

GenCore version 6.2.1
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OM protein - protein search, using sw model

Run on: November 29, 2007, 17:17:13 ; Search time 46 Seconds
(without alignments) 328.583 Million cell updates

Title: US-10-692-299-2

perfect score:

Sequence: 1 MRGATRVSIMLLLVTVSDCA.....CSRFPDGRYRCMDLKNINF 105

Scoring table: BLOSUM62

scoring cadre: BLOS06Z
Gapop 10.0 , Gapext 0.5

Searched: 983262 seqs, 142787483 residues

Total number of hits satisfying chosen parameters: 983262

Minimum DB seq length: 0

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%

POSS-PROCESSING: MINIMUM MATCH 0%
MAXIMUM MATCH 100%

Maximum Match 100%
Listing first 1500 summaries

Database : Issued Patents AA:**

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Database : ISSUED_PATENTS_AA:
1: /EMC Celerra_SIDS2/ptodata/1/iaa/5 COMB.rep:*
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1: /EMC_Celerra_SIDS2/ptodata/1/1aa/5_COMB.pcp:*
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2: /EMC_Celerra_SIDS2/ptodata/1/iaa/6 COMB.pcp:*
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3: /EMC_Celerra_SIDS2/ptodata/1/iaa/H_COMB.pcp:
4: /EMC_Celerra_SIDS2/ptodata/1/iaa/H_COMB.pcp:

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1: /EMC_Celerra_SIDS2/ptodata/1/iaa/COMB.pep:
5: /EMC_Celerra_SIDS2/ptodata/1/iaa/PCTUS COMB.pep:*

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6: /EMC_Celerra_SIDS2/ptodata/1/iaa/RE_COMB.pep:*

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7: /EMC_Celerra_SIDS2/ptodata/1/iaa/backfiles1.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	589	100.0	105	2	US-09-712-529-5	Sequence 5, Appli
2	589	100.0	105	2	US-10-212-201A-5	Sequence 5, Appli
3	589	100.0	105	2	US-10-212-355-5	Sequence 5, Appli
4	589	100.0	105	2	US-09-991-181-371	Sequence 371, App
5	589	100.0	105	2	US-09-990-444-371	Sequence 371, App
6	589	100.0	105	2	US-09-997-333-371	Sequence 371, App
7	589	100.0	105	2	US-09-992-598-371	Sequence 371, App
8	589	100.0	105	2	US-09-989-735-371	Sequence 371, App
9	589	100.0	105	3	US-09-989-726-371	Sequence 371, App
10	589	100.0	105	3	US-09-997-554-371	Sequence 371, App
11	589	100.0	105	3	US-09-989-728-371	Sequence 371, App
12	589	100.0	105	3	US-09-997-349-371	Sequence 371, App
13	589	100.0	105	3	US-09-997-653-371	Sequence 371, App
14	589	100.0	105	3	US-09-989-293A-371	Sequence 371, App
15	589	100.0	105	3	US-09-989-732-371	Sequence 371, App
16	589	100.0	105	3	US-09-990-441-371	Sequence 371, App
17	589	100.0	105	3	US-10-333-192-23	Sequence 23, Appl
18	589	100.0	105	3	US-10-123-292-470	Sequence 470, App
19	589	100.0	105	3	US-10-323-157A-2	Sequence 2, Appli
20	589	100.0	105	3	US-09-989-328-371	Sequence 371, App
21	589	100.0	105	3	US-09-989-724-371	Sequence 371, App
22	589	100.0	105	3	US-09-989-733-371	Sequence 371, App
23	589	100.0	105	3	US-09-993-583-371	Sequence 371, App
24	589	100.0	105	3	US-10-152-398-470	Sequence 470, App
25	589	100.0	105	3	US-09-989-279-371	Sequence 371, App
26	589	100.0	105	3	US-10-123-907-470	Sequence 470, App

100	303	51.4	108	3	US-10-811-328-5	Sequence 5, Appli	173	100.5	17.1	350	2	US-09-905-381A-236	Sequence 236, App
101	303	51.4	108	3	US-10-982-168-2	Sequence 2, Appli	174	100.5	17.1	350	2	US-09-906-618-236	Sequence 236, App
102	303	51.4	108	3	US-10-980-246-2	Sequence 2, Appli	175	100.5	17.1	350	2	US-09-906-646-236	Sequence 236, App
103	303	51.4	108	3	US-10-680-755A-2	Sequence 2, Appli	176	100.5	17.1	350	2	US-09-904-462-236	Sequence 236, App
104	303	51.4	116	3	US-10-680-755A-26	Sequence 26, Appli	177	100.5	17.1	350	2	US-09-902-736A-236	Sequence 236, App
105	298	50.6	107	3	US-10-231-411A-6	Sequence 6, Appli	178	100.5	17.1	350	2	US-09-906-722A-236	Sequence 236, App
106	291	49.4	81	3	US-10-323-157A-6	Sequence 6, Appli	179	100.5	17.1	350	2	US-09-905-449-236	Sequence 236, App
107	291	49.4	81	3	US-10-811-328-6	Sequence 6, Appli	180	100.5	17.1	350	2	US-09-903-562B-236	Sequence 236, App
108	287.5	48.8	96	3	US-10-323-157A-11	Sequence 11, Appli	181	100.5	17.1	350	2	US-09-906-679A-236	Sequence 236, App
109	287.5	48.8	96	3	US-10-811-328-11	Sequence 11, Appli	182	100.5	17.1	350	3	US-09-907-841-236	Sequence 2, Appli
110	286	48.6	81	3	US-10-811-328-29	Sequence 29, Appli	183	100.5	17.1	350	3	US-09-906-838B-236	Sequence 236, App
111	286	48.6	81	3	US-10-811-328-31	Sequence 31, Appli	184	100.5	17.1	350	3	US-09-909-320-236	Sequence 236, App
112	282.5	48.0	129	3	US-10-231-411A-2	Sequence 2, Appli	185	100.5	17.1	350	3	US-10-063-639A-8	Sequence 8, Appli
113	282.5	48.0	129	3	US-10-680-755A-29	Sequence 29, Appli	186	100.5	17.1	350	3	US-10-063-639A-8	Sequence 236, App
114	278.5	47.3	77	3	US-10-811-328-32	Sequence 32, Appli	187	100.5	17.1	350	3	US-09-907-942-236	Sequence 236, App
115	109	18.5	23	3	US-10-680-755A-9	Sequence 9, Appli	188	100.5	17.1	350	3	US-10-063-638A-8	Sequence 8, Appli
116	107.5	18.3	224	2	US-09-161-241-14	Sequence 14, Appli	189	100.5	17.1	350	3	US-10-063-510-8	Sequence 8, Appli
117	107.5	18.3	224	3	US-09-972-473-5	Sequence 5, Appli	190	100.5	17.1	350	3	US-10-223-081-50	Sequence 50, Appli
118	107.5	18.3	350	3	US-09-972-473-38	Sequence 38, Appli	191	100.5	17.1	350	3	US-10-063-741-8	Sequence 8, Appli
119	102	17.3	179	3	US-09-972-473-11	Sequence 11, Appli	192	100.5	17.1	350	3	US-10-063-584-8	Sequence 8, Appli
120	102	17.3	186	2	US-09-949-016-7146	Sequence 7146, Ap	193	100.5	17.1	350	3	US-10-223-087-50	Sequence 50, Appli
121	102	17.3	207	2	US-09-161-241-13	Sequence 13, Appli	194	100.5	17.1	350	3	US-09-903-749A-236	Sequence 236, App
122	102	17.3	259	2	US-09-161-241-12	Sequence 12, Appli	195	100.5	17.1	350	3	US-09-904-532B-236	Sequence 236, App
123	102	17.3	259	2	US-09-949-016-6872	Sequence 6872, Ap	196	100.5	17.1	350	3	US-10-006-867-8	Sequence 8, Appli
124	102	17.3	259	2	US-10-012-231A-70	Sequence 70, Appli	197	100.5	17.1	350	3	US-10-223-082-50	Sequence 50, Appli
125	102	17.3	259	2	US-10-015-389A-70	Sequence 70, Appli	198	100.5	17.1	350	3	US-10-223-084-50	Sequence 50, Appli
126	102	17.3	259	2	US-10-006-768A-70	Sequence 70, Appli	199	100.5	17.1	350	3	US-09-905-075-236	Sequence 236, App
127	102	17.3	259	2	US-10-015-671A-70	Sequence 70, Appli	200	100.5	17.1	350	3	US-10-063-659-8	Sequence 8, Appli
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132	102	17.3	259	2	US-10-015-392A-70	Sequence 70, Appli	205	100.5	17.1	350	3	US-10-063-583-8	Sequence 8, Appli
133	102	17.3	259	3	US-10-011-795B-70	Sequence 70, Appli	206	100.5	17.1	350	3	US-10-063-593-8	Sequence 8, Appli
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135	102	17.3	259	3	US-10-012-121A-70	Sequence 70, Appli	208	100.5	17.1	350	3	US-10-063-660-8	Sequence 8, Appli
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139	102	17.3	259	3	US-10-017-253A-70	Sequence 70, Appli	212	100.5	17.1	350	3	US-10-063-530-8	Sequence 8, Appli
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142	102	17.3	259	3	US-10-007-236A-70	Sequence 70, Appli	215	100.5	17.1	350	3	US-10-063-657-8	Sequence 8, Appli
143	102	17.3	259	3	US-10-012-149A-70	Sequence 70, Appli	216	100.5	17.1	350	3	US-10-063-702-8	Sequence 8, Appli
144	102	17.3	259	3	US-10-007-194A-70	Sequence 70, Appli	217	100.5	17.1	350	3	US-10-063-529-8	Sequence 8, Appli
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146	102	17.3	259	3	US-10-006-117A-70	Sequence 70, Appli	219	100.5	17.1	350	3	US-10-063-585-8	Sequence 8, Appli
147	102	17.3	259	3	US-10-015-480A-70	Sequence 70, Appli	220	100.5	17.1	350	3	US-10-063-591A-8	Sequence 8, Appli
148	102	17.3	259	3	US-10-006-172A-70	Sequence 70, Appli	221	100.5	17.1	350	3	US-10-063-516-8	Sequence 8, Appli
149	102	17.3	259	3	US-10-015-395A-70	Sequence 70, Appli	222	100.5	17.1	350	3	US-10-063-532-8	Sequence 8, Appli
150	102	17.3	259	3	US-10-183-001-250	Sequence 250, App	223	100.5	17.1	350	3	US-10-063-654-8	Sequence 8, Appli
151	102	17.3	259	3	US-10-015-610A-70	Sequence 70, Appli	224	100.5	17.1	350	3	US-10-063-582-8	Sequence 8, Appli
152	102	17.3	259	3	US-10-180-998-250	Sequence 250, App	225	100.5	17.1	350	3	US-10-063-524-8	Sequence 8, Appli
153	102	17.3	259	3	US-10-201-769-250	Sequence 250, App	226	100.5	17.1	350	3	US-09-903-640A-236	Sequence 236, App
154	102	17.3	259	3	US-10-006-130A-70	Sequence 70, Appli	227	100.5	17.1	350	3	US-10-448-580-236	Sequence 236, App
155	102	17.3	259	3	US-10-174-576-250	Sequence 250, App	228	100.5	17.1	350	3	US-10-972-317-8	Sequence 8, Appli
156	102	17.3	259	3	US-10-174-581-250	Sequence 250, App	229	100.5	17.1	350	3	US-10-063-551-8	Sequence 8, Appli
157	102	17.3	259	3	US-10-015-869A-70	Sequence 70, Appli	230	100.5	17.1	350	3	US-10-063-551-8	Sequence 8, Appli
158	102	17.3	259	3	US-10-207-916-250	Sequence 250, App	231	100.5	17.1	350	3	US-10-063-650-8	Sequence 8, Appli
159	102	17.3	259	3	US-10-174-583-250	Sequence 250, App	232	100.5	17.1	350	3	US-10-063-523-8	Sequence 8, Appli
160	102	17.3	259	3	US-10-187-745-250	Sequence 250, App	233	100.5	17.1	350	3	US-10-063-582A-8	Sequence 8, Appli
161	102	17.3	263	3	US-09-972-473-21	Sequence 21, Appli	234	100.5	17.1	350	3	US-10-063-705-8	Sequence 8, Appli
162	101	17.1	272	2	US-09-161-241-11	Sequence 11, Appli	235	100.5	17.1	350	3	US-10-963-467-236	Sequence 236, App
163	101	17.1	272	3	US-09-972-473-36	Sequence 36, Appli	236	100.5	17.1	350	3	US-10-063-598-8	Sequence 8, Appli
164	100.5	17.1	215	2	US-10-104-047-2196	Sequence 2196, Ap	237	100.5	17.1	350	3	US-10-063-554-8	Sequence 8, Appli
165	100.5	17.1	350	2	US-09-161-241-9	Sequence 9, Appli	238	100.5	17.1	350	3	US-10-063-597-8	Sequence 8, Appli
166	100.5	17.1	350	2	US-09-907-794A-236	Sequence 236, App	239	100.5	17.1	350	3	US-10-063-600-8	Sequence 8, Appli
167	100.5	17.1	350	2	US-09-905-125A-236	Sequence 236, App	240	100.5	17.1	350	3	US-10-063-652A-8	Sequence 8, Appli
168	100.5	17.1	350	2	US-09-902-775A-236	Sequence 236, App	241	100.5	17.1	350	3	US-10-063-602-8	Sequence 8, Appli
169	100.5	17.1	350	2	US-09-906-700-236	Sequence 236, App	242	100.5	17.1	350	3	US-10-063-560-8	Sequence 8, Appli
170	100.5	17.1	350	2	US-09-903-603A-236	Sequence 236, App	243	100.5	17.1	350	3	US-10-063-517-8	Sequence 8, Appli
171	100.5	17.1	350	2	US-09-904-920A-236	Sequence 236, App	244	100.5	17.1	350	3	US-10-063-548-8	Sequence 8, Appli
172	100.5	17.1	350	2	US-09-909-064-236	Sequence 236, App	245	100.5	17.1	350	3	US-10-063-548-8	Sequence 8, Appli

246	100.5	17.1	350	3	US-10-063-553-8	Sequence 8, Appli	319	79	13.4	124	2	US-09-949-016-11293	Sequence 11293, A
247	100.5	17.1	350	3	US-10-063-653A-8	Sequence 8, Appli	320	79	13.4	1664	3	US-10-055-877-212	Sequence 212, App
248	100.5	17.1	350	3	US-10-448-923-236	Sequence 236, App	321	78.5	13.3	163	1	US-08-219-237B-5	Sequence 5, Appli
249	100.5	17.1	350	3	US-10-063-595-8	Sequence 8, Appli	322	78.5	13.3	163	2	US-08-477-347-13	Sequence 13, Appli
250	100.5	17.1	350	3	US-10-063-587-8	Sequence 8, Appli	323	78.5	13.3	163	2	US-08-476-862-4	Sequence 4, Appli
251	100.5	17.1	350	3	US-10-063-586-8	Sequence 8, Appli	324	78.5	13.3	163	2	US-08-468-560C-5	Sequence 5, Appli
252	100.5	17.1	350	3	US-10-223-090-50	Sequence 50, Appli	325	78.5	13.3	163	2	US-08-800-909-4	Sequence 4, Appli
253	100.5	17.1	375	2	US-09-949-016-7856	Sequence 7856, Ap	326	78.5	13.3	163	2	US-09-800-908-13	Sequence 13, Appli
254	100.5	17.1	375	2	US-09-949-016-7857	Sequence 7857, Ap	327	78.5	13.3	163	2	US-09-884-987-5	Sequence 5, Appli
255	100.5	17.1	375	2	US-09-949-016-7858	Sequence 7858, Ap	328	77	13.1	145	3	US-10-703-032-196520	Sequence 196520,
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257	98.5	16.7	349	2	US-09-972-473-17	Sequence 17, Appli	330	76	12.9	14	3	US-10-811-328-19	Sequence 19, Appli
258	97	16.5	266	2	US-09-161-241-10	Sequence 10, Appli	331	75.5	12.8	1101	2	US-09-561-709B-5	Sequence 5, Appli
259	97	16.5	266	2	US-09-976-594-1086	Sequence 1086, Ap	332	75.5	12.8	1574	3	US-10-055-877-211	Sequence 211, App
260	97	16.5	266	2	US-09-999-833A-456	Sequence 456, App	333	75.5	12.8	1761	2	US-09-561-709B-1	Sequence 1, Appli
261	97	16.5	266	2	US-10-020-445A-456	Sequence 456, App	334	75	12.7	546	2	US-09-949-016-10394	Sequence 10394, A
262	97	16.5	266	2	US-09-978-189-456	Sequence 456, App	335	75	12.7	651	1	US-08-264-101-2	Sequence 2, Appli
263	97	16.5	266	2	US-10-017-085A-456	Sequence 456, App	336	75	12.7	651	1	US-08-765-243-2	Sequence 2, Appli
264	97	16.5	266	3	US-10-145-129A-456	Sequence 456, App	337	75	12.7	651	5	PCT-US95-07295-2	Sequence 2, Appli
265	97	16.5	266	3	US-10-013-929A-456	Sequence 456, App	338	75	12.7	734	1	US-08-765-243-8	Sequence 8, Appli
266	97	16.5	266	3	US-10-013-917A-456	Sequence 456, App	339	75	12.7	734	5	PCT-US95-07295-8	Sequence 8, Appli
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268	97	16.5	266	3	US-10-123-292-428	Sequence 428, App	341	75	12.7	3075	1	US-08-460-309-5	Sequence 5, Appli
269	97	16.5	266	3	US-09-972-473-8	Sequence 8, Appli	342	75	12.7	3075	1	US-08-125-077-5	Sequence 5, Appli
270	97	16.5	266	3	US-10-162-521A-456	Sequence 456, App	343	74.5	12.6	451	2	US-10-915-160-6	Sequence 6, Appli
271	97	16.5	266	3	US-10-145-016A-456	Sequence 456, App	344	74	12.6	1620	3	US-10-055-877-213	Sequence 213, App
272	97	16.5	266	3	US-10-013-926A-456	Sequence 456, App	345	73	12.4	87	3	US-09-972-473-25	Sequence 25, Appli
273	97	16.5	266	3	US-10-152-398-428	Sequence 428, App	346	73	12.4	163	2	US-08-828-683A-13	Sequence 13, Appli
274	97	16.5	266	3	US-10-162-522A-456	Sequence 456, App	347	73	12.4	163	2	US-09-523-323-54	Sequence 54, Appli
275	97	16.5	266	3	US-10-123-907-428	Sequence 428, App	348	73	12.4	164	1	US-08-232-087A-9	Sequence 9, Appli
276	97	16.5	266	3	US-10-147-512-428	Sequence 428, App	349	73	12.4	189	2	US-09-422-680A-25	Sequence 25, Appli
277	97	16.5	266	3	US-10-147-485-428	Sequence 428, App	350	73	12.4	227	2	US-08-974-022-48	Sequence 48, Appli
278	97	16.5	266	3	US-10-124-814-428	Sequence 428, App	351	73	12.4	227	2	US-08-795-445A-48	Sequence 48, Appli
279	97	16.5	266	3	US-10-143-029A-456	Sequence 456, App	352	73	12.4	227	2	US-08-795-447A-48	Sequence 48, Appli
280	97	16.5	266	3	US-10-124-822-428	Sequence 428, App	353	73	12.4	227	2	US-08-974-186-48	Sequence 48, Appli
281	97	16.5	266	3	US-10-165-247A-456	Sequence 456, App	354	73	12.4	227	2	US-08-795-446B-48	Sequence 48, Appli
282	97	16.5	266	3	US-10-017-086A-456	Sequence 456, App	355	73	12.4	227	2	US-08-706-945D-134	Sequence 134, App
283	97	16.5	266	3	US-09-999-833A-456	Sequence 456, App	356	73	12.4	227	3	US-08-577-788C-48	Sequence 48, Appli
284	97	16.5	266	3	US-10-131-833A-428	Sequence 428, App	357	73	12.4	227	3	US-09-613-591F-131	Sequence 131, App
285	97	16.5	266	3	US-10-142-419-428	Sequence 428, App	358	73	12.4	235	2	US-09-326-394-4	Sequence 4, Appli
286	97	16.5	266	3	US-10-152-375-428	Sequence 428, App	359	73	12.4	235	2	US-09-580-235-2	Sequence 2, Appli
287	97	16.5	266	3	US-10-143-031A-456	Sequence 456, App	360	73	12.4	235	2	US-09-580-235-4	Sequence 4, Appli
288	97	16.5	266	3	US-10-131-818A-428	Sequence 428, App	361	73	12.4	235	2	US-09-580-235-6	Sequence 6, Appli
289	97	16.5	266	3	US-10-013-923A-456	Sequence 456, App	362	73	12.4	235	2	US-09-580-235-8	Sequence 8, Appli
290	97	16.5	266	3	US-10-013-927A-456	Sequence 456, App	363	73	12.4	235	2	US-09-580-181-2	Sequence 2, Appli
291	97	16.5	266	3	US-10-145-873-428	Sequence 428, App	364	73	12.4	235	2	US-09-580-181-4	Sequence 4, Appli
292	97	16.5	266	3	US-10-152-395-428	Sequence 428, App	365	73	12.4	235	2	US-09-580-181-6	Sequence 6, Appli
293	97	16.5	266	3	US-10-131-822A-428	Sequence 428, App	366	73	12.4	235	2	US-09-580-181-8	Sequence 8, Appli
294	97	16.5	266	3	US-10-142-763-428	Sequence 428, App	367	73	12.4	235	2	US-09-102-530-2	Sequence 2, Appli
295	97	16.5	266	3	US-10-128-694A-428	Sequence 428, App	368	73	12.4	235	2	US-09-102-530-4	Sequence 4, Appli
296	97	16.5	266	3	US-10-123-213-428	Sequence 428, App	369	73	12.4	235	2	US-09-102-530-6	Sequence 6, Appli
297	97	16.5	266	3	US-10-123-909-428	Sequence 428, App	370	73	12.4	235	2	US-09-102-530-8	Sequence 8, Appli
298	97	16.5	266	3	US-10-145-087A-456	Sequence 456, App	371	73	12.4	235	2	US-09-882-735A-16	Sequence 16, Appli
299	97	16.5	266	3	US-09-978-564A-456	Sequence 456, App	372	73	12.4	235	3	US-10-243-230-2	Sequence 2, Appli
300	97	16.5	266	3	US-09-978-375A-456	Sequence 456, App	373	73	12.4	235	3	US-10-243-230-4	Sequence 4, Appli
301	97	16.5	266	3	US-10-165-353A-456	Sequence 456, App	374	73	12.4	235	3	US-10-243-230-6	Sequence 6, Appli
302	97	16.5	266	3	US-10-143-030A-456	Sequence 456, App	375	73	12.4	235	3	US-10-243-230-8	Sequence 8, Appli
303	97	16.5	266	3	US-10-131-826A-428	Sequence 428, App	376	73	12.4	257	2	US-09-579-845-10	Sequence 10, Appli
304	97	16.5	266	3	US-10-145-089A-456	Sequence 456, App	377	73	12.4	439	2	US-10-360-101-226	Sequence 226, App
305	97	16.5	266	3	US-10-170-481A-456	Sequence 456, App	378	73	12.4	461	1	US-08-385-229-2	Sequence 2, Appli
306	97	16.5	266	3	US-10-147-513-428	Sequence 428, App	379	73	12.4	461	1	US-08-650-000-2	Sequence 2, Appli
307	97	16.5	266	3	US-10-121-043-428	Sequence 428, App	380	73	12.4	461	2	US-09-042-785A-7	Sequence 7, Appli
308	97	16.5	266	3	US-10-160-502A-456	Sequence 456, App	381	73	12.4	461	2	US-08-477-347-3	Sequence 3, Appli
309	97	16.5	266	3	US-10-139-980-428	Sequence 428, App	382	73	12.4	461	2	US-09-006-353A-4	Sequence 4, Appli
310	95.5	16.2	259	3	US-09-972-473-37	Sequence 37, Appli	383	73	12.4	461	2	US-08-476-862-2	Sequence 2, Appli
311	91	15.4	19	3	US-10-323-157A-9	Sequence 9, Appli	384	73	12.4	461	2	US-09-573-986-4	Sequence 4, Appli
312	91	15.4	19	3	US-10-811-328-9	Sequence 9, Appli	385	73	12.4	461	2	US-08-406-824A-2	Sequence 2, Appli
313	83.5	14.2	508	2	US-10-915-160-2	Sequence 2, Appli	386	73	12.4	461	2	US-09-800-909-2	Sequence 2, Appli
314	82	13.9	1342	2	US-09-561-709B-13	Sequence 13, Appli	387	73	12.4	461	2	US-09-758-124-2	Sequence 2, Appli
315	81.5	13.8	425	3	US-10-108-260A-4381	Sequence 4381, Ap	388	73	12.4	461	2	US-09-800-908-3	Sequence 3, Appli
316	81.5	13.8	446	2	US-10-104-047-2665	Sequence 2665, Ap	389	73	12.4	461	2	US-09-896-096A-17	Sequence 17, Appli
317	81	13.8	1964	2	US-09-467-997-1	Sequence 1, Appli	390	73	12.4	461	2	US-09-949-016-6019	Sequence 6019, Ap
318	79.5	13.5	446	3	US-10-108-260A-3580	Sequence 3580, Ap	391	73	12.4	461	2	US-10-046-433-6	Sequence 6, Appli

538	67.5	11.5	69	2	US-09-894-882-232	Sequence 232, App	611	65.5	11.1	182	2	US-10-104-047-3287	Sequence 3287, App
539	67.5	11.5	311	3	US-10-703-032-122198	Sequence 122198,	612	65.5	11.1	269	2	US-10-012-231A-372	Sequence 372, App
540	67.5	11.5	1480	2	US-09-191-647-7	Sequence 7, Appli	613	65.5	11.1	269	2	US-10-015-389A-372	Sequence 372, App
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542	67.5	11.5	1480	2	US-09-540-153-7	Sequence 7, Appli	615	65.5	11.1	269	2	US-10-015-671A-372	Sequence 372, App
543	67.5	11.5	1480	2	US-09-182-024A-5	Sequence 5, Appli	616	65.5	11.1	269	2	US-10-015-393A-372	Sequence 372, App
544	67.5	11.5	1480	2	US-10-289-776-7	Sequence 7, Appli	617	65.5	11.1	269	2	US-10-011-833A-372	Sequence 372, App
545	67.5	11.5	1480	5	PCT-US91-09055-2	Sequence 2, Appli	618	65.5	11.1	269	2	US-10-006-041A-372	Sequence 372, App
546	67.5	11.5	1504	2	US-10-037-417-98	Sequence 98, Appli	619	65.5	11.1	269	2	US-10-012-064A-372	Sequence 372, App
547	67	11.4	98	3	US-10-703-032-115297	Sequence 115297,	620	65.5	11.1	269	2	US-10-015-392A-372	Sequence 372, App
548	67	11.4	116	3	US-10-703-032-156175	Sequence 156175,	621	65.5	11.1	269	3	US-10-011-795B-372	Sequence 372, App
549	67	11.4	1172	1	US-08-313-288B-19	Sequence 19, Appl	622	65.5	11.1	269	3	US-10-015-388A-372	Sequence 372, App
550	67	11.4	1172	2	US-09-949-015-6333	Sequence 6333, Ap	623	65.5	11.1	269	3	US-10-012-121A-372	Sequence 372, App
551	67	11.4	1172	3	US-10-296-733A-26	Sequence 26, Appl	624	65.5	11.1	269	3	US-10-006-485A-372	Sequence 372, App
552	67	11.4	1193	1	US-08-400-159-10	Sequence 10, Appl	625	65.5	11.1	269	3	US-10-006-746A-372	Sequence 372, App
553	67	11.4	1193	2	US-08-611-729A-10	Sequence 10, Appl	626	65.5	11.1	269	3	US-10-012-752A-372	Sequence 372, App
554	67	11.4	1193	2	US-09-195-524-10	Sequence 10, Appl	627	65.5	11.1	269	3	US-10-017-253A-372	Sequence 372, App
555	67	11.4	1193	2	US-09-310-685-8	Sequence 8, Appli	628	65.5	11.1	269	3	US-10-015-519A-372	Sequence 372, App
556	67	11.4	1219	2	US-08-882-046-5	Sequence 5, Appli	629	65.5	11.1	269	3	US-10-015-715A-372	Sequence 372, App
557	67	11.4	1219	2	US-09-566-047-5	Sequence 5, Appli	630	65.5	11.1	269	3	US-10-007-236A-372	Sequence 372, App
558	67	11.4	1450	3	US-10-055-877-48	Sequence 48, Appl	631	65.5	11.1	269	3	US-10-012-149A-372	Sequence 372, App
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560	67	11.4	2321	2	US-09-612-226B-2	Sequence 2, Appli	633	65.5	11.1	269	3	US-10-123-292-532	Sequence 532, App
561	67	11.4	2321	3	US-10-356-625-2	Sequence 2, Appli	634	65.5	11.1	269	3	US-10-013-910A-372	Sequence 372, App
562	67	11.4	3597	2	US-10-037-417-6	Sequence 6, Appli	635	65.5	11.1	269	3	US-10-006-117A-372	Sequence 372, App
563	67	11.4	3600	2	US-10-037-417-2	Sequence 2, Appli	636	65.5	11.1	269	3	US-10-152-398-532	Sequence 532, App
564	66.5	11.3	70	2	US-09-894-882-233	Sequence 253, App	637	65.5	11.1	269	3	US-10-015-480A-372	Sequence 372, App
565	66.5	11.3	70	2	US-09-894-882-262	Sequence 262, App	638	65.5	11.1	269	3	US-10-006-172A-372	Sequence 372, App
566	66.5	11.3	589	1	US-07-668-648-2	Sequence 2, Appli	639	65.5	11.1	269	3	US-10-015-395A-372	Sequence 372, App
567	66.5	11.3	589	1	US-07-668-648-6	Sequence 6, Appli	640	65.5	11.1	269	3	US-10-123-907-532	Sequence 532, App
568	66.5	11.3	589	1	US-08-429-998-6	Sequence 2, Appli	641	65.5	11.1	269	3	US-10-015-610A-372	Sequence 372, App
569	66.5	11.3	589	1	US-08-429-998-6	Sequence 6, Appli	642	65.5	11.1	269	3	US-10-147-485-532	Sequence 532, App
570	66.5	11.3	589	1	US-08-431-333-2	Sequence 2, Appli	643	65.5	11.1	269	3	US-10-147-485-532	Sequence 532, App
571	66.5	11.3	589	1	US-08-431-333-6	Sequence 6, Appli	644	65.5	11.1	269	3	US-10-006-130A-372	Sequence 372, App
572	66.5	11.3	589	2	US-08-991-862-2	Sequence 2, Appli	645	65.5	11.1	269	3	US-10-124-814-532	Sequence 532, App
573	66.5	11.3	589	2	US-09-813-156-2	Sequence 2, Appli	646	65.5	11.1	269	3	US-10-124-822-532	Sequence 532, App
574	66.5	11.3	589	2	US-09-456-886-2	Sequence 2, Appli	647	65.5	11.1	269	3	US-10-223-081-254	Sequence 254, App
575	66.5	11.3	589	2	US-09-824-647-2	Sequence 2, Appli	648	65.5	11.1	269	3	US-10-223-087-254	Sequence 254, App
576	66.5	11.3	589	2	US-09-880-842-2	Sequence 2, Appli	649	65.5	11.1	269	3	US-10-131-833A-532	Sequence 532, App
577	66.5	11.3	589	3	US-10-281-160-2	Sequence 2, Appli	650	65.5	11.1	269	3	US-10-142-419-532	Sequence 532, App
578	66.5	11.3	589	5	PCT-US91-02321-2	Sequence 2, Appli	651	65.5	11.1	269	3	US-10-152-375-532	Sequence 532, App
579	66.5	11.3	589	5	PCT-US91-02321-6	Sequence 6, Appli	652	65.5	11.1	269	3	US-10-213-044-10	Sequence 10, Appl
580	66.5	11.3	5179	2	US-10-042-865-108	Sequence 108, App	653	65.5	11.1	269	3	US-10-223-082-254	Sequence 254, App
581	66.5	11.3	714	3	US-09-538-092-1258	Sequence 1258, Ap	654	65.5	11.1	269	3	US-10-223-084-254	Sequence 254, App
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584	66	11.2	70	2	US-09-894-882-256	Sequence 353, App	657	65.5	11.1	269	3	US-10-145-873-532	Sequence 532, App
585	66	11.2	158	2	US-09-832-129-39	Sequence 39, Appl	658	65.5	11.1	269	3	US-10-152-395-532	Sequence 532, App
586	66	11.2	1055	2	US-09-214-278-2	Sequence 2, Appli	659	65.5	11.1	269	3	US-10-131-822A-532	Sequence 532, App
587	66	11.2	1055	2	US-09-855-723-2	Sequence 2, Appli	660	65.5	11.1	269	3	US-10-142-763-532	Sequence 532, App
588	66	11.2	1055	3	US-10-219-248-2	Sequence 2, Appli	661	65.5	11.1	269	3	US-10-128-694A-532	Sequence 532, App
589	66	11.2	1065	1	US-08-400-159-8	Sequence 8, Appli	662	65.5	11.1	269	3	US-10-123-213-532	Sequence 532, App
590	66	11.2	1140	3	US-10-055-877-215	Sequence 215, App	663	65.5	11.1	269	3	US-10-123-909-532	Sequence 532, App
591	66	11.2	1148	2	US-08-882-046-4	Sequence 4, Appli	664	65.5	11.1	269	3	US-10-131-826A-532	Sequence 532, App
592	66	11.2	1148	2	US-09-566-047-4	Sequence 4, Appli	665	65.5	11.1	269	3	US-10-147-513-532	Sequence 532, App
593	66	11.2	1212	2	US-09-214-278-3	Sequence 3, Appli	666	65.5	11.1	269	3	US-10-121-043-532	Sequence 532, App
594	66	11.2	1212	2	US-09-855-723-3	Sequence 3, Appli	667	65.5	11.1	269	3	US-10-139-980-532	Sequence 532, App
595	66	11.2	1212	3	US-10-219-248-3	Sequence 3, Appli	668	65.5	11.1	269	3	US-10-223-090-254	Sequence 254, App
596	66	11.2	1238	2	US-09-214-278-5	Sequence 5, Appli	669	65.5	11.1	299	2	US-09-188-930-192	Sequence 192, App
597	66	11.2	1238	3	US-09-855-722-5	Sequence 5, Appli	670	65.5	11.1	299	2	US-09-188-930-332	Sequence 332, App
598	66	11.2	1238	3	US-10-219-248-5	Sequence 5, Appli	671	65.5	11.1	299	2	US-09-312-283C-192	Sequence 332, App
599	66	11.2	1257	2	US-08-611-729A-8	Sequence 8, Appli	672	65.5	11.1	299	2	US-09-312-283C-332	Sequence 332, App
600	66	11.2	1257	2	US-09-195-524-8	Sequence 8, Appli	673	65.5	11.1	683	2	US-08-979-847B-198	Sequence 198, App
601	66	11.2	1257	2	US-09-310-685-6	Sequence 6, Appli	674	65.5	11.1	683	2	US-08-979-847B-208	Sequence 208, App
602	65.5	11.1	94	3	US-10-976-102-47	Sequence 47, Appl	675	65.5	11.1	683	2	US-08-979-847B-210	Sequence 210, App
603	65.5	11.1	99	3	US-10-846-374B-192	Sequence 192, App	676	65.5	11.1	720	2	US-08-872-855-4	Sequence 4, Appli
604	65.5	11.1	144	3	US-10-703-032-128595	Sequence 128595,	677	65.5	11.1	722	2	US-08-981-392-12	Sequence 12, Appl
605	65.5	11.1	144	3	US-10-703-032-128595	Sequence 128595,	678	65.5	11.1	722	2	US-09-908-322-12	Sequence 12, Appl
606	65.5	11.1	166	3	US-10-703-032-117513	Sequence 117513,	679	65.5	11.1	722	2	US-09-310-685-14	Sequence 14, Appl
607	65.5	11.1	178	3	US-10-703-032-132027	Sequence 132027,	680	65.5	11.1	722	3	US-09-783-931C-12	Sequence 12, Appl
608	65.5	11.1	179	2	US-09-148-545-177	Sequence 177, App	681	65.5	11.1	722	3	US-10-042-865-107	Sequence 107, App
609	65.5	11.1	179	2	US-09-621-011-177	Sequence 177, App	682	65.5	11.1	768	2	US-08-979-847B-89	Sequence 89, Appl
610	65.5	11.1	179	3	US-09-981-876-177	Sequence 177, App	683	65.5	11.1				

684	65.5	11.1	925	3	US-10-865-978A-25	Sequence 25, Appl	757	64.5	11.0	2214	2	US-09-919-039-40	Sequence 40, Appl
685	65.5	11.1	1068	1	US-08-537-210A-2	Sequence 2, Appl	758	64.5	11.0	2743	2	US-10-037-182-36	Sequence 36, Appl
686	65.5	11.1	1068	2	US-09-113-825-2	Sequence 2, Appl	759	64.5	11.0	3695	2	US-10-037-182-2	Sequence 2, Appl
687	65.5	11.1	2213	1	US-08-727-034-3	Sequence 3, Appl	760	64	10.9	159	1	US-08-232-087A-11	Sequence 11, Appl
688	65.5	11.1	2471	1	US-08-185-432-16	Sequence 16, Appl	761	64	10.9	207	2	US-08-974-022-47	Sequence 47, Appl
689	65.5	11.1	2471	1	US-08-083-590A-19	Sequence 19, Appl	762	64	10.9	207	2	US-08-795-445A-47	Sequence 47, Appl
690	65.5	11.1	2471	1	US-08-532-384-19	Sequence 19, Appl	763	64	10.9	207	2	US-08-795-447A-47	Sequence 47, Appl
691	65.5	11.1	2471	2	US-08-899-232-1	Sequence 1, Appl	764	64	10.9	207	2	US-08-974-186-47	Sequence 47, Appl
692	65.5	11.1	2471	2	US-09-121-457-1	Sequence 1, Appl	765	64	10.9	207	2	US-08-795-446B-47	Sequence 47, Appl
693	65.5	11.1	2556	1	US-08-185-432-17	Sequence 17, Appl	766	64	10.9	207	2	US-08-706-945D-133	Sequence 133, Appl
694	65.5	11.1	2556	1	US-08-083-590A-20	Sequence 20, Appl	767	64	10.9	207	2	US-08-577-788C-47	Sequence 47, Appl
695	65.5	11.1	2556	2	US-08-532-384-20	Sequence 20, Appl	768	64	10.9	207	2	Sequence 130, Appl	Sequence 130, Appl
696	65.5	11.1	2556	2	US-08-899-232-2	Sequence 2, Appl	769	64	10.9	235	2	Sequence 15031, A	Sequence 15031, A
697	65.5	11.1	2556	2	US-09-121-457-2	Sequence 2, Appl	770	64	10.9	325	1	Sequence 2, Appl	Sequence 2, Appl
698	65.5	11.1	3635	2	US-09-845-583A-2	Sequence 2, Appl	771	64	10.9	325	1	Sequence 9, Appl	Sequence 9, Appl
699	65.5	11.1	3635	2	US-10-037-417-47	Sequence 47, Appl	772	64	10.9	325	5	PCT-US91-02207-2	Sequence 2, Appl
700	65.5	11.1	3635	2	US-10-037-182-4	Sequence 4, Appl	773	64	10.9	335	2	US-09-252-991A-32163	Sequence 32163, A
701	65	11.0	77	2	US-08-866-545-2	Sequence 2, Appl	774	64	10.9	340	2	US-09-748-537-14	Sequence 14, Appl
702	65	11.0	77	2	US-09-627-775-2	Sequence 2, Appl	775	64	10.9	425	2	US-09-605-042A-41	Sequence 41, Appl
703	65	11.0	142	2	US-10-094-749-1973	Sequence 1973, Ap	776	64	10.9	459	2	US-09-949-016-10099	Sequence 10099, A
704	65	11.0	236	2	US-09-252-991A-25980	Sequence 25980, A	777	64	10.9	1282	2	US-09-627-650B-1	Sequence 1, Appl
705	65	11.0	383	1	US-08-597-545-2	Sequence 2, Appl	778	64	10.9	1652	2	US-09-436-063C-1	Sequence 1, Appl
706	65	11.0	383	1	US-08-457-135-2	Sequence 2, Appl	779	64	10.9	1652	2	US-10-156-240-1	Sequence 1, Appl
707	65	11.0	383	1	US-09-482-273-159	Sequence 159, App	780	64	10.9	1917	2	US-09-627-650B-5	Sequence 5, Appl
708	65	11.0	575	2	US-10-103-295-160	Sequence 160, App	781	64	10.9	1917	2	US-09-436-063C-5	Sequence 5, Appl
709	65	11.0	638	2	US-09-482-273-245	Sequence 245, App	782	64	10.9	1917	2	US-10-156-240-5	Sequence 5, Appl
710	65	11.0	638	3	US-10-103-295-248	Sequence 248, App	783	64	10.9	1917	2	US-09-627-650B-7	Sequence 7, Appl
711	65	11.0	993	1	US-08-348-143-1	Sequence 1, Appl	784	64	10.9	2508	2	US-09-436-063C-7	Sequence 7, Appl
712	65	11.0	993	1	US-08-571-785-1	Sequence 1, Appl	785	64	10.9	2508	3	US-10-156-240-7	Sequence 7, Appl
713	65	11.0	993	1	US-09-192-435-1	Sequence 1, Appl	786	64	10.9	2544	2	US-09-627-650B-3	Sequence 3, Appl
714	65	11.0	993	2	US-09-558-340-1	Sequence 1, Appl	787	64	10.9	2544	2	US-09-436-063C-3	Sequence 3, Appl
715	65	11.0	1010	2	US-08-882-046-7	Sequence 7, Appl	788	64	10.9	2544	3	US-10-156-240-3	Sequence 3, Appl
716	65	11.0	1010	2	US-09-566-047-7	Sequence 7, Appl	789	64	10.9	2544	3	US-09-627-650B-9	Sequence 9, Appl
717	65	11.0	1036	2	US-09-068-740A-6	Sequence 6, Appl	790	64	10.9	2601	2	US-09-436-063C-9	Sequence 9, Appl
718	65	11.0	1036	3	US-09-995-593A-6	Sequence 6, Appl	791	64	10.9	2601	3	US-10-156-240-9	Sequence 9, Appl
719	65	11.0	1036	3	US-11-043-357-6	Sequence 6, Appl	792	64	10.9	2601	3	US-10-002-344A-257	Sequence 257, App
720	65	11.0	1036	3	US-11-051-631-6	Sequence 6, Appl	793	63.5	10.8	121	2	US-10-002-344A-257	Sequence 257, App
721	65	11.0	1067	2	US-09-579-536C-18	Sequence 18, Appl	794	63.5	10.8	163	2	US-09-252-991A-29129	Sequence 29129, A
722	65	11.0	1187	2	US-09-068-740A-7	Sequence 7, Appl	795	63.5	10.8	194	2	US-09-252-991A-32646	Sequence 32646, A
723	65	11.0	1187	3	US-09-995-593A-7	Sequence 7, Appl	796	63.5	10.8	606	2	US-09-460-295B-12	Sequence 12, Appl
724	65	11.0	1187	3	US-11-043-357-7	Sequence 7, Appl	797	63.5	10.8	606	2	US-09-460-295B-12	Sequence 12, Appl
725	65	11.0	1187	3	US-11-051-631-7	Sequence 7, Appl	798	63.5	10.8	713	2	US-08-872-855-5	Sequence 5, Appl
726	65	11.0	1208	2	US-09-199-865-1	Sequence 1, Appl	799	63.5	10.8	721	2	US-08-981-392-5	Sequence 5, Appl
727	65	11.0	1208	2	US-10-213-329-1	Sequence 1, Appl	800	63.5	10.8	721	2	US-09-908-322-5	Sequence 5, Appl
728	65	11.0	1218	1	US-08-400-159-6	Sequence 6, Appl	801	63.5	10.8	721	2	US-09-908-322-5	Sequence 5, Appl
729	65	11.0	1218	2	US-08-882-046-2	Sequence 2, Appl	802	63.5	10.8	721	2	US-09-310-685-12	Sequence 12, Appl
730	65	11.0	1218	2	US-08-611-729A-6	Sequence 6, Appl	803	63.5	10.8	721	3	US-09-783-931C-5	Sequence 5, Appl
731	65	11.0	1218	2	US-09-214-278-7	Sequence 7, Appl	804	63.5	10.8	721	3	US-10-042-865-109	Sequence 109, App
732	65	11.0	1218	2	US-09-068-740A-11	Sequence 11, Appl	805	63.5	10.8	1128	2	US-10-042-865-109	Sequence 11, Appl
733	65	11.0	1218	2	US-09-855-722-7	Sequence 7, Appl	806	63.5	10.8	1128	2	US-09-436-063C-11	Sequence 11, Appl
734	65	11.0	1218	2	US-09-566-047-2	Sequence 2, Appl	807	63.5	10.8	1128	2	US-10-156-240-11	Sequence 11, Appl
735	65	11.0	1218	2	US-09-917-254-85	Sequence 85, Appl	808	63.5	10.8	3647	2	US-09-949-016-10932	Sequence 10932, A
736	65	11.0	1218	2	US-09-195-524-6	Sequence 6, Appl	809	63	10.7	70	2	US-09-894-882-350	Sequence 350, App
737	65	11.0	1218	2	US-09-579-536C-1	Sequence 1, Appl	810	63	10.7	100	2	US-09-894-882-350	Sequence 40, Appl
738	65	11.0	1218	2	US-09-949-016-5902	Sequence 5902, Ap	811	63	10.7	100	3	US-10-976-102-40	Sequence 40, Appl
739	65	11.0	1218	2	US-09-310-685-4	Sequence 4, Appl	812	63	10.7	129	2	US-10-104-047-2669	Sequence 2669, Ap
740	65	11.0	1218	3	US-10-219-248-7	Sequence 7, Appl	813	63	10.7	222	3	US-10-104-047-2669	Sequence 111480,
741	65	11.0	1218	3	US-09-995-593A-11	Sequence 11, Appl	814	63	10.7	258	2	US-09-578-845-7	Sequence 7, Appl
742	65	11.0	1218	3	US-11-043-357-11	Sequence 11, Appl	815	63	10.7	298	2	US-09-902-540-12595	Sequence 12595, A
743	65	11.0	1218	3	US-11-051-631-11	Sequence 11, Appl	816	63	10.7	487	2	US-09-578-845-14	Sequence 14, Appl
744	65	11.0	1254	2	US-09-949-016-10297	Sequence 10297, A	817	62.5	10.6	69	2	US-09-894-882-268	Sequence 268, App
745	65	11.0	4654	2	US-08-476-515A-84	Sequence 84, Appl	818	62.5	10.6	70	2	US-09-894-882-235	Sequence 235, App
746	65	11.0	4655	2	US-08-652-877-84	Sequence 84, Appl	819	62.5	10.6	143	3	US-10-703-032-110377	Sequence 110377
747	65	11.0	4655	2	US-08-652-877-86	Sequence 86, Appl	820	62.5	10.6	277	2	US-08-469-633A-4	Sequence 4, Appl
748	65	11.0	4655	2	US-08-652-877-88	Sequence 88, Appl	821	62.5	10.6	297	2	US-09-270-767-44071	Sequence 2, Appl
749	65	11.0	4655	2	US-08-652-877-90	Sequence 90, Appl	822	62.5	10.6	347	2	US-09-582-337-2	Sequence 2, Appl
750	64.5	11.0	147	3	US-10-703-032-127195	Sequence 127195,	823	62.5	10.6	1080	2	US-09-904-380-2	Sequence 292, App
751	64.5	11.0	310	3	US-10-703-032-140673	Sequence 140673,	824	62	10.5	70	2	US-09-894-882-232	Sequence 86, Appl
752	64.5	11.0	969	3	US-10-055-877-214	Sequence 214, App	825	62	10.5	102	2	US-09-950-933A-86	Sequence 86, Appl
753	64.5	11.0	1581	2	US-09-949-002-414	Sequence 414, App	826	62	10.5	102	3	US-10-976-102-86	Sequence 86, Appl
754	64.5	11.0	1587	2	US-09-949-002-354	Sequence 354, App	827	62	10.5	113	2	US-09-270-767-37873	Sequence 37873, A
755	64.5	11.0	1788	3	US-09-619-049-777	Sequence 777, App	828	62	10.5	113	2	US-09-270-767-53090	Sequence 53090, A
756	64.5	11.0	2214	1	US-08-727-034-7	Sequence 7, Appl	829	62	10.5	148	2	US-09-252-991A-32322	Sequence 32322, A

830	62	10.5	402	1	US-08-709-979A-3	Sequence 3, Appli	903	61.5	10.4	282	3	US-09-906-838B-127	Sequence 127, App
831	62	10.5	402	2	US-08-709-974A-1	Sequence 1, Appli	904	61.5	10.4	282	3	US-09-909-320-127	Sequence 127, App
832	62	10.5	402	2	US-08-709-974A-5	Sequence 5, Appli	905	61.5	10.4	282	3	US-10-152-398-312	Sequence 312, App
833	62	10.5	415	1	US-08-833-642A-5	Sequence 5, Appli	906	61.5	10.4	282	3	US-10-123-907-312	Sequence 312, App
834	62	10.5	415	2	US-08-709-974A-4	Sequence 4, Appli	907	61.5	10.4	282	3	US-10-147-512-312	Sequence 312, App
835	62	10.5	415	2	US-09-069-632-1	Sequence 1, Appli	908	61.5	10.4	282	3	US-09-907-942-127	Sequence 127, App
836	62	10.5	435	1	US-08-361-920-27	Sequence 27, Appl	909	61.5	10.4	282	3	US-09-906-815C-127	Sequence 127, App
837	62	10.5	435	1	US-08-479-939-27	Sequence 27, Appl	910	61.5	10.4	282	3	US-10-147-485-312	Sequence 312, App
838	62	10.5	435	1	US-08-483-432-27	Sequence 27, Appl	911	61.5	10.4	282	3	US-10-124-814-312	Sequence 312, App
839	62	10.5	435	2	US-09-069-632-3	Sequence 3, Appli	912	61.5	10.4	282	3	US-10-124-822-312	Sequence 312, App
840	62	10.5	578	2	US-08-981-322-13	Sequence 13, Appl	913	61.5	10.4	282	3	US-10-131-833A-312	Sequence 312, App
841	62	10.5	578	2	US-09-908-322-13	Sequence 13, Appl	914	61.5	10.4	282	3	US-09-903-749A-127	Sequence 127, App
842	62	10.5	578	3	US-09-783-931C-13	Sequence 13, Appl	915	61.5	10.4	282	3	US-09-904-532B-127	Sequence 127, App
843	62	10.5	623	3	US-10-496-799-3	Sequence 3, Appli	916	61.5	10.4	282	3	US-10-142-419-312	Sequence 312, App
844	62	10.5	831	2	US-09-939-853A-97	Sequence 97, Appl	917	61.5	10.4	282	3	US-10-152-375-312	Sequence 312, App
845	62	10.5	831	2	US-09-939-853A-98	Sequence 98, Appl	918	61.5	10.4	282	3	US-10-131-818A-312	Sequence 312, App
846	62	10.5	998	1	US-08-449-645A-20	Sequence 20, Appl	919	61.5	10.4	282	3	US-09-905-075-127	Sequence 127, App
847	62	10.5	998	1	US-08-702-367A-20	Sequence 20, Appl	920	61.5	10.4	282	3	US-10-145-873-312	Sequence 312, App
848	62	10.5	998	2	US-09-378-759-20	Sequence 20, Appl	921	61.5	10.4	282	3	US-10-152-395-312	Sequence 312, App
849	62	10.5	998	5	PCT-US95-04681-20	Sequence 20, Appl	922	61.5	10.4	282	3	US-10-131-822A-312	Sequence 312, App
850	62	10.5	1113	2	US-09-959-392-4	Sequence 4, Appli	923	61.5	10.4	282	3	US-10-142-763-312	Sequence 312, App
851	62	10.5	1150	3	US-10-296-733A-1	Sequence 1, Appli	924	61.5	10.4	282	3	US-10-128-694A-312	Sequence 312, App
852	62	10.5	1170	1	US-08-313-288B-20	Sequence 20, Appl	925	61.5	10.4	282	3	US-10-123-213-312	Sequence 312, App
853	62	10.5	1833	2	US-08-479-722B-2	Sequence 2, Appli	926	61.5	10.4	282	3	US-10-123-909-312	Sequence 312, App
854	62	10.5	1833	2	US-09-592-685-2	Sequence 2, Appli	927	61.5	10.4	282	3	US-10-131-826A-312	Sequence 312, App
855	62	10.5	1833	5	PCT-US95-02251-18	Sequence 18, Appl	928	61.5	10.4	282	3	US-09-903-640A-127	Sequence 127, App
856	62	10.5	4440	3	US-10-183-001-525	Sequence 525, App	929	61.5	10.4	282	3	US-10-448-580-127	Sequence 127, App
857	62	10.5	4440	3	US-10-180-998-525	Sequence 525, App	930	61.5	10.4	282	3	US-10-147-513-312	Sequence 312, App
858	62	10.5	4440	3	US-10-201-769-525	Sequence 525, App	931	61.5	10.4	282	3	US-10-121-043-312	Sequence 312, App
859	62	10.5	4440	3	US-10-174-576-525	Sequence 525, App	932	61.5	10.4	282	3	US-10-963-467-127	Sequence 127, App
860	62	10.5	4440	3	US-10-174-581-525	Sequence 525, App	933	61.5	10.4	282	3	US-10-448-923-127	Sequence 127, App
861	62	10.5	4440	3	US-10-207-916-525	Sequence 525, App	934	61.5	10.4	282	3	US-10-139-980-312	Sequence 312, App
862	62	10.5	4440	3	US-10-174-583-525	Sequence 525, App	935	61.5	10.4	310	1	US-07-704-288C-6	Sequence 6, Appli
863	62	10.5	4440	3	US-10-187-745-525	Sequence 525, App	936	61.5	10.4	310	1	US-08-379-259-6	Sequence 6, Appli
864	61.5	10.4	69	2	US-09-894-882-359	Sequence 259, App	937	61.5	10.4	510	2	US-10-104-047-2580	Sequence 2580, Ap
865	61.5	10.4	92	3	US-10-703-032-141830	Sequence 141830, App	938	61.5	10.4	523	3	US-09-792-200C-14	Sequence 14, Appl
866	61.5	10.4	105	3	US-10-703-031C-24	Sequence 24, Appl	939	61.5	10.4	1345	2	US-09-949-016-8313	Sequence 8313, Ap
867	61.5	10.4	156	2	US-09-270-767-33322	Sequence 33322, A	940	61.5	10.4	2157	2	US-09-466-778-2	Sequence 2, Appli
868	61.5	10.4	156	2	US-09-270-767-48539	Sequence 48539, A	941	61.5	10.4	2157	2	US-10-960-275-2	Sequence 2, Appli
869	61.5	10.4	180	2	US-09-904-615-78	Sequence 78, Appl	942	61.5	10.4	2873	1	US-08-466-033-15	Sequence 15, Appl
870	61.5	10.4	180	2	US-10-054-988-78	Sequence 78, Appl	943	61.5	10.4	2873	1	US-08-638-911A-2	Sequence 2, Appli
871	61.5	10.4	226	3	US-10-703-032-123140	Sequence 123140, App	944	61.5	10.4	2873	1	US-08-444-733-15	Sequence 15, Appl
872	61.5	10.4	277	1	US-08-147-784-2	Sequence 2, Appli	945	61.5	10.4	2873	1	US-08-464-134-15	Sequence 15, Appl
873	61.5	10.4	277	2	US-08-195-967-2	Sequence 2, Appli	946	61.5	10.4	2873	1	US-08-461-361-15	Sequence 15, Appl
874	61.5	10.4	277	2	US-09-006-353A-12	Sequence 12, Appl	947	61.5	10.4	2873	1	US-08-485-910-15	Sequence 15, Appl
875	61.5	10.4	277	2	US-08-472-940-2	Sequence 2, Appli	948	61.5	10.4	2873	5	PCT-US95-06266-15	Sequence 15, Appl
876	61.5	10.4	277	2	US-09-573-986-12	Sequence 12, Appl	949	61.5	10.4	3571	2	US-09-911-842A-2	Sequence 2, Appli
877	61.5	10.4	277	2	US-09-880-939-2	Sequence 2, Appli	950	61.5	10.4	3571	2	US-10-150-821-2	Sequence 2, Appli
878	61.5	10.4	277	2	US-09-804-200-2	Sequence 2, Appli	951	61	10.4	70	2	US-09-894-882-289	Sequence 289, App
879	61.5	10.4	277	2	US-10-046-433-3	Sequence 3, Appli	952	61	10.4	93	2	US-09-950-933A-95	Sequence 95, Appl
880	61.5	10.4	277	3	US-09-826-212A-12	Sequence 12, Appl	953	61	10.4	93	3	US-10-976-102-95	Sequence 95, Appl
881	61.5	10.4	277	3	US-10-323-274C-2	Sequence 2, Appli	954	61	10.4	123	3	US-10-703-032-147084	Sequence 147084, App
882	61.5	10.4	277	3	US-10-326-929A-2	Sequence 2, Appli	955	61	10.4	233	3	US-10-703-032-114880	Sequence 114880, App
883	61.5	10.4	277	3	US-09-518-931-14	Sequence 14, Appl	956	61	10.4	336	2	US-09-248-796A-20058	Sequence 20058, A
884	61.5	10.4	282	2	US-09-907-794A-127	Sequence 127, App	957	61	10.4	348	1	US-08-468-847B-14	Sequence 14, Appl
885	61.5	10.4	282	2	US-09-905-125A-127	Sequence 127, App	958	61	10.4	359	2	US-09-270-767-42534	Sequence 42534, A
886	61.5	10.4	282	2	US-09-902-775A-127	Sequence 127, App	959	61	10.4	405	3	US-09-540-209B-9253	Sequence 9253, Ap
887	61.5	10.4	282	2	US-09-906-700-127	Sequence 127, App	960	61	10.4	722	3	US-10-703-032-116051	Sequence 116051, App
888	61.5	10.4	282	2	US-09-808-847-1	Sequence 1, Appli	961	61	10.4	724	2	US-10-094-749-2240	Sequence 2240, Ap
889	61.5	10.4	282	2	US-09-903-620A-127	Sequence 127, App	962	61	10.4	787	1	US-08-720-484A-4	Sequence 4, Appli
890	61.5	10.4	282	2	US-09-904-903A-127	Sequence 127, App	963	61	10.4	787	2	US-08-953-823A-4	Sequence 4, Appli
891	61.5	10.4	282	2	US-09-905-064-127	Sequence 127, App	964	61	10.4	787	2	US-09-398-239-4	Sequence 4, Appli
892	61.5	10.4	282	2	US-09-905-381A-127	Sequence 127, App	965	61	10.4	787	2	US-09-560-876A-4	Sequence 4, Appli
893	61.5	10.4	282	2	US-09-906-618-127	Sequence 127, App	966	61	10.4	1170	2	US-09-657-472-2	Sequence 2, Appli
894	61.5	10.4	282	2	US-09-906-646-127	Sequence 127, App	967	61	10.4	1170	2	US-09-949-002-350	Sequence 350, App
895	61.5	10.4	282	2	US-09-904-462-127	Sequence 127, App	968	61	10.4	1171	2	US-09-560-385A-36	Sequence 36, Appl
896	61.5	10.4	282	2	US-09-902-736A-127	Sequence 127, App	969	61	10.4	1192	2	US-09-560-385A-34	Sequence 34, Appl
897	61.5	10.4	282	2	US-09-906-722A-127	Sequence 127, App	970	61	10.4	1192	2	US-10-053-662A-32	Sequence 32, Appl
898	61.5	10.4	282	2	US-09-905-449-127	Sequence 127, App	971	61	10.4	1248	2	US-08-882-046-6	Sequence 6, Appli
899	61.5	10.4	282	2	US-09-903-562B-127	Sequence 127, App	972	61	10.4	1248	2	US-09-566-047-6	Sequence 6, Appli
900	61.5	10.4	282	2	US-09-906-679A-127	Sequence 127, App	973	61	10.4	1251	5	PCT-US95-02251-3	Sequence 3, Appli
901	61.5	10.4	282	3	US-09-907-841-127	Sequence 127, App	974	61	10.4	1252	1	US-08-199-780-3	Sequence 3, Appli
902	61.5	10.4	282	3	US-10-123-292-312	Sequence 312, Appl	975	61	10.4	1252	1	US-08-316-650-3	Sequence 3, Appli

976	61	10.4	2476	1	US-08-276-967-2	Sequence 2, Appli	1049	60.5	10.3	723	3	US-10-152-398-346	Sequence 346, App
977	61	10.4	2794	3	US-10-042-865-2	Sequence 2, Appli	1050	60.5	10.3	723	3	US-10-123-907-346	Sequence 346, App
978	60.5	10.3	75	3	US-10-703-032-141698	Sequence 141698,	1051	60.5	10.3	723	3	US-10-147-512-346	Sequence 346, App
979	60.5	10.3	92	3	US-10-703-032-141780	Sequence 141780,	1052	60.5	10.3	723	3	US-10-147-815-346	Sequence 346, App
980	60.5	10.3	98	3	US-09-950-933A-48	Sequence 48, Appl	1053	60.5	10.3	723	3	US-10-124-814-346	Sequence 346, App
981	60.5	10.3	98	3	US-10-976-102-48	Sequence 82, Appl	1054	60.5	10.3	723	3	US-10-124-822-346	Sequence 346, App
982	60.5	10.3	99	3	US-09-950-933A-82	Sequence 82, Appl	1055	60.5	10.3	723	3	US-09-950-933A-9	Sequence 9, Appli
983	60.5	10.3	99	3	US-10-976-102-82	Sequence 133593,	1056	60.5	10.3	723	3	US-10-131-833A-346	Sequence 346, App
984	60.5	10.3	110	3	US-10-703-032-133593	Sequence 39, Appl	1057	60.5	10.3	723	3	US-10-142-419-346	Sequence 346, App
985	60.5	10.3	115	3	US-09-950-933A-39	Sequence 39, Appl	1058	60.5	10.3	723	3	US-10-152-375-346	Sequence 346, App
986	60.5	10.3	115	3	US-10-976-102-39	Sequence 122834,	1059	60.5	10.3	723	3	US-10-131-818A-346	Sequence 9, Appli
987	60.5	10.3	121	3	US-10-703-032-122834	Sequence 122834,	1060	60.5	10.3	723	3	US-11-043-357-9	Sequence 346, App
988	60.5	10.3	141	2	US-09-248-796A-17570	Sequence 17570, A	1061	60.5	10.3	723	3	US-10-145-873-346	Sequence 346, App
989	60.5	10.3	170	2	US-09-252-991A-22362	Sequence 22362, A	1062	60.5	10.3	723	3	US-10-152-395-346	Sequence 346, App
990	60.5	10.3	180	2	US-09-461-688-4	Sequence 4, Appli	1063	60.5	10.3	723	3	US-10-131-822A-346	Sequence 346, App
991	60.5	10.3	182	2	US-09-252-991A-25189	Sequence 25189, A	1064	60.5	10.3	723	3	US-10-128-694A-346	Sequence 346, App
992	60.5	10.3	310	2	US-07-791-931-6	Sequence 6, Appli	1065	60.5	10.3	723	3	US-10-142-763-346	Sequence 346, App
993	60.5	10.3	324	1	US-08-047-413-11	Sequence 11, Appl	1066	60.5	10.3	723	3	US-10-123-213-346	Sequence 346, App
994	60.5	10.3	324	2	US-08-229-050-11	Sequence 11, Appl	1067	60.5	10.3	723	3	US-10-123-909-346	Sequence 346, App
995	60.5	10.3	324	1	US-08-801-563-11	Sequence 11, Appl	1068	60.5	10.3	723	3	US-11-051-631-9	Sequence 9, Appli
996	60.5	10.3	349	1	US-08-167-628-2	Sequence 2, Appli	1069	60.5	10.3	723	3	US-10-131-826A-346	Sequence 346, App
997	60.5	10.3	349	1	US-08-386-680-2	Sequence 2, Appli	1070	60.5	10.3	723	3	US-10-147-513-346	Sequence 346, App
998	60.5	10.3	349	1	US-08-459-717-2	Sequence 2, Appli	1071	60.5	10.3	723	3	US-10-121-043-346	Sequence 346, App
999	60.5	10.3	349	1	US-08-880-031-2	Sequence 2, Appli	1072	60.5	10.3	723	3	US-10-139-880-346	Sequence 346, App
1000	60.5	10.3	349	2	US-09-054-368-2	Sequence 2, Appli	1073	60.5	10.3	723	3	US-09-866-028-15	Sequence 15, Appl
1001	60.5	10.3	349	2	US-09-097-179-2	Sequence 2, Appli	1074	60.5	10.3	723	3	US-09-944-457-15	Sequence 15, Appl
1002	60.5	10.3	349	2	US-09-054-274-2	Sequence 2, Appli	1075	60.5	10.3	723	3	US-09-945-584-15	Sequence 15, Appl
1003	60.5	10.3	349	2	US-09-080-715-2	Sequence 2, Appli	1076	60.5	10.3	723	3	US-09-944-944-15	Sequence 15, Appl
1004	60.5	10.3	349	2	US-09-056-704-2	Sequence 2, Appli	1077	60.5	10.3	723	3	US-09-945-587-15	Sequence 15, Appl
1005	60.5	10.3	349	2	US-09-292-036-4	Sequence 2, Appli	1078	60.5	10.3	723	3	US-09-944-884-15	Sequence 15, Appl
1006	60.5	10.3	349	2	US-09-233-316-26	Sequence 26, Appl	1079	60.5	10.3	723	3	US-10-183-001-38	Sequence 38, Appl
1007	60.5	10.3	349	2	US-09-142-569-8	Sequence 8, Appli	1080	60.5	10.3	723	3	US-10-174-576-38	Sequence 38, Appl
1008	60.5	10.3	349	2	US-09-461-688-2	Sequence 2, Appli	1081	60.5	10.3	723	3	US-10-174-581-38	Sequence 38, Appl
1009	60.5	10.3	349	2	US-09-495-448A-8	Sequence 8, Appli	1082	60.5	10.3	723	3	US-09-944-896-15	Sequence 15, Appl
1010	60.5	10.3	349	2	US-09-949-016-6141	Sequence 6141, Ap	1083	60.5	10.3	723	3	US-10-207-916-38	Sequence 38, Appl
1011	60.5	10.3	349	2	US-10-053-753A-8	Sequence 8, Appli	1084	60.5	10.3	723	3	US-10-174-583-38	Sequence 38, Appl
1012	60.5	10.3	349	3	US-09-461-646-2	Sequence 2, Appli	1085	60.5	10.3	723	3	US-10-187-745-38	Sequence 38, Appl
1013	60.5	10.3	349	3	US-10-171-311-46	Sequence 46, Appl	1086	60.5	10.3	723	3	US-08-936-135-18	Sequence 18, Appl
1014	60.5	10.3	349	3	US-10-902-895-8	Sequence 8, Appli	1087	60.5	10.3	723	3	US-08-936-135-18	Sequence 18, Appl
1015	60.5	10.3	349	3	PCT-US96-08140-2	Sequence 46, Appl	1088	60.5	10.3	723	3	US-08-936-135-18	Sequence 18, Appl
1016	60.5	10.3	349	3	US-09-252-991A-31718	Sequence 31718, A	1089	60.5	10.3	723	3	US-08-936-135-18	Sequence 18, Appl
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1018	60.5	10.3	371	3	US-08-597-545-1	Sequence 1, Appli	1091	60.5	10.3	723	3	US-08-936-135-18	Sequence 18, Appl
1019	60.5	10.3	385	1	US-08-457-135-1	Sequence 1, Appli	1092	60.5	10.3	723	3	US-08-936-135-18	Sequence 18, Appl
1020	60.5	10.3	385	1	US-09-142-027A-10	Sequence 10, Appl	1093	60.5	10.3	723	3	US-08-936-135-18	Sequence 18, Appl
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1023	60.5	10.3	515	2	US-09-636-077A-6	Sequence 6, Appli	1096	60.5	10.3	723	3	US-08-936-135-18	Sequence 18, Appl
1024	60.5	10.3	515	2	US-09-636-060C-6	Sequence 6, Appli	1097	60.5	10.3	723	3	US-08-936-135-18	Sequence 18, Appl
1025	60.5	10.3	515	2	US-09-986-552-6	Sequence 6, Appli	1098	60.5	10.3	723	3	US-08-936-135-18	Sequence 18, Appl
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1030	60.5	10.3	515	2	US-10-023-888-18	Sequence 18, Appl	1103	60.5	10.3	723	3	US-08-936-135-18	Sequence 18, Appl
1031	60.5	10.3	515	2	US-10-023-888-18	Sequence 18, Appl	1104	60.5	10.3	723	3	US-08-936-135-18	Sequence 18, Appl
1032	60.5	10.3	515	2	US-10-901-216-18	Sequence 18, Appl	1105	60.5	10.3	723	3	US-08-936-135-18	Sequence 18, Appl
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1035	60.5	10.3	520	3	US-11-043-357-3	Sequence 3, Appli	1108	60.5	10.3	723	3	US-08-936-135-18	Sequence 18, Appl
1036	60.5	10.3	520	3	US-11-051-631-3	Sequence 3, Appli	1109	60.5	10.3	723	3	US-08-936-135-18	Sequence 18, Appl
1037	60.5	10.3	520	3	US-09-248-796A-17571	Sequence 17571, A	1110	60.5	10.3	723	3	US-08-936-135-18	Sequence 18, Appl
1038	60.5	10.3	563	2	US-10-455-719-273	Sequence 273, App	1111	60.5	10.3	723	3	US-08-936-135-18	Sequence 18, Appl
1039	60.5	10.3	702	2	US-09-068-740A-4	Sequence 4, Appli	1112	60.5	10.3	723	3	US-08-936-135-18	Sequence 18, Appl
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1126	60	10.2	399	2	US-09-807-802A-9	Sequence 9, Appl	1199	60	10.2	1523	3	US-10-015-610A-198	Sequence 198, App
1127	60	10.2	399	3	US-10-696-282-9	Sequence 9, Appl	1200	60	10.2	1523	3	US-10-180-998-290	Sequence 290, App
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1130	60	10.2	623	2	US-09-807-802A-2	Sequence 2, Appl	1203	60	10.2	1523	3	US-10-174-576-290	Sequence 290, App
1131	60	10.2	623	3	US-09-807-802A-5	Sequence 5, Appl	1204	60	10.2	1523	3	US-10-174-581-290	Sequence 290, App
1132	60	10.2	623	4	US-10-696-282-2	Sequence 2, Appl	1205	60	10.2	1523	3	US-10-015-869A-198	Sequence 198, App
1133	60	10.2	623	5	US-10-696-282-5	Sequence 5, Appl	1206	60	10.2	1523	3	US-10-207-916-290	Sequence 290, App
1134	60	10.2	623	6	US-10-696-900-2	Sequence 2, Appl	1207	60	10.2	1523	3	US-10-174-583-290	Sequence 290, App
1135	60	10.2	623	7	US-10-696-900-5	Sequence 5, Appl	1208	60	10.2	1523	3	US-10-187-745-290	Sequence 290, App
1136	60	10.2	795	2	US-09-133-562D-11	Sequence 11, Appl	1209	59.5	10.1	70	2	US-09-894-882-238	Sequence 238, App
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1139	60	10.2	802	3	US-10-020-445A-169	Sequence 169, App	1212	59.5	10.1	74	1	US-08-420-526-2	Sequence 2, Appl
1140	60	10.2	802	4	US-09-978-189-169	Sequence 169, App	1213	59.5	10.1	78	3	US-10-703-032-139163	Sequence 139163, App
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1147	60	10.2	802	11	US-10-145-016A-169	Sequence 169, App	1220	59.5	10.1	886	2	US-09-631-603-14	Sequence 14, Appl
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1151	60	10.2	802	15	US-10-165-247A-169	Sequence 169, App	1224	59	10.0	175	2	US-09-252-991A-30055	Sequence 30055, A
1152	60	10.2	802	16	US-10-017-086A-169	Sequence 169, App	1225	59	10.0	258	2	US-09-579-845-9	Sequence 9, Appl
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1158	60	10.2	802	22	US-09-978-564A-169	Sequence 169, App	1231	59	10.0	348	3	US-10-245-752-74	Sequence 74, Appl
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1162	60	10.2	802	26	US-10-145-089A-169	Sequence 169, App	1235	59	10.0	372	2	US-09-252-991A-20108	Sequence 20108, A
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1164	60	10.2	802	28	US-10-160-502A-169	Sequence 169, App	1237	59	10.0	383	2	US-09-142-027A-12	Sequence 12, Appl
1165	60	10.2	821	2	US-09-193-562D-12	Sequence 12, Appl	1238	59	10.0	474	1	US-08-650-000-4	Sequence 4, Appl
1166	60	10.2	821	3	US-10-055-412B-12	Sequence 12, Appl	1239	59	10.0	474	2	US-09-042-785A-8	Sequence 8, Appl
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1168	60	10.2	905	2	US-09-193-562D-2	Sequence 2, Appl	1241	59	10.0	474	3	US-10-420-785A-4	Sequence 4, Appl
1169	60	10.2	905	3	US-09-193-562D-2	Sequence 2, Appl	1242	59	10.0	474	7	5395760-4	Patent No. 5395760
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1171	60	10.2	1523	2	US-09-182-024A-2	Sequence 2, Appl	1244	59	10.0	621	2	US-09-996-620-6	Sequence 6, Appl
1172	60	10.2	1523	3	US-10-012-231A-198	Sequence 198, App	1245	59	10.0	836	3	US-10-108-260A-3700	Sequence 3700, App
1173	60	10.2	1523	4	US-10-015-389A-198	Sequence 198, App	1246	59	10.0	1153	2	US-09-560-385A-16	Sequence 16, Appl
1174	60	10.2	1523	5	US-10-006-768A-198	Sequence 198, App	1247	59	10.0	1170	2	US-09-561-709B-12	Sequence 12, Appl
1175	60	10.2	1523	6	US-10-015-671A-198	Sequence 198, App	1248	59	10.0	1170	2	US-09-560-385A-14	Sequence 14, Appl
1176	60	10.2	1523	7	US-10-015-393A-198	Sequence 198, App	1249	59	10.0	1253	2	US-08-479-722B-4	Sequence 4, Appl
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1178	60	10.2	1523	9	US-10-006-041A-198	Sequence 198, App	1251	59	10.0	1404	1	US-08-400-159-2	Sequence 2, Appl
1179	60	10.2	1523	10	US-10-012-064A-198	Sequence 198, App	1252	59	10.0	1404	2	US-08-611-729A-2	Sequence 2, Appl
1180	60	10.2	1523	11	US-10-015-392A-198	Sequence 198, App	1253	59	10.0	1404	2	US-09-195-524-2	Sequence 2, Appl
1181	60	10.2	1523	12	US-10-011-795B-198	Sequence 198, App	1254	58.5	9.9	84	3	US-10-000-986A-206	Sequence 206, App
1182	60	10.2	1523	13	US-10-015-386A-198	Sequence 198, App	1255	58.5	9.9	84	3	US-09-992-600B-206	Sequence 206, App
1183	60	10.2	1523	14	US-10-012-121A-198	Sequence 198, App	1256	58.5	9.9	84	3	US-09-999-570A-206	Sequence 206, App
1184	60	10.2	1523	15	US-10-006-485A-198	Sequence 198, App	1257	58.5	9.9	84	3	US-10-001-142C-206	Sequence 206, App
1185	60	10.2	1523	16	US-10-006-746A-198	Sequence 198, App	1258	58.5	9.9	124	3	US-09-252-691C-10808	Sequence 10808, A
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1187	60	10.2	1523	18	US-10-017-253A-198	Sequence 198, App	1260	58.5	9.9	139	3	US-10-108-260A-3259	Sequence 3259, App
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1189	60	10.2	1523	20	US-10-015-715A-198	Sequence 198, App	1262	58.5	9.9	143	2	US-09-270-767-3302	Sequence 3302, A
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1192	60	10.2	1523	23	US-10-007-194A-198	Sequence 198, App	1265	58.5	9.9	164	3	US-10-703-032-182470	Sequence 182470, App
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ALIGNMENTS

RESULT 1
US-09-712-529-5
; Sequence 5, Application US/09712529
; Patent No. 6485938
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Thompson, Penny P.
; TITLE OF INVENTION: Human Zven Proteins
; FILE REFERENCE: 99-81
; CURRENT APPLICATION NUMBER: US/09/712,529
; CURRENT FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-712-529-5

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Best Local Similarity 100.0%; Pred. No. 2.1e-58;
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; Patent No. 6756479
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Thompson, Penny P.
; TITLE OF INVENTION: Human Zven Proteins
; FILE REFERENCE: 99-81
; CURRENT APPLICATION NUMBER: US/10/212,201A
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US/09/712,529
; PRIOR FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 7
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; ORGANISM: Homo sapiens
US-10-212-201A-5

Query Match      100.0%; Score 589; DB 2; Length 105;
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; Patent No. 6828425
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Thompson, Penny P.
; TITLE OF INVENTION: Human Zven Proteins
; FILE REFERENCE: 99-81
; CURRENT APPLICATION NUMBER: US/10/212.355
; CURRENT FILING DATE: 2002-08-02
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; ORGANISM: Homo sapiens
US-10-212-355-5

Query Match      100.0%; Score 589; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 2.le-58;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 HPGSHKVPFFRKHKHTCPCLPNLLCSRFDPGRYRCSDMLKNINF 105

RESULT 4
US-09-991-181-371
; Sequence 371, Application US/09991181
; Patent No. 6913919
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann

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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zenin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C53
; CURRENT APPLICATION NUMBER: US/09/991.181
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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Query Match 100.0%; Score 589; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 2.1e-58;

Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5

US-09-990-444-371
; Sequence 371, Application US/09990444
; Patent No. 6930170
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.

Fri Nov 30 07:56:32 2007

us-10-692-299-2.spdi.ra1

APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C19
CURRENT FILING DATE: 2001-11-14
CURRENT APPLICATION NUMBER: US/09/990,444
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Query Match 100.0%; Score 589; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 2.1e-58;

Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGATRVSIIMLLVTVSDCAVITGACERDVCGAGTCCCAISLWLRGLRMCTPLGREGSEC 60
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RESULT 6

US-09-997-333-371
; Sequence 371, Application US/09997333

; Patent No. 6953836

; GENERAL INFORMATION:

- ; APPLICANT: Ashkenazi, Avi J.
- ; APPLICANT: Baker, Kevin P.
- ; APPLICANT: Botstein, David
- ; APPLICANT: Desnoyers, Luc
- ; APPLICANT: Eaton, Dan L.
- ; APPLICANT: Ferrara, Napoleone
- ; APPLICANT: Fong, Sherman
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- ; APPLICANT: Goddard, Audrey
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- ; APPLICANT: Napier, Mary A.
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- ; APPLICANT: Roy, Margaret Ann
- ; APPLICANT: Stewart, Timothy A.
- ; APPLICANT: Tumas, Daniel
- ; APPLICANT: Watanabe, Colin K.
- ; APPLICANT: Williams, P. Mickey
- ; APPLICANT: Wood, William I.
- ; APPLICANT: Zhang, Zemin

;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2730FIC27
;; CURRENT APPLICATION NUMBER: US/09/997,333
;; CURRENT FILING DATE: 2001-11-15
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RESULT 7
US-09-9992-598-371
US-9992 371, Application US/09992598
/ Patent No. 6956108
GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi J.
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Botstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Eaton, Dan L.
/ APPLICANT: Ferrara, Napoleone
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Kijavits, Ivar J.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: Secured and Tra
/ TITLE OF INVENTION: Acids Encoding
/ FILE REFERENCE: P2730P1C20

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to 220, 1180

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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 589; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 2.le-58;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 8
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; Sequence 371, Application US/09989735
; Patent No. 6972185
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P27301C61
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US/09/989,735
; PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR FILING DATE: 1998-06-25
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 589; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 2.1e-58;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 9
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; Sequence 371, Application US/09989726
; Patent No. 7018811
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deanoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
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; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C60
; CURRENT APPLICATION NUMBER: US/09/989,726
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; PRIOR APPLICATION NUMBER: 60/049787
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Best Local Similarity 100.08; Pred. No. 2.le-58;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 10
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PC46
; CURRENT APPLICATION NUMBER: US/09/997,514
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;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 589; DB 3; Length 105;
Best Local Similarity 100.0%; Pred. No. 2.1e-58;
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; Sequence 371, Application US/09989728
; Patent No. 7029873
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deanovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
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Query Match      100.0%; Score 589; DB 3; Length 105;
Best Local Similarity 100.0%; Pred. No. 2.1e-58;
Matches 105; Conservative 0; Mismatches 0; Indels
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Db 61 HPGSHKVPFFFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKINNF 105			

RESULT 13

US-09-997-653-371
; Sequence 371, Application US/09997653
; Patent No. 7034122

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; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey E.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
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; TITLE OF INVENTION: Acids Encoding
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GenCore version 6.2.1
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Listing first 1500 summaries

Database : UniProt_8.4.*

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2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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58	100.5	17.1	350	2	Q4R4I7_MACFA
59	99.5	16.9	277	2	Q9ES33_RAT
60	99.5	16.9	348	2	Q5RKL1_RAT
61	98.5	16.7	349	1	DKK3_MOUSE
62	97	16.5	266	1	DKK1_HUMAN
63	96.5	16.4	268	1	Q6FVU5_RABIT
64	95.5	16.2	259	2	Q57464_XENLA
65	95	16.1	177	2	Q4SL69_TETNG
66	94.5	16.0	350	2	Q6PQ81_HUMAN
67	94	16.0	240	2	Q9FWH3_BRARE
68	94	16.0	418	2	Q4T860_TETNG
69	93.5	15.9	1233	2	Q4S163_TETNG
70	93	15.8	88	2	Q5D229_HADSP
71	92	15.6	88	2	Q5D228_HADSP
72	90.5	15.4	400	2	Q3UIZ8_MOUSE
73	90.5	15.4	425	1	CNI30_MOUSE
74	90.5	15.4	425	2	Q52KCO_MOUSE
75	90.5	15.4	425	2	Q642A8_RAT
76	89	15.1	88	2	Q5D230_HADSP
77	88.5	15.0	640	2	Q96397_CHLRE
78	86	14.6	241	2	Q9W6D9_BRARE
79	85	14.4	107	1	COL_RABIT
80	84.5	14.3	102	2	Q3UW21_MOUSE
81	84	14.3	1331	2	Q4S572_TETNG
82	83.5	14.2	110	2	Q4PML0_IPOSC
83	83.5	14.2	504	2	Q1XB78_MYTED
84	83	14.1	708	2	P87363_CHICK
85	83	14.1	966	2	Q22378_CABEL
86	82.5	14.0	274	2	Q5RCC3_PONPY
87	82.5	14.0	425	1	CNI30_HUMAN
88	82	13.9	1013	2	Q28CM0_XENTR
89	82	13.9	1165	2	Q5BKF5_XENTR
90	81.5	13.8	446	2	Q8NB03_HUMAN
91	81	13.8	1964	1	NOTC4_MOUSE
92	80.5	13.7	113	2	Q9D2R7_MOUSE
93	80.5	13.7	386	2	Q32NM5_XENLA
94	80.5	13.7	388	2	Q6JA22_XENLA
95	80.5	13.7	388	2	Q68Y16_XENLA
96	80.5	13.7	729	2	Q8BNH3_MOUSE
97	80.5	13.7	787	2	Q8K061_MOUSE
98	80.5	13.7	1193	2	Q4S758_TETNG
99	80.5	13.7	1293	2	Q16M09_AEDAE
100	80	13.6	412	2	Q557F1_DICDI
101	80	13.6	412	2	Q68HY9_DICDI
102	79.5	13.5	191	2	Q62QW6_HUMAN
103	79.5	13.5	404	2	Q6ZQR7_HUMAN
104	79.5	13.5	446	2	Q8N1N5_HUMAN

Q8JFY2	bombina max
Q2TBS7	bos taurus
Q50E35	arvicanthus
Q50E36	arvicanthus
Q50E61	arvicanthus
Q56R10	penaeus mon
Q8UUX3	gallus gall
Q56R11	pacifastacu
Q8VEJ3	mus musculus
Q9UBT3	homo sapien
Q3KNX0	homo sapien
Q90839	gallus gall
Q9DDA4	xenopus lae
Q4RJF1	tetraodon n
Q9UBU2	homo sapien
Q5EHU6	gecko japon
Q9QYZ8	mus musculus
Q8BFW0	m 10, 11 da
Q54908	mus musculus
Q8OUL5	m dickkopf
Q43532	homo sapien
Q8N294	homo sapien
Q5R8T0	pongo pygma
Q2HWR5	sus scrofa
Q9UBP4	homo sapien
Q5R4Q2	pongo pygma
Q4R4I7	macaca fasc
Q9ES33	rattus norv
Q5RKL1	rattus norv
Q9QUN9	mus musculus
Q94907	homo sapien
Q6PVU5	oryctolagus
Q57464	xenopus lae
Q4SL69	tetraodon n
Q6PQ81	homo sapien
Q9FWH3	brachydanio
Q4T860	tetraodon n
Q4S163	tetraodon n
Q5D229	hadronyche
Q5D228	hadronyche
Q3UIZ8	mus musculus
Q8BU04	mus musculus
Q52KCO	m hypotheti
Q642A8	rattus norv
Q5D230	hadronyche
Q96397	chlamydomon
Q9W6D9	brachydanio
P42890	oryctolagus
Q3UW21	mus musculus
Q4S572	tetraodon n
Q4PML0	ixodes scap
Q1XB78	mytilus edu
P87363	gallus gall
Q22378	caenorhabdi
Q5RCC3	pongo pygma
Q8N306	homo sapien
Q28CM0	xenopus tro
Q5BKF5	xenopus tro
Q8NB03	homo sapien
P31695	mus musculus
Q9D2R7	mus musculus
Q32NM5	xenopus lae
Q6JA22	xenopus lae
Q68Y16	xenopus lae
Q8BNH3	mus musculus
Q8K061	mus musculus
Q4S758	tetraodon n
Q16M09	aedes aegypt
Q557F1	dictyostell
Q68HY9	dictyostell
Q62QW6	homo sapien
Q6ZQR7	homo sapien
Q8N1N5	homo sapien

105	79.5	13.5	704	1	FBLN1_CHICK	073775 gallus gall	178	74.5	12.6	392	2	Q6NUF1_XENLA	Q6nuf1 xenopus lae
106	79.5	13.5	870	2	Q8IOG6_DROME	Q8iqs6 drosoephila	179	74.5	12.6	429	2	Q1XBT6_MYTED	Q1xibt6 mytilus edu
107	79.5	13.5	1353	2	Q4UGZ9_HUMAN	Q4ugs9 thelieria a	180	74.5	12.6	720	2	Q2U318_ASPOR	Q2u318 aspergillus
108	79	13.4	109	2	Q5U809_HUMAN	Q5u809 homo sapien	181	74.5	12.6	1426	2	Q4RTA6_TETNG	Q4arta6 tetraodon n
109	79	13.4	112	1	COL_HUMAN	P04118 homo sapien	182	74.5	12.6	2327	2	Q9IBG7_XENLA	Q9ibg7 xenopus lae
110	79	13.4	112	2	Q5T9G7_HUMAN	Q5t9g7 homo sapien	183	74.5	12.6	5644	2	Q16KQ9_AEDAE	Q16kq9 aedes aegypt
111	79	13.4	224	2	Q4H3Q2_CIOIN	Q4h3q2 ciona intes	184	74	12.6	92	2	Q6ISU9_ORYSA	Q6isu9 oryza sativ
112	79	13.4	225	2	Q4H3Q3_CIOIN	Q4h3q3 ciona intes	185	74	12.6	111	1	COL_SPEPTR	Q91xl7 spermothillu
113	79	13.4	919	2	Q61V24_CAEBR	Q61v24 caenorhabdi	186	74	12.6	112	1	COL_RAT	P17084 rattus norv
114	79	13.4	1651	2	Q9TVQ2_CAEBL	Q9tvq2 caenorhabdi	187	74	12.6	112	2	Q29ID9_DROPS	Q29id9 drosoephila
115	79	13.4	2447	2	O13149_FUGRU	O13149 fugu rubrip	188	74	12.6	211	2	Q21QC1_RHOFD	Q21qc1 rhodofera
116	79	13.4	5533	2	Q5RIP6_BRARE	Q5rip6 brachydanio	189	74	12.6	212	2	Q16TD8_AEDAE	Q16td8 aedes aegypt
117	78.5	13.3	162	2	Q5JHV8_PVRKO	Q5jhw8 pyrococcus	190	74	12.6	623	2	Q4P8A3_USTWA	Q4p8a3 uscillego ma
118	78.5	13.3	593	2	Q5RST2_PONPY	Q5r5t2 pongo pygma	191	74	12.6	1168	2	Q60XC0_CAEBR	Q60xc0 caenorhabdi
119	78	13.2	70	1	CKIX_CONBE	Q9u3x3 conus betul	192	74	12.6	1171	2	Q4RLR5_TETNG	Q4rlr5 tetraodon n
120	78	13.2	425	2	Q53RA0_HUMAN	Q53ra0 homo sapien	193	74	12.6	1216	2	Q5TZK7_BRARE	Q5tzk7 brachydanio
121	78	13.2	1408	2	Q4RX38_TETNG	Q4rx38 tetraodon n	194	74	12.6	1216	2	Q5TZK8_BRARE	Q5tzk8 brachydanio
122	78	13.2	4599	1	LRPIB_HUMAN	Q9nzt2 homo sapien	195	74	12.6	1254	2	Q90Y56_BRARE	Q90y56 brachydanio
123	77.5	13.2	350	2	Q54EN7_DICDI	Q54en7 dictyosteli	196	74	12.6	1254	2	Q9YHU2_BRARE	Q9yhu2 brachydanio
124	77.5	13.2	473	1	FP2_MYTGA	Q25464 mytilus gal	197	74	12.6	3461	2	Q16KR1_AEDAE	Q16kr1 aedes aegypt
125	77.5	13.2	911	2	Q7ZZT0_BRARE	Q7zzt0 brachydanio	198	74	12.6	4680	2	Q7PV66_ANOGA	Q7pv66 anopheles g
126	77.5	13.2	2559	1	STABQ2_MOUSE	Q7zzt0 mus musculu	199	74	12.6	701	2	Q8AVE8_XENLA	Q8ave8 xenopus lae
127	77	13.1	251	2	Q70LQ4_ENCBU	Q70lq4 enchytraeus	200	73.5	12.5	2146	2	Q4T7A2_TETNG	Q4t7a2 tetraodon n
128	77	13.1	251	2	Q24774_ENCBU	Q24774 enchytraeus	201	73.5	12.5	2715	1	MLL4_HUMAN	Q9umn6 homo sapien
129	77	13.1	693	2	Q505M8_XENLA	Q505m8 xenopus lae	202	73.5	12.5	64	1	TX16_PHORI	P83893 phoneutria
130	77	13.1	762	2	Q8ML23_DROME	Q8ml23 drosoephila	203	73	12.4	172	2	Q8RU50_ORYSA	Q8ru50 oryza sativ
131	77	13.1	1961	2	Q1EC02_DROME	Q1ec02 drosoephila	204	73	12.4	417	2	TNR16_MOUSE	Q920w1 mus musculu
132	77	13.1	3570	2	Q7Q737_ANOGA	Q7q737 anopheles g	205	73	12.4	417	2	Q8BY11_MOUSE	Q8byy1 mus musculu
133	77	13.1	81	2	Q54HP8_DICDI	Q54hpf dictyosteli	206	73	12.4	418	2	Q5ZMNA_CHICK	Q5zmn4 gallus gall
134	76.5	13.0	425	2	Q4R222_MACPA	Q4r222 macaca fasc	207	73	12.4	427	2	Q8CFT3_MOUSE	Q8cft3 mus musculu
135	76.5	13.0	1637	2	Q9XSV8_BOVIN	Q9xsv8 bos taurus	208	73	12.4	457	2	Q8IVS6_HUMAN	Q8ivs6 homo sapien
136	76.5	13.0	5146	1	SSPO_BOVIN	P98167 bos taurus	209	73	12.4	461	2	TNR1B_HUMAN	P20333 h tumor nec
137	76.5	13.0	264	2	Q5HZW5_RAT	Q5hzw5 rattus norv	210	73	12.4	461	2	Q5THJ6_HUMAN	Q5thj6 homo sapien
138	76	12.9	299	2	Q1HDL3_HUMAN	Q1hdl3 homo sapien	211	73	12.4	667	2	Q1WKW9_DROTE	Q1kwk9 drosoephila
139	76	12.9	496	2	Q54L19_DICDI	Q54li9 dictyosteli	212	73	12.4	835	2	Q9RH03_AZOIR	Q9rh03 azospirillu
140	76	12.9	496	2	Q6TMQ0_DICDI	Q6tmj0 dictyosteli	213	73	12.4	1123	2	Q69ZY6_MOUSE	Q69zy6 mus musculu
141	76	12.9	1259	2	Q385C6_9TRYP	Q385c6 trypanosoma	214	73	12.4	2871	1	Q4H346_CIOIN	Q4h346 ciona intes
142	76	12.9	749	2	Q86TP7_HUMAN	Q86tp7 homo sapien	215	73	12.4	3075	1	FEN1_PIG	Q9lv36 sus scrofa
143	75.5	12.8	1099	2	Q60V58_CAEBR	Q60v58 caenorhabdi	216	73	12.4	3857	2	LWAI1_HUMAN	P23391 homo sapien
144	75.5	12.8	1574	1	MEGR6_RAT	Q88x21 rattus norv	217	73	12.4	103	2	Q6Z331_ORYSA	Q6z331 oryza sativ
145	75.5	12.8	1761	2	Q86XN2_HUMAN	Q86xn2 homo sapien	218	73	12.4	315	2	Q9NP01_HUMAN	Q9np01 homo sapien
146	75	12.7	60	2	Q20AU5_CRAGI	Q20a05 crassostrea	219	72.5	12.3	615	2	Q22886_CAEBL	Q22886 caenorhabdi
147	75	12.7	60	2	Q20A06_CRAGI	Q20a06 crassostrea	220	72.5	12.3	986	2	Q1L889_BRARE	Q1l8e9 brachydanio
148	75	12.7	130	2	Q4PMW2_IXOSC	Q4pmw2 ixodes scap	221	72.5	12.3	1269	2	Q1L926_BRARE	Q1l926 brachydanio
149	75	12.7	303	2	Q3TTU9_MOUSE	Q3ttu9 mus musculu	222	72.5	12.3	1365	2	Q7SN88_HUMAN	Q7sn88 homo sapien
150	75	12.7	490	1	TPWS2_MOUSE	Q9jiq8 mus musculu	223	72.5	12.3	1428	2	Q1A5L3_BRARE	Q1a5l3 brachydanio
151	75	12.7	490	2	Q3UKE3_MOUSE	Q3uke3 mus musculu	224	72.5	12.3	1778	2	Q45VP9_DERVA	Q45vp9 dermacentor
152	75	12.7	490	2	Q7TN04_MOUSE	Q7tn04 mus musculu	225	72.5	12.3	2871	1	FEN1_BOVIN	P81333 bos taurus
153	75	12.7	579	2	Q6P2G0_HUMAN	Q6p2g0 homo sapien	226	72.5	12.3	2871	1	FEN1_HUMAN	P35555 homo sapien
154	75	12.7	647	2	Q6P3V5_HUMAN	Q6p3v5 homo sapien	227	72.5	12.3	3277	2	Q6VU67_HUMAN	Q6vu67 homo sapien
155	75	12.7	735	1	ADAM2_HUMAN	Q99965 homo sapien	228	72.5	12.3	3333	2	Q76E14_HUMAN	Q76e14 homo sapien
156	75	12.7	1051	2	Q5U4U1_XENLA	Q5u4u1 xenopus lae	229	72.5	12.3	3333	2	Q6VU68_HUMAN	Q6vu68 homo sapien
157	75	12.7	1214	2	Q90YD2_XENLA	Q90yd2 xenopus lae	230	72.5	12.3	101	2	Q65313_9ROSI	Q65313 lavatera th
158	75	12.7	1581	1	LAMC3_MOUSE	Q9r0b6 mus musculu	231	72	12.2	146	2	Q5K4P7_SCHGR	Q5k4f7 schistocerc
159	75	12.7	1581	1	LAMC3_MOUSE	Q9r0b6 mus musculu	232	72	12.2	269	2	Q4I3B1_GIBEZE	Q4i3b1 gibberella
160	75	12.7	1581	2	Q4VAI3_MOUSE	Q4vai3 mus musculu	233	72	12.2	348	2	Q54KB6_DICDI	Q54kb6 dictyosteli
161	75	12.7	1957	2	Q4SUZ8_TETNG	Q4su28 tetraodon n	234	72	12.2	576	2	Q6YID6_PENMO	Q6yid6 penaeus mon
162	75	12.7	2003	1	NOTC4_HUMAN	Q99466 homo sapien	235	72	12.2	655	2	Q1WKX2_DROER	Q1wxk2 drosoephila
163	75	12.7	2003	2	Q5SPL1_HUMAN	Q5spl1 homo sapien	236	72	12.2	661	2	Q1WKX0_DROSI	Q1wxk0 drosoephila
164	75	12.7	2003	2	Q5SSY7_HUMAN	Q5ssy7 homo sapien	237	72	12.2	661	2	Q1WKX1_DROOR	Q1wxk1 drosoephila
165	75	12.7	2005	2	Q5STG5_HUMAN	Q5stg5 homo sapien	238	72	12.2	665	2	Q1WKX1_DROOR	Q1wxk1 drosoephila
166	75	12.7	2318	1	NOTC3_MOUSE	Q61982 mus musculu	239	72	12.2	682	2	Q1WKW8_DROYA	Q1wkw8 drosoephila
167	75	12.7	2319	1	NOTC3_RAT	Q9r172 rattus norv	240	72	12.2	1361	2	Q9NGV2_DROME	Q9ngv2 drosoephila
168	75	12.7	2531	2	Q16004_LYTVA	O16004 lytechinus	241	72	12.2	1361	2	Q9V714_DROME	Q9v714 drosoephila
169	75	12.7	2884	2	Q4SHN1_TETNG	Q4shn1 tetraodon n	242	72	12.2	1639	2	LAMC1_DROME	P15215 drosoephila
170	75	12.7	3667	2	Q29F13_DROPS	Q29f13 drosoephila	243	72	12.2	1639	2	Q5BI30_DROME	Q5bi30 drosoephila
171	74.5	12.6	104	2	Q7XZ46_GRIJA	Q7xz46 griffithsia	244	72	12.2	170	2	Q5ZVJ8_CTOIN	Q5zvj8 ciona intes
172	74.5	12.6	113	1	COL_MOUSE	Q9cqc2 mus musculu	245	71.5	12.1	453	2	Q64767_ADEG1	Q64767 avian adeno
173	74.5	12.6	190	2	Q4T7E9_TETNG	Q4t7e9 tetraodon n	246	71.5	12.1	466	2	Q1XBT7_MYTED	Q1xibt7 mytilus edu
174	74.5	12.6	194	2	Q4SIA7_TETNG	Q4sia7 tetraodon n	247	71.5	12.1	591	1	GRN_CAVPO	P28797 cavia porce
175	74.5	12.6	286	2	Q7R5C8_GIALA	Q7r5c8 giardia lam	248	71.5	12.1	638	2	Q8NBH6_HUMAN	Q8nbh6 homo sapien
176	74.5	12.6	387	2	Q4KLX7_XENLA	Q4klx7 xenopus lae	249	71.5	12.1	703	1	FBLN1_HUMAN	P23142 homo sapien
177	74.5	12.6	387	2	Q9PVD4_XENLA	Q9pvd4 xenopus lae	250	71.5	12.1				

251	71.5	12.1	1064	2	Q2HD56_CHAGB	Q2hd56 chaetomium	324	69.5	11.8	1147	2	Q3TLU3_MOUSE	Q3tlu3 mus musculus
252	71.5	12.1	1170	1	TSP2_BOVIN	Q95116 bos taurus	325	69.5	11.8	2352	2	Q61240_HALRO	Q61240 halocynthia
253	71.5	12.1	1178	1	TSP2_CHICK	P35440 gallus galli	326	69.5	11.8	2653	2	Q25253_LUCCU	Q25253 laccalia cup
254	71.5	12.1	1285	1	CRUM2_HUMAN	Q51j48 homo sapien	327	69.5	11.8	4545	2	Q912X7_MOUSE	Q912x7 mus musculus
255	71.5	12.1	1466	2	Q1A512_BRARE	Q1a512 brachydanio	328	69.5	11.8	4545	2	Q920V4_MOUSE	Q920v4 mus musculus
256	71.5	12.1	1519	2	Q8WPN0_OIKDI	Q8wpn0 oikopleura	329	69.5	11.8	4545	2	Q61291_MOUSE	Q61291 mus musculus
257	71.5	12.1	1744	2	Q8CHH1_MOUSE	Q8chh1 mus musculus	330	69	11.7	106	2	Q3QA05_ORYSA	Q3qa05 oryza sativ
258	71.5	12.1	1809	1	F1VL_DROME	Q96838 drosophila	331	69	11.7	217	2	Q7XZ34_GRIJA	Q7xz34 griffithsia
259	71.5	12.1	2013	2	Q6PHU4_MOUSE	Q6phu4 mus musculus	332	69	11.7	220	1	UPAS_RAT	P51573 rattus norv
260	71.5	12.1	2713	2	Q5NUO9_MOUSE	Q5nuo9 mus musculus	333	69	11.7	220	1	UPAS_RAT	P51573 rattus norv
261	71.5	12.1	3652	1	Q16PL9_AEDA	Q16pl9 aedes aegyp	334	69	11.7	294	2	Q8IRV4_DROME	Q8irv4 drosophila
262	71	12.1	286	2	Q7JMU0_MELIC	Q7jmu0 meloidogyne	335	69	11.7	328	1	UPAR_RAT	P49616 rattus norv
263	71	12.1	288	2	Q5RIP8_BRARE	Q5rip8 brachydanio	336	69	11.7	388	2	Q66JK7_XENTR	Q66jk7 xenopus tro
264	71	12.1	305	2	Q25467_MELIC	Q25467 meloidogyne	337	69	11.7	403	2	Q4R3X4_MACFA	Q4r3x4 macaca fasc
265	71	12.1	438	2	Q53Y88_HUMAN	Q53y88 homo sapien	338	69	11.7	611	2	Q4SZZ8_TETNG	Q4szz8 tetraodon n
266	71	12.1	442	2	Q55GL3_DICDI	Q55gl3 dictyosteli	339	69	11.7	949	2	Q3V7A7_9PRIM	Q3v7a7 macaca fusc
267	71	12.1	457	2	Q8TEC5_HUMAN	Q8tec5 homo sapien	340	69	11.7	1599	2	Q616G7_CAEBR	Q616g7 caenorhabdi
268	71	12.1	587	2	Q2HJ16_BOVIN	Q2hj16 bos taurus	341	69	11.7	1976	2	Q59ES6_HUMAN	Q59es6 homo sapien
269	71	12.1	593	1	GRN_HUMAN	P28799 h granulins	342	69	11.7	2360	2	Q7YZP0_EINMA	Q7yzp0 eimeria max
270	71	12.1	593	2	Q540U8_HUMAN	Q540u8 homo sapien	343	69	11.7	2911	1	FBN2_HUMAN	P35556 homo sapien
271	71	12.1	593	2	Q53HQ8_HUMAN	Q53hq8 homo sapien	344	69	11.7	3133	1	HMCT_BOMMO	P98092 bombyx mori
272	71	12.1	719	2	Q1CX64_MYXXA	Q1cx64 myxococcus	345	68.5	11.6	3712	1	LAMA_DROME	Q00174 drosophila
273	71	12.1	1379	2	Q59H72_HUMAN	Q59h72 homo sapien	346	68.5	11.6	143	2	Q330K6_TRIMU	Q330k6 trimeresuru
274	71	12.1	1568	2	Q5VUP0_HUMAN	Q5vup0 homo sapien	347	68.5	11.6	182	2	Q307E7_SHEEP	Q307e7 ovis aries
275	71	12.1	1587	1	LAMC3_HUMAN	Q9vup0 homo sapien	348	68.5	11.6	295	2	Q9NEG3_DROME	Q9neg3 drosophila
276	71	12.1	1587	2	Q5VUP1_HUMAN	Q5vup1 homo sapien	349	68.5	11.6	328	2	Q8MQG3_CAEBL	Q8mqg3 caenorhabdi
277	71	12.1	1624	2	Q17AS8_AEDA	Q17as8 aedes aegyp	350	68.5	11.6	333	2	Q3HTT8_CANFA	Q3htt8 canis fami
278	71	12.1	1637	2	Q29CY8_DROPS	Q29cy8 drosophila	351	68.5	11.6	369	2	Q565Y9_9BACT	Q565y9 uncultured
279	71	12.1	2359	2	Q59FC2_HUMAN	Q59fc2 homo sapien	352	68.5	11.6	469	2	Q5BLE3_BRARE	Q5ble3 brachydanio
280	70.5	12.0	172	2	Q19QV7_9CNIID	Q19qv7 nematostell	353	68.5	11.6	587	2	Q3QVQ5_PROAE	Q3qvq5 prosthecoch
281	70.5	12.0	239	2	Q1FAJ6_9CHLR	Q1faj6 roseiflexus	354	68.5	11.6	598	1	FBLN1_CERAB	Q8mj39 cercopithec
282	70.5	12.0	287	2	Q75212_BRARE	Q75212 brachydanio	355	68.5	11.6	671	2	Q6BET7_CAEBL	Q6bet7 caenorhabdi
283	70.5	12.0	444	2	Q6QW08_AZOB	Q6qw08 azospirillu	356	68.5	11.6	708	2	Q7F803_ORYSA	Q7f803 oryza sativ
284	70.5	12.0	490	2	Q6P7D7_RAT	Q6p7d7 rattus norv	357	68.5	11.6	726	2	Q9AW87_CYNPY	Q9aw87 cynops pyrr
285	70.5	12.0	555	2	Q4RN57_TETNG	Q4rn57 tetraodon n	358	68.5	11.6	728	2	Q90656_CHICK	Q90656 gallus gall
286	70.5	12.0	701	2	Q4T4W9_TETNG	Q4t4w9 tetraodon n	359	68.5	11.6	850	2	Q04384_BRAOL	Q04384 brassica ol
287	70.5	12.0	1063	2	Q7QU10_GIALA	Q7qu10 giardia lam	360	68.5	11.6	894	2	Q17429_CAEBL	Q17429 caenorhabdi
288	70.5	12.0	1212	2	Q42347_CHICK	Q42347 gallus galli	361	68.5	11.6	898	2	Q8MQG2_CAEBL	Q8mqg2 caenorhabdi
289	70.5	12.0	1847	2	Q76952_AEDA	Q76952 aedes aegyp	362	68.5	11.6	909	2	Q5ZEL8_ORYSA	Q5zel8 oryza sativ
290	70.5	12.0	1847	2	Q171G8_AEDA	Q171g8 aedes aegyp	363	68.5	11.6	931	2	Q61FT4_CAEBR	Q61ft4 caenorhabdi
291	70.5	12.0	1847	2	Q16GY3_AEDA	Q16gy3 aedes aegyp	364	68.5	11.6	960	2	Q8MM07_CAEBL	Q8mm07 caenorhabdi
292	70.5	12.0	2871	1	FBN1_MOUSE	Q61554 mus musculu	365	68.5	11.6	969	2	Q8IV28_HUMAN	Q8iv28 homo sapien
293	70.5	12.0	2872	2	Q9WUH8_RAT	Q9wuh8 rattus norv	366	68.5	11.6	1172	1	TSP2_MOUSE	Q7tmt3 mus musculu
294	70	11.9	68	1	TX16_PHONI	P83997 phoneutria	367	68.5	11.6	1172	2	Q8CG21_MOUSE	Q8cg21 mus musculu
295	70	11.9	92	2	Q2MCN5_HYDMA	Q2mcn5 hydra magni	368	68.5	11.6	1180	2	Q5CZ12_HUMAN	Q5cz12 homo sapien
296	70	11.9	315	2	Q56JU1_CANFA	Q56jj1 canis fami	369	68.5	11.6	1375	1	NID2_HUMAN	Q14112 homo sapien
297	70	11.9	399	2	Q2E3D9_ACICE	Q2e3d9 acidothermu	370	68.5	11.6	1801	2	Q8WSJ2_BOMMO	Q8wsj2 bombyx mori
298	70	11.9	426	2	Q6TMJ6_DICDI	Q6tmj6 dictyosteli	371	68.5	11.6	1827	2	Q8JHV6_BRARE	Q8jhw6 brachydanio
299	70	11.9	426	2	Q55FY2_DICDI	Q55fy2 dictyosteli	372	68.5	11.6	1838	2	Q28XF3_DROPS	Q28xf3 drosophila
300	70	11.9	460	2	Q5SY22_HUMAN	Q5sy22 homo sapien	373	68.5	11.6	1952	2	Q95SN5_DROME	Q95sn5 drosophila
301	70	11.9	490	2	Q920K3_RAT	Q920k3 rattus norv	374	68.5	11.6	4547	2	Q9W343_DROME	Q9w343 drosophila
302	70	11.9	706	2	Q4H3Q7_CIOIN	Q4h3q7 ciona intes	375	68	11.5	112	1	COL_CANFA	P19090 canis fami
303	70	11.9	729	2	Q7T3M4_BRARE	Q7t3m4 brachydanio	376	68	11.5	113	2	Q5T5G1_HUMAN	Q5t5g1 homo sapien
304	70	11.9	729	2	Q4V9K5_BRARE	Q4v9k5 brachydanio	377	68	11.5	314	2	Q5XTR8_MACMU	Q5xtr8 macaca mula
305	70	11.9	750	2	Q4RQ92_TETNG	Q4rq92 tetraodon n	378	68	11.5	345	2	Q7JKP2_CAEBL	Q7jkp2 caenorhabdi
306	70	11.9	841	1	TS1R1_HUMAN	Q7rtx1 homo sapien	379	68	11.5	358	2	Q9U362_CAEBL	Q9u362 caenorhabdi
307	70	11.9	947	2	Q8BK7_MOUSE	Q8bk7 mus musculu	380	68	11.5	427	1	TNR16_HUMAN	P08138 homo sapien
308	70	11.9	950	2	Q802C1_XENLA	Q802c1 xenopus lae	381	68	11.5	448	2	Q2GPN1_CHAGB	Q2gpn1 chaetomium
309	70	11.9	1140	2	Q80T91_MOUSE	Q80t91 mus musculu	382	68	11.5	489	1	MA2A1_RAT	P28494 rattus norv
310	70	11.9	1790	2	Q55F41_DICDI	Q55f41 dictyosteli	383	68	11.5	497	2	Q4AQCI_9CHLB	Q4aqci chlorobium
311	70	11.9	2428	2	Q816X6_BOOMI	Q816x6 boophilus m	384	68	11.5	586	1	UL84_HCMVA	P16727 human cytom
312	69.5	11.8	89	2	Q5D232_HADSP	Q5d232 hadronyche	385	68	11.5	586	2	Q6RXF3_HCMV	Q6rxf3 human cytom
313	69.5	11.8	111	2	Q4PN79_IXOSC	Q4pn79 ixodes scap	386	68	11.5	587	2	Q6SW58_HCMV	Q6sw58 human cytom
314	69.5	11.8	113	2	Q8MKJ5_DROME	Q8mkj5 drosophila	387	68	11.5	593	2	Q4R529_MACFA	Q4r529 macaca fasc
315	69.5	11.8	123	2	Q3XNW9_9PROT	Q3xnw9 magnetococc	388	68	11.5	677	2	Q4T3P3_TETNG	Q4t3p3 tetraodon n
316	69.5	11.8	413	2	Q9H8S1_HUMAN	Q9h8s1 homo sapien	389	68	11.5	729	2	Q6GPT6_XENLA	Q6gpt6 xenopus lae
317	69.5	11.8	540	2	Q4CXJ4_TRYCR	Q4cxj4 trypanosoma	390	68	11.5	794	2	Q8T4P0_LYTVA	Q8t4p0 lytechinus
318	69.5	11.8	551	2	Q61MD2_CAEBR	Q61md2 caenorhabdi	391	68	11.5	893	2	Q9Y1Y3_9METZ	Q9y1y3 ephydatia f
319	69.5	11.8	587	2	Q61T62_CAEBR	Q61t62 caenorhabdi	392	68	11.5	944	2	Q4SLY2_TETNG	Q4sly2 tetraodon n
320	69.5	11.8	802	2	Q7JL02_CAEBL	Q7jl02 caenorhabdi	393	68	11.5	964	2	Q4STC1_TETNG	Q4stc1 tetraodon n
321	69.5	11.8	818	2	Q4V7B3_RAT	Q4v7b3 rattus norv	394	68	11.5	1090	2	Q5SPG5_BRARE	Q5spg5 brachydanio
322	69.5	11.8	847	2	Q90W12_ONCMY	Q90w12 oncorhynch	395	68	11.5	1119	2	Q18034_CAEBL	Q18034 caenorhabdi
323	69.5	11.8	949	2	P90956_CAEBL	P90956 caenorhabdi	396	68	11.5	1150	1	MA2A1_MOUSE	P27046 mus musculu

397	11.5	1984	1	YL DROME	P98163 drosophila	470	66.5	11.3	480	2	Q34XA1_9GAMM	Q34xa1 alkallimmi
398	68	2906	2	Q9WU9 RAT	P93450 rattus norv	471	66.5	11.3	511	1	Q6IN42 RAT	Q6in42 rattus norv
399	68	5147	1	FAT DROME	P33450 drosophila	472	66.5	11.3	588	1	GRN RAT	P23785 r granulin
400	67.5	11.5	1	LCE2D HUMAN	Q5ta82 homo sapien	473	66.5	11.3	589	1	GRN MOUSE	P28798 mus musculus
401	67.5	200	2	Q7PWE6 ANOGA	Q7pw6e anopheles g	474	66.5	11.3	589	2	Q3TX66 MOUSE	Q3tx66 mus musculus
402	67.5	269	2	Q583F5 9TRYF	Q583f5 trypanosoma	475	66.5	11.3	589	2	Q3TVQ3 MOUSE	Q3tvq3 mus musculus
403	67.5	395	2	Q941Y3 ORYSA	Q941y3 oryza sativ	476	66.5	11.3	589	2	Q3UC19 MOUSE	Q3uc19 mus musculus
404	67.5	358	2	Q5TV39 ANOGA	Q5tv39 anopheles g	477	66.5	11.3	589	2	Q544Y8 MOUSE	Q544y8 m adult mal
405	67.5	413	2	Q6ZP14 HUMAN	Q6zpl4 homo sapien	478	66.5	11.3	593	2	Q3U9K2 MOUSE	Q3u9k2 mus musculus
406	67.5	442	2	Q6ZP14 HUMAN	Q6zpl4 homo sapien	479	66.5	11.3	597	2	Q54X44 DICDI	Q54x44 dictyosteli
407	67.5	442	2	Q6ZP14 HUMAN	Q6zpl4 homo sapien	480	66.5	11.3	602	2	Q3U9N4 MOUSE	Q3u9n4 m bone marr
408	67.5	443	2	Q2TAU8 XENLA	Q2tau8 xenopus lae	481	66.5	11.3	602	2	Q3U9N4 MOUSE	Q3u9n4 m bone marr
409	67.5	509	2	Q4SU37 TETNG	Q4su37 tetraodon n	482	66.5	11.3	602	2	Q3U5Q6 MOUSE	Q3u5q6 mus musculus
410	67.5	576	2	Q9Y3V7 HUMAN	Q9y3v7 homo sapien	483	66.5	11.3	602	2	Q3U8W3 MOUSE	Q3u8w3 mus musculus
411	67.5	608	2	Q627A0 CAERH	Q627a0 caenorhabdi	484	66.5	11.3	602	2	Q3U8W3 MOUSE	Q3u8w3 mus musculus
412	67.5	793	2	Q16MF7 AEDAE	Q16mf7 aedes aegyp	485	66.5	11.3	674	1	Q8TAN9 STRPU	Q8tan9 strongyloce
413	67.5	884	2	Q7QT01 GIALA	Q7qt01 giardia lam	486	66.5	11.3	714	1	DL11 RAT	P97677 rattus norv
414	67.5	892	2	Q178R8 AEDAE	Q178r8 aedes aegyp	487	66.5	11.3	907	2	Q4R1B4 LEUMA	Q4r1b4 leucophaea
415	67.5	895	2	Q9LX29 ARATH	Q9lx29 arabidopsis	488	66.5	11.3	949	1	PCDAB PANTR	Q5drf3 pan troglod
416	67.5	896	2	Q16Q03 AEDAE	Q16q03 aedes aegyp	489	66.5	11.3	996	2	Q16ZG2 AEDAE	Q16zg2 aedes aegyp
417	67.5	1068	2	Q6QHS4 STRPU	Q6qhs4 strongyloce	490	66.5	11.3	1045	2	Q8T3A6 CAEEL	Q8t3a6 caenorhabdi
418	67.5	1184	1	FBLN2 HUMAN	P98095 homo sapien	491	66.5	11.3	1070	2	Q8T3A7 CAEEL	Q8t3a7 caenorhabdi
419	67.5	1184	2	Q86V58 HUMAN	Q86v58 homo sapien	492	66.5	11.3	1070	2	Q8T3A7 CAEEL	Q8t3a7 caenorhabdi
420	67.5	1231	2	Q8IUI0 HUMAN	Q8iui0 homo sapien	493	66.5	11.3	1111	2	Q9XW66 CAEEL	Q9xw66 caenorhabdi
421	67.5	1231	2	Q8IUI1 HUMAN	Q8iui1 homo sapien	494	66.5	11.3	1111	2	Q9XW66 CAEEL	Q9xw66 caenorhabdi
422	67.5	1294	2	Q8C622 MOUSE	Q8c622 mus musculu	495	66.5	11.3	1174	2	Q3TGL4 MOUSE	Q3tgl4 mus musculu
423	67.5	1356	2	Q4N8M7 THEPA	Q4n8m7 theileria p	496	66.5	11.3	1174	2	Q3TGL4 MOUSE	Q3tgl4 mus musculu
424	67.5	1403	1	NID2 MOUSE	Q88322 mus musculu	497	66.5	11.3	1221	1	PBLN2 MOUSE	P37889 mus musculu
425	67.5	1403	2	Q3TPN0 MOUSE	Q3tpn0 mus musculu	498	66.5	11.3	1444	2	Q6A051 MOUSE	Q6a051 mus musculu
426	67.5	1403	2	Q3U545 MOUSE	Q3u545 mus musculu	499	66.5	11.3	1713	2	Q5RH37 BRARE	Q5rh37 brachydanio
427	67.5	1403	2	Q7TOF0 MOUSE	Q7tqf0 mus musculu	500	66.5	11.3	1732	2	Q1LY17 BRARE	Q1ly17 brachydanio
428	67.5	1403	2	Q8CPA3 MOUSE	Q8cpa3 mus musculu	501	66.5	11.3	1945	2	Q4RQ96 TETNG	Q4rq96 tetraodon n
429	67.5	1403	2	Q8R5G0 MOUSE	Q8r5g0 mus musculu	502	66.5	11.3	3224	2	Q4RVG6 TETNG	Q4rvg6 tetraodon n
430	67.5	1504	1	SLIT DROME	P24014 drosophila	503	66	11.2	5179	1	MUC2 HUMAN	Q02817 homo sapien
431	67.5	1687	2	Q6K1204 MOUSE	Q6k1204 mus musculu	504	66	11.2	64	1	CX13 CONIM	P69497 conus imper
432	67.5	1751	2	Q4SK18 TETNG	Q4sk18 tetraodon n	505	66	11.2	85	1	Q59AA9 CONIM	Q59aa9 conus imper
433	67.5	4525	2	Q16UK9 AEDAE	Q16uk9 aedes aegyp	506	66	11.2	94	2	HPCP MORCS	P82951 caenorhabdi
434	67.5	4699	2	Q3V383 DROME	Q3v383 drosophila	507	66	11.2	149	2	Q1XF21 CAEEL	Q1xf21 caenorhabdi
435	67.5	23015	2	Q8IQ18 DROME	Q8iq18 drosophila	508	66	11.2	174	2	Q8GA35 ECOLI	Q8ga35 escherichia
436	67.5	237	1	Q2CGN9 9RHOB	Q2cgn9 oceanicola	509	66	11.2	208	2	Q9N2N0 BOMMO	Q9n2n0 bombyx mori
437	67.5	237	1	ALG14 YEAST	P38242 saccharomyc	510	66	11.2	234	2	Q8K6H7 ORYSA	Q8k6h7 oryza sativ
438	67.5	328	2	Q35771 RAT	Q35771 rattus norv	511	66	11.2	258	2	Q7QG12 ANOGA	Q7qg12 anopheles g
439	67.5	371	2	Q5U215 RAT	Q5u215 rattus norv	512	66	11.2	274	2	Q7Q953 ANOGA	Q7q953 anopheles g
440	67.5	463	2	Q88QF3 LITFO	Q88qf3 lithobius f	513	66	11.2	350	2	Q6NCDB RHOPA	Q6ncdb rhodopseudo
441	67.5	473	2	Q3TS72 MOUSE	Q3ts72 mus musculu	514	66	11.2	399	2	Q1D2N0 WYXXA	Q1d2n0 myxococcus
442	67.5	495	2	Q54QC5 DICDI	Q54qc5 dictyosteli	515	66	11.2	488	2	Q29GV6 DROPS	Q29gv6 drosophila
443	67.5	601	2	Q1RMN3 BOVIN	Q1rmn3 bos taurus	516	66	11.2	722	2	Q7R168 GIALA	Q7r168 giardia lam
444	67.5	724	2	Q4ZJ75 XENLA	Q4zj75 xenopus lae	517	66	11.2	724	2	Q32NV6 XENLA	Q32nv6 xenopus lae
445	67.5	885	2	Q7R1C5 GIALA	Q7r1c5 giardia lam	518	66	11.2	728	2	Q54DV5 DICDI	Q54dv5 dictyosteli
446	67.5	993	1	EPHB3 MOUSE	P54754 mus musculu	519	66	11.2	792	2	Q90Z43 CHICK	Q90z43 gallus gall
447	67.5	993	2	Q91Y89 MOUSE	Q91y89 mus musculu	520	66	11.2	898	2	Q60UE2 CAEEL	Q60ue2 caenorhabdi
448	67.5	1050	2	Q71G60 RSIV	Q71g60 red sea bre	521	66	11.2	1057	2	Q4N4P8 THEPA	Q4n4p8 theileria p
449	67.5	1172	1	TSP2 HUMAN	P35442 homo sapien	522	66	11.2	1062	2	Q3UG73 MOUSE	Q3ug73 mus musculu
450	67.5	1172	2	Q5R152 HUMAN	Q5r152 homo sapien	523	66	11.2	1095	2	Q90XG4 CHICK	Q90xg4 gallus gall
451	67.5	1193	2	Q90819 CHICK	Q90819 gallus gall	524	66	11.2	1140	2	Q68DE5 HUMAN	Q68de5 homo sapien
452	67.5	1218	1	JAG1 MOUSE	Q9qxo0 mus musculu	525	66	11.2	1140	2	Q96KG7 HUMAN	Q96kg7 homo sapien
453	67.5	1218	2	Q3UVN4 MOUSE	Q3uvn4 mus musculu	526	66	11.2	1147	2	Q6DIB5 MOUSE	Q6dib5 mus musculu
454	67.5	1219	1	JAG1 RAT	Q63722 rattus norv	527	66	11.2	1238	1	JAG2 HUMAN	Q9y219 homo sapien
455	67.5	1229	1	MEGF6 HUMAN	Q75095 homo sapien	528	66	11.2	1327	1	Y2006 MYCTU	Q10850 mycobacteri
456	67.5	1289	2	Q59FL3 HUMAN	Q59fl3 homo sapien	529	66	11.2	1327	2	Q7TZ61 MYCBO	Q7tz61 mycobacteri
457	67.5	1640	2	QACB8 HUMAN	Q4ac86 homo sapien	530	66	11.2	1416	2	Q39WC4 GROMG	Q39wc4 geobacter m
458	67.5	1722	2	Q19350 CAEEL	Q19350 caenorhabdi	531	66	11.2	1523	1	SLIT3 MOUSE	Q3uhn1 mus musculu
459	67.5	2225	2	Q571J3 MOUSE	Q571j3 mus musculu	532	66	11.2	1523	2	Q3UHN1 MOUSE	Q3uhn1 mus musculu
460	67.5	2321	1	NOTC1 HUMAN	Q9um47 homo sapien	533	66	11.2	1523	2	Q5SS56 MOUSE	Q5ss56 mus musculu
461	67.5	2437	1	NOTC1 BRARE	P46530 brachydanio	534	66	11.2	1743	2	Q9XW55 CAEEL	Q9xw55 caenorhabdi
462	67.5	2825	2	Q70465 MOUSE	Q70465 mus musculu	535	66	11.2	1914	2	Q499U7 RAT	Q499u7 rattus norv
463	67.5	2907	1	FN2 MOUSE	Q61555 mus musculu	536	66	11.2	2289	2	Q4S3T6 TETNG	Q4s3t6 tetraodon n
464	66.5	84	2	Q5D231 HADSP	Q5d231 hadronyche	537	66	11.2	2378	2	Q4RW31 TETNG	Q4rw31 tetraodon n
465	66.5	98	1	KRA33 HUMAN	Q9byr6 homo sapien	538	66	11.2	2809	1	FN3 HUMAN	Q75n90 homo sapien
466	66.5	98	2	Q6NTD4 HUMAN	Q6ntd4 homo sapien	539	66	11.2	5374	2	Q99ND0 MOUSE	Q99nd0 mus musculu
467	66.5	170	2	Q2BNK4 9GAMM	Q2bnk4 oceanospiri	540	66	11.2	99	2	Q9D7P0 MOUSE	Q9d7p0 mus musculu
468	66.5	287	2	Q81PJ1 DROME	Q81pj1 drosophila	541	65.5	11.1	99	2	Q9CPW1 MOUSE	Q9cpw1 m adult mal
469	66.5	362	2	Q72B35 DRSVH	Q72b35 desulfovibr	542	65.5	11.1	99	2	Q9CPW1 MOUSE	Q9cpw1 m adult mal
470	66.5	462	2	Q3UDD6 MOUSE	Q3udd6 mus musculu							

543	65.5	11.1	110	1	LCE2B_HUMAN	O14633	homo sapien	616	65	11.0	263	2	O99740_HUMAN	O99740	homo sapien
544	65.5	11.1	110	1	LCE2C_HUMAN	O5ta81	homo sapien	617	65	11.0	289	2	O1PG03_HYDSY	O1PG03	hydractinia
545	65.5	11.1	110	2	Q5TA90_HUMAN	Q5ta80	homo sapien	618	65	11.0	289	2	O1PG01_HYDSY	O1PG01	hydractinia
546	65.5	11.1	110	2	Q4PMX5_ORYSA	Q4pmx5	ixodes scap	619	65	11.0	289	2	O1PG29_HYDSY	O1PG29	hydractinia
547	65.5	11.1	113	2	Q8H3W9_ORYSA	Q8h3w9	oryza sativ	620	65	11.0	289	2	O1PG16_HYDSY	O1PG16	hydractinia
548	65.5	11.1	176	2	Q4V4J0_DROME	Q4v4j0	drosophila	621	65	11.0	289	2	O1PG00_HYDSY	O1PG00	hydractinia
549	65.5	11.1	208	2	Q4DH08_TRYCR	Q4dh08	trypanosoma	622	65	11.0	289	2	O1PG02_HYDSY	O1PG02	hydractinia
550	65.5	11.1	208	2	Q4CWR8_TRYCR	Q4cwr8	trypanosoma	623	65	11.0	289	2	O1PG10_HYDSY	O1PG10	hydractinia
551	65.5	11.1	230	2	Q5VTG9_HUMAN	Q5vtg9	homo sapien	624	65	11.0	289	2	O1PG05_HYDSY	O1PG05	hydractinia
552	65.5	11.1	236	2	Q8WUQ9_HUMAN	Q8wuq9	homo sapien	625	65	11.0	302	1	CHI4_SOLTU	P52406	solanum tub
553	65.5	11.1	236	2	Q7Z3S9_HUMAN	Q7z3s9	homo sapien	626	65	11.0	306	2	Q2KJ78_BOVIN	Q2k78	bos taurus
554	65.5	11.1	244	2	Q2Y7J9_NITMU	Q2y7j9	nitrospir	627	65	11.0	315	2	Q4U3E1_HUMAN	Q4u3e1	homo sapien
555	65.5	11.1	249	2	Q5BKT8_HUMAN	Q5bkt8	homo sapien	628	65	11.0	320	2	O9PUK3_CHICK	O9puK3	gallus gall
556	65.5	11.1	254	2	Q5UCC6_HUMAN	Q5ucc6	homo sapien	629	65	11.0	322	2	O2OCF5_PETMA	Q2ocf5	petromyzon
557	65.5	11.1	256	1	F5TLI3_MOUSE	Q9eqc7	mus musculus	630	65	11.0	329	2	O8I145_SOLTU	O8i145	solanum tub
558	65.5	11.1	256	2	Q542M9_MOUSE	Q542m9	mus musculus	631	65	11.0	329	2	O8I144_SOLTU	O8i144	solanum tub
559	65.5	11.1	262	2	Q8N541_HUMAN	Q8n541	homo sapien	632	65	11.0	362	2	O9PVN4_CHICK	O9pvN4	gallus gall
560	65.5	11.1	262	2	Q5UCC4_HUMAN	Q5ucc4	homo sapien	633	65	11.0	379	2	O7SKV0_BRARE	O7skv0	brachydanio
561	65.5	11.1	266	2	Q86YL4_HUMAN	Q86yl4	homo sapien	634	65	11.0	383	2	Q969Y6_HUMAN	Q969y6	homo sapien
562	65.5	11.1	269	2	Q6UWP3_HUMAN	Q6uwp3	homo sapien	635	65	11.0	400	2	Q22B14_TETTH	Q22b14	tetrahymena
563	65.5	11.1	269	2	Q8NC23_HUMAN	Q8nc23	homo sapien	636	65	11.0	426	2	O8I499_CUPSA	O8i499	cupienius
564	65.5	11.1	323	2	Q4Q266_LEIMA	Q4q266	leishmania	637	65	11.0	433	2	Q3V346_MOUSE	Q3v346	mus musculus
565	65.5	11.1	337	2	Q8NHD3_HUMAN	Q8nhd3	homo sapien	638	65	11.0	448	2	O9I2M6_RAT	O9i2m6	rattus norv
566	65.5	11.1	342	2	Q6P192_HUMAN	Q6p192	homo sapien	639	65	11.0	448	2	O8P7W2_XANCP	O8p7w2	xanthomonas
567	65.5	11.1	342	2	Q8NHD5_HUMAN	Q8nhd5	homo sapien	640	65	11.0	461	2	Q6VAU8_RAT	Q6vaU8	rattus norv
568	65.5	11.1	343	2	Q5XG84_HUMAN	Q5xg84	homo sapien	641	65	11.0	474	1	TNR1B_RAT	Q80wy6	rattus norv
569	65.5	11.1	343	2	Q42607_XENLA	Q42607	xenopus lae	642	65	11.0	474	2	Q5YLP0_RAT	Q5yLp0	rattus norv
570	65.5	11.1	356	2	Q96FY1_HUMAN	Q96fy1	homo sapien	643	65	11.0	474	2	Q2WV02_CLOBE	Q2wv02	clostridium
571	65.5	11.1	363	2	Q4AL35_9CHLB	Q4al35	chlorobium	644	65	11.0	531	1	PKLL1_MOUSE	PKll1	rhizobium l
572	65.5	11.1	409	2	Q3TV46_MOUSE	Q3tv46	mus musculus	645	65	11.0	647	2	Q1M7N7_RHIL3	Q1m7n7	rhizobium l
573	65.5	11.1	410	2	Q171B0_AEDAE	Q171b0	aedes aegypt	646	65	11.0	773	2	Q53TLO_HUMAN	Q53tlo	homo sapien
574	65.5	11.1	433	2	Q7ZX39_XENLA	Q7zx39	xenopus lae	647	65	11.0	823	2	Q80V13_MOUSE	Q80v13	mus musculus
575	65.5	11.1	438	2	Q6INJ1_XENLA	Q6inj1	xenopus lae	648	65	11.0	1218	1	JAG1_HUMAN	JAG1	homo sapien
576	65.5	11.1	459	2	Q62327_MOUSE	Q62327	mus musculus	649	65	11.0	1295	1	GLP1_MOUSE	GLP1	caenorhabdi
577	65.5	11.1	474	2	Q3U2A9_MOUSE	Q3u2a9	mus musculus	650	65	11.0	2107	2	Q297B9_DROPS	Q297b9	drosophila
578	65.5	11.1	516	2	Q60S84_CAEBR	Q60s84	caenorhabdi	651	65	11.0	2146	1	CRB_DROME	P10040	drosophila
579	65.5	11.1	546	2	Q3UYW9_MOUSE	Q3uyw9	mus musculus	652	65	11.0	2524	1	Q9GPA5_BRAFL	Q9gpa5	branchiosto
580	65.5	11.1	569	2	Q8NHD4_HUMAN	Q8nhd4	homo sapien	653	65	11.0	2524	2	Q9GPA5_BRAFL	Q9gpa5	branchiosto
581	65.5	11.1	589	2	Q3TW74_MOUSE	Q3tw74	mus musculus	654	65	11.0	3447	2	Q4DJJ6_TRYCR	Q4dja6	trypanosoma
582	65.5	11.1	602	2	Q3UAD3_MOUSE	Q3uaj3	mus musculus	655	65	11.0	3467	2	Q4D2A3_TRYCR	Q4d2a3	trypanosoma
583	65.5	11.1	602	2	Q3UD85_MOUSE	Q3ud85	mus musculus	656	65	11.0	3481	2	Q4DJK2_TRYCR	Q4djK2	trypanosoma
584	65.5	11.1	656	1	MSGF6_MOUSE	Q80v70	mus musculus	657	65	11.0	3481	2	Q4DNCO_TRYCR	Q4dnco	trypanosoma
585	65.5	11.1	722	1	DLL1_MOUSE	Q61483	mus musculus	658	65	11.0	4599	1	LRP1B_MOUSE	LRP1b	mus musculus
586	65.5	11.1	722	2	Q6PFV7_MOUSE	Q6pfv7	mus musculus	659	65	11.0	4655	1	LRP2_HUMAN	P98164	homo sapien
587	65.5	11.1	744	2	Q8NHD2_HUMAN	Q8nhd2	homo sapien	660	65	11.0	4655	2	Q725C0_HUMAN	Q725c0	homo sapien
588	65.5	11.1	768	2	Q36581_9RETR	Q36581	multiple sc	661	65	11.0	4655	2	Q725C1_HUMAN	Q725c1	homo sapien
589	65.5	11.1	804	2	Q3UK93_MOUSE	Q3uk95	mus musculus	662	65	11.0	90	2	Q5T9G3_HUMAN	Q5t9g3	homo sapien
590	65.5	11.1	818	2	Q8CCS9_MOUSE	Q8ccs9	mus musculus	663	65	11.0	98	1	KRA32_HUMAN	Q8mrx1	caerostriis
591	65.5	11.1	826	2	Q16Q60_AEDAE	Q9dbc8	mus musculus	664	64.5	11.0	102	1	TXCA_CAEBR	Q6zr78	homo sapien
592	65.5	11.1	830	1	SREC_HUMAN	Q16q60	aedes aegypt	665	64.5	11.0	134	2	O6ZR78_HUMAN	O6zr78	homo sapien
593	65.5	11.1	877	2	Q3UMW1_MOUSE	Q3umw1	mus musculus	666	64.5	11.0	153	2	Q52VJ2_CIONA	Q52vJ2	ciona intes
594	65.5	11.1	1062	1	ATX1_ARATH	Q9c5x4	arabidopsis	667	64.5	11.0	170	2	Q52VK0_CIOIN	Q52vk0	ciona intes
595	65.5	11.1	1110	2	Q614U4_CAEBR	Q614u4	caenorhabdi	668	64.5	11.0	191	1	Y064_TREPA	O83103	treponema p
596	65.5	11.1	1114	2	Q3UKW7_MOUSE	Q9jkw7	mus musculus	669	64.5	11.0	197	2	Q8WQ21_LOCM1	O8wq21	locusta mig
597	65.5	11.1	1114	2	Q3U2A7_MOUSE	Q3u2a7	mus musculus	670	64.5	11.0	245	2	O6ZT26_HUMAN	O6zt26	homo sapien
598	65.5	11.1	1114	2	Q3U2A7_MOUSE	Q6iq50	homo sapien	671	64.5	11.0	325	2	O614Z3_CAEBR	O614z3	caenorhabdi
599	65.5	11.1	1235	2	Q6IQ50_HUMAN	Q6iq50	homo sapien	672	64.5	11.0	343	2	Q17CJ7_AEDAE	Q17cj7	aedes aegypt
600	65.5	11.1	1465	2	QARN50_TETNG	Q4rn50	tetraodon n	673	64.5	11.0	369	2	Q83KX8_SHIFL	Q83kx8	shigella fl
601	65.5	11.1	2067	2	Q59E8B_HUMAN	Q59ed8	homo sapien	674	64.5	11.0	375	2	Q7PR44_ANOGA	Q7pr44	anopheles g
602	65.5	11.1	2213	1	SORL_RABIT	Q95209	o sortilin-	675	64.5	11.0	397	2	O72VK2_CIOIN	O72vk2	ciona intes
603	65.5	11.1	2471	1	NOTC2_HUMAN	Q04721	homo sapien	676	64.5	11.0	405	2	Q8BKSA_MOUSE	Q8bks4	mus musculus
604	65.5	11.1	2471	2	Q5VTD0_HUMAN	Q5vtd0	homo sapien	677	64.5	11.0	420	2	Q3FHB1_9BURK	Q3fbb1	burkholderi
605	65.5	11.1	2555	2	Q5SXM3_HUMAN	Q5axm3	homo sapien	678	64.5	11.0	450	2	Q3F7Z1_HUMAN	Q3f7z1	homo sapien
606	65.5	11.1	2556	1	NOTC1_HUMAN	P45531	homo sapien	679	64.5	11.0	456	2	Q54IG3_DICDI	Q54ig3	dictyosteli
607	65.5	11.1	3718	1	LAMAS_MOUSE	Q61001	mus musculus	680	64.5	11.0	500	1	LRP11_HUMAN	LRP11	homo sapien
608	65.5	11.1	4532	2	Q29ID0_DROPS	Q29id0	drosophila	681	64.5	11.0	626	2	Q2ILJ6_ANADE	Q2ilj6	anaeronyxob
609	65	11.0	78	2	Q9MB66_TOBAC	Q9mb66	nicotiana t	682	64.5	11.0	705	2	Q8R0X1_MOUSE	Q8r0x1	mus musculus
610	65	11.0	90	2	Q5D233_HADIN	Q5d233	hadronyche	683	64.5	11.0	727	2	Q7Q8A1_ANOGA	Q7q8a1	anopheles g
611	65	11.0	95	2	Q9RJN7_STRCO	Q9rjn7	streptomyce	684	64.5	11.0	744	2	Q1L8H4_BRARE	Q1l8h4	brachydanio
612	65	11.0	131	1	CHHB1_BOMMO	P05688	bombyx mori	685	64.5	11.0	754	2	Q1L8H4_BRARE	Q1l8h4	brachydanio
613	65	11.0	147	2	Q6QXV5_ORYSA	Q6qxv5	oryza sativ	686	64.5	11.0	772	2	Q4QBY8_LEIMA	Q4qby8	leishmania
614	65	11.0	181	2	Q4AFA9_9CHLB	Q4afa9	chlorobium	687	64.5	11.0	804	2	Q7TPT4_MOUSE	Q7tpt4	mus musculus
615	65	11.0	212	2	Q45KX0_HUMAN	Q45kx0	homo sapien	688	64.5	11.0					

689	64.5	11.0	822	2	Q62287 MOUSE	Q62287 mus musculus
690	64.5	11.0	841	2	Q4YVB8 PLABE	Q4YVB8 Plasmodium
691	64.5	11.0	853	2	Q8I719 PLAF7	Q8I719 Plasmodium
692	64.5	11.0	853	2	Q8MM24 PLAF7	Q8MM24 Plasmodium
693	64.5	11.0	873	2	Q8QGN9 BRARE	Q8QGN9 brachydanio
694	64.5	11.0	969	2	Q96KG6 HUMAN	Q96KG6 homo sapien
695	64.5	11.0	987	2	Q6XLI8 CALJA	Q6XLI8 callithrix
696	64.5	11.0	1021	2	Q3UGU1 MOUSE	Q3UGU1 mus musculus
697	64.5	11.0	1026	2	Q8SWY0 DROME	Q8SWY0 drosophila
698	64.5	11.0	1044	2	Q17R86 HUMAN	Q17R86 homo sapien
699	64.5	11.0	1162	2	Q2Q422 CANFA	Q2Q422 canis famill
700	64.5	11.0	1211	2	Q383K6 TRYPA	Q383K6 trypanosoma
701	64.5	11.0	1296	2	Q6ANW6 DROME	Q6ANW6 drosophila
702	64.5	11.0	1308	2	Q9GPM8 CAERE	Q9GPM8 caenorhabdi
703	64.5	11.0	1378	2	Q3UHB0 MOUSE	Q3UHB0 mus musculus
704	64.5	11.0	1378	2	Q68HV2 MOUSE	Q68HV2 mus musculus
705	64.5	11.0	1505	2	Q5S3N1 SALSA	Q5S3N1 salmo salar
706	64.5	11.0	1557	2	Q75412 HUMAN	Q75412 homo sapien
707	64.5	11.0	1587	2	Q00508 HUMAN	Q00508 homo sapien
708	64.5	11.0	1624	2	Q75413 HUMAN	Q75413 homo sapien
709	64.5	11.0	1633	2	Q61G22 CAEBR	Q61G22 caenorhabdi
710	64.5	11.0	1737	2	Q7PXF5 ANOGA	Q7PXF5 anopheles g
711	64.5	11.0	1790	1	LAMB1 DROME	P11046 drosophila
712	64.5	11.0	1793	2	Q69ZV8 MOUSE	Q69ZV8 mus musculus
713	64.5	11.0	1946	2	Q4S290 TETNG	Q4S290 tetraodon n
714	64.5	11.0	2214	1	SORL HUMAN	Q26273 h sortiilin-
715	64.5	11.0	2771	2	Q9WTS7 MOUSE	Q9WTS7 mus musculus
716	64.5	11.0	2796	2	Q3UHK6 MOUSE	Q3UHK6 mus musculus
717	64.5	11.0	2833	2	Q2UHS2 MOUSE	Q2UHS2 mus musculus
718	64.5	11.0	3664	2	Q2Q1W5 BRARE	Q2Q1W5 brachydanio
719	64.5	11.0	3695	1	LAMAS HUMAN	Q15230 homo sapien
720	64.5	11.0	3695	2	Q8TDF8 HUMAN	Q8TDF8 homo sapien
721	64	10.9	112	1	COL PIG	P02703 sus scrofa
722	64	10.9	115	2	Q38C22 9TRYP	Q38C22 trypanosoma
723	64	10.9	116	2	Q5Q981 IXOSC	Q5Q981 ixodes scap
724	64	10.9	117	2	Q9YD41 AERPE	Q9YD41 aeropyrum p
725	64	10.9	130	1	KRA3A SHEEP	P02443 ovis aries
726	64	10.9	146	1	TXVB TRIPL	P67862 trimeresuru
727	64	10.9	148	2	Q71RP9 TRIST	Q71RP9 trimeresuru
728	64	10.9	163	2	Q4SFU4 TETNG	Q4SFU4 tetraodon n
729	64	10.9	178	1	CHHB2 BOMMO	P20730 bombyx mori
730	64	10.9	199	2	Q9H557 HUMAN	Q9H557 homo sapien
731	64	10.9	217	2	Q7A9R9 ECOS7	Q7A9R9 escherichia
732	64	10.9	217	2	Q85613 ECOLI	Q85613 escherichia
733	64	10.9	225	2	Q8XCA3 ECOS7	Q8XCA3 escherichia
734	64	10.9	285	2	Q868R9 ANOGA	Q868R9 anopheles g
735	64	10.9	285	2	Q5CAG9 ORYSA	Q5CAG9 oryza sativ
736	64	10.9	309	2	Q74ZS4 ASHGO	Q74ZS4 aahbya goas
737	64	10.9	315	2	Q616A1 CAEBR	Q616A1 caenorhabdi
738	64	10.9	322	2	Q65113 ORYSA	Q65113 oryza sativ
739	64	10.9	325	1	V72 SFVKA	P25943 shope fibro
740	64	10.9	325	2	Q77PB3 9POXV	Q77PB3 rabbit fibr
741	64	10.9	363	2	Q1CYN7 WYXXA	Q1CYN7 myxococcus
742	64	10.9	368	2	Q2BRZ1 LACRE	Q2BRZ1 lactobacill
743	64	10.9	370	2	Q6DSV5 ERWCT	Q6DSV5 erwinia car
744	64	10.9	389	2	Q8R226 MOUSE	Q8R226 mus musculus
745	64	10.9	425	1	TNR16 RAT	P07174 rattus norv
746	64	10.9	426	2	Q8LAF6 ARATH	Q8LAF6 arabidopsis
747	64	10.9	426	2	Q33X5 ARATH	Q33X5 arabidopsis
748	64	10.9	475	1	U3IP2 HUMAN	Q43818 homo sapien
749	64	10.9	479	2	Q3G7J0 9DELT	Q3G7J0 pelobacter
750	64	10.9	578	1	TRBM CANFA	Q5W7P8 canis famill
751	64	10.9	581	2	Q5LU50 SILPO	Q5LU50 silicibacte
752	64	10.9	587	1	UI84 HGVT	P29835 human cytom
753	64	10.9	588	2	Q43FM5 9CHLB	Q43FM5 chlorobium
754	64	10.9	590	2	Q8C088 MOUSE	Q8C088 mus musculus
755	64	10.9	657	2	Q4PIC7 USTMA	Q4PIC7 ustilago ma
756	64	10.9	682	2	Q3A3T0 PELCD	Q3A3T0 pelobacter
757	64	10.9	687	2	Q1AWM1 9ACTN	Q1AWM1 rubrobacter
758	64	10.9	723	2	Q9QW16 9MURI	Q9QW16 rattus sp.
759	64	10.9	737	2	Q8JZM4 MOUSE	Q8JZM4 mus musculus
760	64	10.9	737	2	Q8VD97 MOUSE	Q8VD97 mus musculus
761	64	10.9	739	2	Q17AY8 AEDAE	Q17AY8 aedes aegyp

762	64	10.9	983	2	Q4T849 TETNG	Q4T849 tetraodon n
763	64	10.9	990	2	Q6BTQ2 DEBHA	Q6BTQ2 debaryomyce
764	64	10.9	1032	2	Q75WG1 PENJP	Q75WG1 penaeus jap
765	64	10.9	1037	2	Q3UV32 MOUSE	Q3UV32 mus musculus
766	64	10.9	1114	2	Q75WG2 PENJP	Q75WG2 penaeus jap
767	64	10.9	1143	2	Q21010 CAEBL	Q21010 caenorhabdi
768	64	10.9	1144	1	MA2A1 HUMAN	Q67706 homo sapien
769	64	10.9	1145	2	Q2PJ74 CAEBL	Q2PJ74 caenorhabdi
770	64	10.9	1180	2	Q3BP15 XANGS	Q3BP15 xanthomonas
771	64	10.9	1364	2	Q4RQ03 TETNG	Q4RQ03 tetraodon n
772	64	10.9	1437	2	Q4UDU8 TRYCR	Q4UDU8 brachydanio
773	64	10.9	1515	2	Q9DEJ7 BRARE	Q9DEJ7 brachydanio
774	64	10.9	1818	2	Q2YI44 BLAGE	Q2YI44 blattella g
775	64	10.9	2030	2	Q2WBY6 PLADU	Q2WBY6 platyneareis
776	64	10.9	2192	2	Q804R1 BRARE	Q804R1 brachydanio
777	64	10.9	2215	1	SORL MOUSE	Q8B307 m sortiilin-
778	64	10.9	2215	2	Q3UHM3 MOUSE	Q3UHM3 mus musculus
779	64	10.9	2523	2	Q61211 CAEBR	Q61211 caenorhabdi
780	64	10.9	2532	2	Q629H6 CAEBR	Q629H6 caenorhabdi
781	64	10.9	2599	2	Q16TK9 AEDAE	Q16TK9 aedes aegyp
782	64	10.9	2602	2	Q7PSV8 ANOGA	Q7PSV8 anopheles g
783	64	10.9	2824	2	Q9W7R3 BRARE	Q9W7R3 brachydanio
784	64	10.9	3019	2	Q4RU98 TETNG	Q4RU98 tetraodon n
785	64	10.9	3235	2	Q61FT2 CAEBR	Q61FT2 caenorhabdi
786	64	10.9	3487	2	Q4D378 TRYCR	Q4D378 trypanosoma
787	64	10.9	4181	2	Q291B2 DROPS	Q291B2 drosophila
788	63.5	10.8	131	2	Q9YZX8 9FLAV	Q9YZX8 gb virus c.
789	63.5	10.8	147	2	Q353G9 9GAMM	Q353G9 alkalilimni
790	63.5	10.8	156	2	Q21VF9 RHOP2	Q21VF9 rhodopseudo
791	63.5	10.8	156	2	Q6N0U5 RHOP2	Q6N0U5 rhodopseudo
792	63.5	10.8	159	2	Q5LKG8 SILPO	Q5LKG8 silicibacte
793	63.5	10.8	168	2	Q8T229 TRYCR	Q8T229 trypanosoma
794	63.5	10.8	208	2	Q2HJ19 9MYRI	Q2HJ19 strigamia m
795	63.5	10.8	225	2	Q851F4 ORYSA	Q851F4 oryza sativ
796	63.5	10.8	225	2	Q626R3 CAEBR	Q626R3 caenorhabdi
797	63.5	10.8	240	1	KCP3 RAT	Q497B3 rattus norv
798	63.5	10.8	261	2	Q39TH1 GEOMG	Q39TH1 geobacter m
799	63.5	10.8	286	2	Q4TKB9 TETNG	Q4TKB9 caenorhabdi
800	63.5	10.8	300	2	Q28KF2 JANSC	Q28KF2 jannaeschia
801	63.5	10.8	349	2	Q54KB3 DICDI	Q54KB3 dictyosteli
802	63.5	10.8	358	2	Q86AK7 DICDI	Q86AK7 dictyosteli
803	63.5	10.8	360	2	Q556S1 DICDI	Q556S1 dictyosteli
804	63.5	10.8	372	2	Q7V1J2 ORYSA	Q7V1J2 oryza sativ
805	63.5	10.8	380	2	Q61ES5 ORYSA	Q61ES5 oryza sativ
806	63.5	10.8	383	2	Q70534 RAT	Q70534 rattus norv
807	63.5	10.8	383	2	Q62779 RAT	Q62779 rattus norv
808	63.5	10.8	407	2	Q3K7E8 PSEPF	Q3K7E8 pseudomonas
809	63.5	10.8	507	2	Q56BV3 9CAUD	Q56BV3 enterobacte
810	63.5	10.8	521	2	Q39NV6 BURS3	Q39NV6 burkholderi
811	63.5	10.8	536	2	Q3RG03 BRARE	Q3RG03 brachydanio
812	63.5	10.8	542	2	Q17H65 AEDAE	Q17H65 aedes aegyp
813	63.5	10.8	562	2	Q26630 METTH	Q26630 methanobact
814	63.5	10.8	721	2	Q91902 XENLA	Q91902 xenopus lae
815	63.5	10.8	721	2	Q4DFR4 TRYCR	Q4DFR4 trypanosoma
816	63.5	10.8	747	2	Q8VHF4 MOUSE	Q8VHF4 mus musculus
817	63.5	10.8	747	2	Q9DGR2 XENLA	Q9DGR2 xenopus lae
818	63.5	10.8	767	2	Q9DGR2 XENLA	Q9DGR2 xenopus lae
819	63.5	10.8	778	2	Q91BG4 XENLA	Q91BG4 xenopus lae
820	63.5	10.8	847	2	Q8JVB9 9VIRU	Q8JVB9 penicillium
821	63.5	10.8	871	2	Q626H3 CAEBR	Q626H3 caenorhabdi
822	63.5	10.8	898	2	Q3URX7 MOUSE	Q3URX7 mus musculus
823	63.5	10.8	905	2	Q18260 CAEBL	Q18260 caenorhabdi
824	63.5	10.8	909	2	Q7SEF5 NEUCR	Q7SEF5 neurospora
825	63.5	10.8	949	2	Q4S2B5 TETNG	Q4S2B5 tetraodon n
826	63.5	10.8	1004	2	Q8CGA7 MOUSE	Q8CGA7 mus musculus
827	63.5	10.8	1034	2	Q8VHL7 MOUSE	Q8VHL7 mus musculus
828	63.5	10.8	1034	2	Q8VHK5 MOUSE	Q8VHK5 mus musculus
829	63.5	10.8	1054	2	Q23JW8 TERTH	Q23JW8 tetrahymena
830	63.5	10.8	1102	2	Q23NT8 TERTH	Q23NT8 tetrahymena
831	63.5	10.8	1398	2	Q24DM6 TERTH	Q24DM6 tetrahymena
832	63.5	10.8	1687	2	Q22QK0 TERTH	Q22QK0 tetrahymena
833	63.5	10.8	1776	2	Q5BG13 EMENI	Q5BG13 emericeilla
834	63.5	10.8				

835	63.5	10.8	1935	2	Q6QHS1_LYTVA	Q6che3 lytechinus	908	63	10.7	1367	2	Q61QY1_CABER	Q61qy1 caenorhabdi
836	63.5	10.8	2019	2	Q68F80_MOUSE	Q6che3 mus musculus	909	63	10.7	1418	2	Q4CR51_TRYCR	Q4cr51 trypanosoma
837	63.5	10.8	2030	2	Q4RH2_TETNG	Q4rh2 tetraodon n	910	63	10.7	1441	2	Q867Q2_CABER	Q867q2 caenorhabdi
838	63.5	10.8	2672	2	Q3UH3_MOUSE	Q3uh3 m 14 days p	911	63	10.7	1553	2	Q29G18_DROPS	Q29g18 drosophila
839	63.5	10.8	2842	2	Q56I18_9FLAV	Q56ih8 gb virus c	912	63	10.7	1897	2	Q29H17_DROPS	Q29h17 drosophila
840	63.5	10.8	3004	2	Q24550_DROME	Q24550 drosophila	913	63	10.7	2433	2	Q24F98_TETTH	Q24f98 tetrahymena
841	63.5	10.8	3004	2	Q3VYN8_DROME	Q3vyn8 drosophila	914	63	10.7	2468	2	Q800E4_BRARE	Q800e4 brachydanio
842	63.5	10.8	3145	2	Q22M95_TETTH	Q22m95 tetrahymena	915	63	10.7	2528	2	Q8AXP0_CYNPY	Q8axp0 cynops pyrr
843	63.5	10.8	3689	2	Q7PPF9_ANOGA	Q7ppf9 anopheles g	916	63	10.7	2660	2	Q7QL19_ANOGA	Q7ql19 anopheles g
844	63.5	10.8	3707	1	PGBM_MOUSE	Q05793 mus musculus	917	63	10.7	3301	1	CELR3_MOUSE	Q91210 mus musculus
845	63.5	10.8	4260	2	Q4T3T2_TETNG	Q4t3t2 tetraodon n	918	63	10.7	3444	2	Q4E1B3_TRYCR	Q4e1b3 trypanosoma
846	63.5	10.8	4981	2	Q2PZL6_MOUSE	Q2pzl6 mus musculus	919	63	10.7	3445	2	Q4DYC9_TRYCR	Q4dyc9 trypanosoma
847	63.5	10.8	5376	1	ZAN_MOUSE	O88799 mus musculus	920	63	10.7	3456	2	Q4DJN1_TRYCR	Q4djn1 trypanosoma
848	63	10.7	65	2	Q4GW4_CRAGI	Q4gww4 crassostrea	921	63	10.7	3474	2	Q4DS23_TRYCR	Q4ds23 trypanosoma
849	63	10.7	92	2	Q2MCN6_HYDAT	Q2mcn6 hydra atten	922	63	10.7	3483	2	Q4DTL6_TRYCR	Q4dtl6 trypanosoma
850	63	10.7	93	2	Q3I3L8_HYDMA	Q3i3l8 hydra magni	923	63	10.7	5141	1	SSFO_RAT	Q700k0 rattus norv
851	63	10.7	94	2	Q7S150_ORYSA	Q7s150 oryza sativ	924	62.5	10.6	128	2	Q6ZWD3_HUMAN	Q6zwd3 homo sapien
852	63	10.7	128	2	Q52VH7_CIOIN	Q52vh7 ciona intes	925	62.5	10.6	131	2	Q9Y2V2_9FLAV	Q9y2v2 gb virus c
853	63	10.7	148	2	Q71RP8_TRIST	Q71rp8 trimeresuru	926	62.5	10.6	135	2	Q3YUP8_9FLAV	Q3yup8 gb virus c
854	63	10.7	173	2	Q9RJ35_STRCO	Q9rj35 streptomyce	927	62.5	10.6	145	2	Q39219_9FLAV	O39219 gb virus c
855	63	10.7	204	1	TNR26_MOUSE	P83626 mus musculus	928	62.5	10.6	153	2	O11434_9ADEN	O11434 duck adenov
856	63	10.7	204	2	Q3U3N2_MOUSE	Q3u3n2 mus musculus	929	62.5	10.6	157	2	Q5ISQ5_MACFA	Q5isq5 macaca fasc
857	63	10.7	215	2	Q80W51_MOUSE	Q80w51 mus musculus	930	62.5	10.6	158	1	KAB3_OLDAP	P58455 oldenlandia
858	63	10.7	289	2	Q1PFZ8_HYDSY	Q1pfz8 hydractinia	931	62.5	10.6	159	2	Q7XZ75_GRIJA	P78455 griffithsia
859	63	10.7	300	2	Q84BD4_WYXXA	Q84bd4 myxococcus	932	62.5	10.6	166	2	Q4CYN2_TRYCR	Q4cyn2 trypanosoma
860	63	10.7	319	2	Q4T826_TETNG	Q4t826 tetraodon n	933	62.5	10.6	169	2	Q3TRB8_MOUSE	Q3trb8 m adult mal
861	63	10.7	322	2	Q1D2V4_MYXXA	Q1d2v4 myxococcus	934	62.5	10.6	170	2	Q52VJ5_CIOIN	Q52vj5 ciona intes
862	63	10.7	349	1	XRCC3_MOUSE	Q9cxe6 mus musculus	935	62.5	10.6	173	2	Q3ZLCO_OREMO	Q3zlc0 oreochromis
863	63	10.7	350	2	O14189_SCHPO	O14189 schizosacch	936	62.5	10.6	208	2	Q4DLA7_TRYCR	Q4dl7 trypanosoma
864	63	10.7	351	2	Q37HL4_RHOPA	Q37hl4 rhodopsendo	937	62.5	10.6	220	2	Q63404_RAT	Q63404 rattus norv
865	63	10.7	368	2	Q86IM1_DICDI	Q86im1 dictyosteli	938	62.5	10.6	227	2	Q7YIM8_9SMEG	Q7yim8 hyporhamphu
866	63	10.7	369	1	YDHH_ECOLI	P77570 escherichia	939	62.5	10.6	237	2	Q3I1U3_MACNE	Q3i1u3 macaca neme
867	63	10.7	369	2	Q32126_SHISS	Q32126 shigella so	940	62.5	10.6	237	2	Q1VKN0_9FLAO	Q1vkn0 psychroflox
868	63	10.7	369	2	Q32FD3_SHIDS	Q32fd3 shigella dy	941	62.5	10.6	286	2	Q6IKY7_DROME	Q6iky7 drosophila
869	63	10.7	369	2	Q32027_SHIBS	Q32027 shigella bo	942	62.5	10.6	288	2	Q9XYT5_TOXCA	Q9xyt5 toxocara ca
870	63	10.7	369	2	Q8X644_ECO57	Q8x644 escherichia	943	62.5	10.6	298	2	Q4CR12_TRYCR	Q4cr12 trypanosoma
871	63	10.7	369	2	Q8FH85_ECOL6	Q8fh85 escherichia	944	62.5	10.6	308	2	O46370_BOVIN	O46370 bos taurus
872	63	10.7	394	2	Q9NGP9_POLPA	Q9ngp9 polysphondy	945	62.5	10.6	350	2	Q20CF4_PETMA	Q20cf4 petromyzon
873	63	10.7	395	2	Q55923_DICDI	Q55923 dictyosteli	946	62.5	10.6	352	2	Q3MZIO_9DELT	Q3mzi0 syntrophoba
874	63	10.7	421	2	Q9DEV1_CYPCA	Q9dev1 cyprinus ca	947	62.5	10.6	360	2	O8YQT4_ANASP	O8yqt4 anabaena sp
875	63	10.7	450	2	Q869J7_9MYRI	Q869j7 gliomeris ma	948	62.5	10.6	360	2	Q3MCS3_ANAVT	Q3mcs3 anabaena va
876	63	10.7	456	2	Q3WTR3_9RHIZ	Q3wtr3 mesorhizobi	949	62.5	10.6	378	2	Q5I0R0_XENTR	Q5i0r0 xenopus tro
877	63	10.7	469	2	Q52V41_CIOIN	Q52v41 ciona intes	950	62.5	10.6	398	2	Q52VK3_CIOIN	Q52vk3 ciona intes
878	63	10.7	528	2	Q9CXD8_MOUSE	Q9cx8 mus musculus	951	62.5	10.6	424	2	Q4SL08_TETNG	Q4sl08 tetraodon n
879	63	10.7	583	2	Q3TSU5_MOUSE	Q3tsu5 mus musculus	952	62.5	10.6	430	2	Q62229_CABER	Q62229 caenorhabdi
880	63	10.7	585	2	Q17EL8_ABDAA	Q17el8 aedes aegypt	953	62.5	10.6	458	2	O1SIS9_MEDTR	O1sisi9 medicago tr
881	63	10.7	601	2	Q52KT2_XENLA	Q52kt2 xenopus lae	954	62.5	10.6	484	2	Q3I1U4_MACMU	Q3i1u4 macaca mula
882	63	10.7	608	2	Q8S1M4_ORYSA	Q8s1m4 oryza sativ	955	62.5	10.6	494	2	Q1FJN7_9CLOT	Q1fjn7 clostridium
883	63	10.7	648	2	Q9VJU4_DROME	Q9vj4 drosophila	956	62.5	10.6	544	2	Q5BW73_SCHJA	Q5bw73 schistosoma
884	63	10.7	669	2	Q4V526_DROME	Q4v526 drosophila	957	62.5	10.6	558	2	Q2HCH0_CHAGB	Q2hch0 chaetomium
885	63	10.7	694	2	Q53QB9_ORYSA	Q53qb9 oryza sativ	958	62.5	10.6	567	2	Q8WUL3_HUMAN	Q8wul3 homo sapien
886	63	10.7	701	2	Q86BL2_DROME	Q86bl2 drosophila	959	62.5	10.6	567	2	Q3G137_9DELT	Q3g137 pelobacter
887	63	10.7	712	2	Q50JF9_CAEEL	Q50jf9 caenorhabdi	960	62.5	10.6	607	2	Q1KXY5_MYXGL	Q1kxy5 myxine glut
888	63	10.7	735	1	ADAM2_MACFA	Q28478 macaca fasc	961	62.5	10.6	645	2	O02261_CABEL	O02261 caenorhabdi
889	63	10.7	735	2	Q4R6R6_MACFA	Q4r6r6 macaca fasc	962	62.5	10.6	665	2	Q1PHR4_SACKO	Q1phr4 saccolossu
890	63	10.7	740	2	Q528V2_ORYSA	Q528v2 oryza sativ	963	62.5	10.6	668	2	Q4S8K6_TETNG	Q4s8k6 tetraodon n
891	63	10.7	780	2	Q3U2X9_MOUSE	Q3u2x9 mus musculus	964	62.5	10.6	705	1	FBLN1_MOUSE	F08879 mus musculus
892	63	10.7	782	2	Q9MU23_MOUSE	Q9mu23 mus musculus	965	62.5	10.6	705	2	Q3TWK8_MOUSE	Q3twk8 mus musculus
893	63	10.7	827	2	Q8BRK9_MOUSE	Q8brk9 mus musculus	966	62.5	10.6	812	2	O77779_BOVIN	O77779 bos taurus
894	63	10.7	909	2	LPD1G4_XENTR	Q6dig4 xenopus tro	967	62.5	10.6	844	2	Q6Y857_MORAM	Q6y857 morone amer
895	63	10.7	917	1	LRP8_CHICK	Q98931 gallus gall	968	62.5	10.6	880	1	CADHF_XENLA	P33148 xenopus lae
896	63	10.7	949	1	PCDAB_HUMAN	Q9y5i1 homo sapien	969	62.5	10.6	907	2	Q9XTS9_CABEL	Q9xts9 caenorhabdi
897	63	10.7	987	2	Q616G9_CABER	Q616g9 caenorhabdi	970	62.5	10.6	919	2	Q298E4_DROPS	Q298e4 drosophila
898	63	10.7	1037	2	Q5VY43_HUMAN	Q5vy43 homo sapien	971	62.5	10.6	919	2	Q28659_RABIT	Q28659 cryptotlagus
899	63	10.7	1107	2	Q4S977_TETNG	Q4s977 tetraodon n	972	62.5	10.6	925	2	Q90B95_CABEL	Q90b95 caenorhabdi
900	63	10.7	1139	1	MA2A2_HUMAN	P49641 homo sapien	973	62.5	10.6	976	2	Q90ZN9_BRARE	Q90zn9 brachydanio
901	63	10.7	1150	2	Q6GQ11_XENLA	Q6gq11 xenopus lae	974	62.5	10.6	1031	2	O42124_CHICK	O42124 gallus gall
902	63	10.7	1152	2	Q197W7_MOUSE	Q197w7 mus musculus	975	62.5	10.6	1159	2	Q410Z0_GIBZE	Q410z0 gibberella
903	63	10.7	1152	2	Q4S7D3_TETNG	Q4s7d3 tetraodon n	976	62.5	10.6	1245	2	Q9Y7V5_TRIHA	Q9y7v5 trichoderma
904	63	10.7	1249	2	Q8VI66_RAT	Q8vi66 rattus norv	977	62.5	10.6	1280	2	Q60YEB_CABER	Q60yeb caenorhabdi
905	63	10.7	1278	2	Q9U350_CABEL	Q9u350 caenorhabdi	978	62.5	10.6	1473	2	Q28WZ1_DROPS	Q28wz1 drosophila
906	63	10.7	1280	2	Q6QHS1_LYTVA	Q6qhs1 lytechinus	979	62.5	10.6	1514	2	Q29BH5_DROPS	Q29bh5 drosophila
907	63	10.7	1356	1	SPIKE_CVHNL	Q6qls2 human coron	980	62.5	10.6	2223	2	Q61T23_CABER	Q61t23 caenorhabdi

981	62.5	10.6	2448	2	Q8WQ55_HUMAN	Q8WQ55 homo sapien	1054	62	10.5	1403	2	Q70E20_MOUSE	Q70E20 mus musculus
982	62.5	10.6	2525	2	Q4QHT5_LEIMA	Q4QHT5 leishmania	1055	62	10.5	1443	2	Q4CNL9_TRYCR	Q4CNL9 trypanosoma
983	62.5	10.6	2529	2	Q2L697_CIOIN	Q2L697 ciona intes	1056	62	10.5	1521	2	Q4CTB2_TRYCR	Q4CTB2 trypanosoma
984	62.5	10.6	2571	1	STAB1_MOUSE	Q8r4y4 mus musculus	1057	62	10.5	1523	1	SLIT3_RAT	Q88280 rattus norv
985	62.5	10.6	2632	2	Q16UT3_ABDAB	Q16ut3 aedes aegypt	1058	62	10.5	1523	2	Q4CNY4_TRYCR	Q4CNY4 trypanosoma
986	62.5	10.6	2843	2	Q96899_9FLAV	Q96899 gb virus c.	1059	62	10.5	1595	2	Q1EBH3_RAT	Q1ebh3 rattus norv
987	62.5	10.6	3623	1	CUBN_MOUSE	Q9j1b4 mus musculus	1060	62	10.5	1599	2	Q09983_CAEEL	Q09983 caenorhabdi
988	62.5	10.6	4135	2	O18977_BOVIN	O18977 bos taurus	1061	62	10.5	1629	2	Q118K6_BRARE	Q118K6 brachydanio
989	62	10.5	92	1	LCM_LOGMI	P80060 locusta mig	1062	62	10.5	1679	2	Q51DQ1_ENTHI	Q51dq1 entanoeba h
990	62	10.5	100	1	VP52_BPAPS	Q9t1p6 bacterioph	1063	62	10.5	1770	2	Q22PS4_TETH	Q22ps4 tetrahymena
991	62	10.5	100	1	Q3LZQ0_9CAUD	Q3lq0 acyrtosiph	1064	62	10.5	1808	2	Q1XD63_RAT	Q1xd63 rattus norv
992	62	10.5	101	2	Q9XGJ3_GERHY	Q9xgj3 gerbera hyb	1065	62	10.5	1813	1	LTBR2_MOUSE	Q08999 mus musculus
993	62	10.5	102	2	Q24040_9ROSI	Q24040 lavatera th	1066	62	10.5	1964	2	Q4CQI1_TRYCR	Q4cq11 trypanosoma
994	62	10.5	112	2	Q2P51_URTDI	Q2p51 urtica dioi	1067	62	10.5	2043	2	Q4Q510_LEIMA	Q4q510 leishmania
995	62	10.5	135	2	Q2AB89_9GEMI	Q2ab9 east africa	1068	62	10.5	2082	1	ZAN_RABIT	P57999 oryctolagus
996	62	10.5	146	1	TXVE_BOVIN	Q90x24 bothrops in	1069	62	10.5	2414	2	Q6DFL6_XENLA	Q6df16 xenopus lae
997	62	10.5	155	2	Q218D3_RHOPB	Q218d3 rhodopseudo	1070	62	10.5	2427	2	Q8MQ36_CAEEL	Q8mq36 caenorhabdi
998	62	10.5	178	2	Q8PPR1_XANAC	Q8ppr1 xanthomonas	1071	62	10.5	2511	2	Q4T9V2_TETNG	Q4t9v2 tetraodon n
999	62	10.5	198	2	Q4WAE1_ASPFU	Q4wae1 aspergillus	1072	62	10.5	2651	2	Q4CTC1_TRYCR	Q4ctc1 trypanosoma
1000	62	10.5	211	2	Q6H8Q4_CANFA	Q6h8q4 canis famil	1073	62	10.5	2705	2	Q4D538_TRYCR	Q4d538 trypanosoma
1001	62	10.5	211	2	Q9RK27_STRCO	Q9rk27 streptomyc	1074	62	10.5	2760	2	Q4T8G9_TETNG	Q4t8g9 tetraodon n
1002	62	10.5	222	2	Q3U697_MOUSE	Q3u697 m bone marr	1075	62	10.5	2838	2	Q4DUG4_TRYCR	Q4dug4 trypanosoma
1003	62	10.5	240	2	Q218M8_RHOPB	Q218m8 rhodopseudo	1076	62	10.5	2976	2	Q4CZM4_TRYCR	Q4czm4 trypanosoma
1004	62	10.5	243	2	Q4TDM7_TETNG	Q4tdm7 tetraodon n	1077	62	10.5	3313	1	CELR3_RAT	Q88278 rattus norv
1005	62	10.5	256	2	Q5ENU2_HETTR	Q5enu2 heterocapsa	1078	62	10.5	3335	2	Q4DZ55_TRYCR	Q4dz55 trypanosoma
1006	62	10.5	289	2	Q6AL36_DESPS	Q6al36 desulforale	1079	62	10.5	3481	2	Q4D8R5_TRYCR	Q4d8r5 trypanosoma
1007	62	10.5	272	2	Q61BN9_CAEER	Q61bn9 caenorhabdi	1080	62	10.5	3482	2	Q4DSH9_TRYCR	Q4dsh9 trypanosoma
1008	62	10.5	282	1	END4_DESVH	Q72cq9 desulfovibr	1081	62	10.5	3483	2	Q4DMZ0_TRYCR	Q4dmz0 trypanosoma
1009	62	10.5	311	2	Q8R1G8_MOUSE	Q8r1g8 mus musculus	1082	62	10.5	3493	2	Q4DHR5_TRYCR	Q4dhr5 trypanosoma
1010	62	10.5	318	2	Q6A853_PROAC	Q6a853 propionibac	1083	62	10.5	3494	2	Q4RU20_TETNG	Q4rj20 tetraodon n
1011	62	10.5	339	2	Q9BLJ2_TOXGO	Q9bli2 toxoplasma	1084	62	10.5	4998	1	SSPO_MOUSE	Q8c965 mus musculus
1012	62	10.5	347	2	Q75JE6_DICDI	Q75je6 dictyosteli	1085	61.5	10.4	83	2	Q9XXT6_CAEEL	Q9xxt6 caenorhabdi
1013	62	10.5	347	2	Q55AL3_DICDI	Q55al3 dictyosteli	1086	61.5	10.4	93	2	Q7MS54_WOLSV	Q7ms54 wolinnella s
1014	62	10.5	369	2	Q1RBF5_ECOUT	Q1rbf5 escherichia	1087	61.5	10.4	131	2	Q9YZW5_9FLAV	Q9yzw5 gb virus c.
1015	62	10.5	380	2	Q60214_METCA	Q60214 methylococc	1088	61.5	10.4	131	2	Q9YZW5_9FLAV	Q9yzw5 gb virus c.
1016	62	10.5	402	1	GUN1_HUMGT	P56680 humicola in	1089	61.5	10.4	135	2	Q77VZ1_9FLAV	Q77vz1 gb virus c.
1017	62	10.5	435	1	GUN1_HUMGT	Q12622 humicola gr	1090	61.5	10.4	135	2	Q9W8H8_9FLAV	Q9w8h8 gb virus c.
1018	62	10.5	435	2	Q616G8_CAEER	Q616g8 caenorhabdi	1091	61.5	10.4	135	2	Q77VZ0_9FLAV	Q77vz0 gb virus c.
1019	62	10.5	469	2	Q161L6_ABDAB	Q161l6 aedes aegypt	1092	61.5	10.4	135	2	Q9YUN7_9FLAV	Q9yun7 gb virus c.
1020	62	10.5	469	2	Q64FJ9_9INFA	Q64fj9 influenza a	1093	61.5	10.4	135	2	Q77VZ3_9FLAV	Q77vz3 gb virus c.
1021	62	10.5	475	1	U3IP2_MOUSE	Q91wm3 mus musculus	1094	61.5	10.4	135	2	Q77VZ2_9FLAV	Q77vz2 gb virus c.
1022	62	10.5	476	2	Q8R1H5_MOUSE	Q8r1h9 mus musculus	1095	61.5	10.4	143	2	Q72441_9FLAV	Q72441 gb virus c.
1023	62	10.5	491	2	P90850_CAEEL	P90850 caenorhabdi	1096	61.5	10.4	162	2	Q9BLH6_APLKU	Q9blh6 apliyea kur
1024	62	10.5	493	2	Q7TNG6_MOUSE	Q7tng6 mus musculus	1097	61.5	10.4	166	1	ZCH13_HUMAN	Q8w36 homo sapien
1025	62	10.5	504	2	Q5ZB09_ORYSA	Q5zb09 oryza sativ	1098	61.5	10.4	176	2	Q87WA2_PESRM	Q87wa2 pseudomonas
1026	62	10.5	583	2	Q1EG87_PIG	Q1eg87 sus scrofa	1099	61.5	10.4	177	2	Q7RYN5_NEUCR	Q7ryn5 neurospora
1027	62	10.5	592	2	Q61834_MOUSE	Q61834 mus musculus	1100	61.5	10.4	190	2	Q3ZDR4_PIG	Q3zdr4 sus scrofa
1028	62	10.5	615	2	Q58E52_MOUSE	Q58e52 mus musculus	1101	61.5	10.4	202	2	O55254_9FLAV	O55254 gb virus c.
1029	62	10.5	625	2	Q8JQP9_9VIRU	Q8jq9 adeno-aseoc	1102	61.5	10.4	220	2	Q92V20_RHIME	Q92v20 rhizobium m
1030	62	10.5	657	2	Q8R0K8_MOUSE	Q8r0k8 mus musculus	1103	61.5	10.4	228	2	Q91NG9_9PARA	Q91ng9 tioman viru
1031	62	10.5	772	1	DLA_BRARE	Q6di48 brachydanio	1104	61.5	10.4	277	2	TNR4_HUMAN	P43489 homo sapien
1032	62	10.5	924	2	Q24457_TETTH	Q24457 tetrahymena	1105	61.5	10.4	282	1	Q2M312_HUMAN	Q2m312 homo sapien
1033	62	10.5	949	1	TSP4_BRARE	Q8igw0 brachydanio	1106	61.5	10.4	282	1	CD320_MOUSE	Q9npf0 homo sapien
1034	62	10.5	949	2	Q502R1_BRARE	Q502r1 brachydanio	1107	61.5	10.4	299	2	Q8BX64_MOUSE	Q8bx64 mus musculus
1035	62	10.5	951	2	Q4D0C3_TRYCR	Q4d0c3 trypanosoma	1108	61.5	10.4	316	2	O57092_9POXV	O57092 ectromelia
1036	62	10.5	988	2	Q22685_CAEEL	Q22685 caenorhabdi	1109	61.5	10.4	322	2	CHIC_LYCES	Q05538 lycopersico
1037	62	10.5	998	1	EPHB3_HUMAN	P54753 homo sapien	1110	61.5	10.4	347	2	Q86T16_HUMAN	Q86t16 homo sapien
1038	62	10.5	1047	2	Q566K6_MOUSE	Q566k6 mus musculus	1111	61.5	10.4	351	2	Q2QTH8_ORYSA	Q2qth8 oryza sativ
1039	62	10.5	1065	2	Q810H2_MOUSE	Q810h2 mus musculus	1112	61.5	10.4	356	2	Q60C70_METCA	Q60c70 methylococc
1040	62	10.5	1095	2	Q41672_GIBZE	Q41672 gibberella	1113	61.5	10.4	368	2	Q82VZ2_NITEU	Q82vz2 nitrosomona
1041	62	10.5	1103	2	Q55A33_DICDI	Q55a33 dictyosteli	1114	61.5	10.4	373	2	Q18197_CAEEL	Q18197 caenorhabdi
1042	62	10.5	1113	1	CORIN_MOUSE	Q92319 mus musculus	1115	61.5	10.4	408	2	Q5SNS5_BRARE	Q5sns5 brachydanio
1043	62	10.5	1170	1	TSPI_HUMAN	P07996 homo sapien	1116	61.5	10.4	408	2	Q29K93_DROPS	Q29k93 drosophiila
1044	62	10.5	1170	1	TSPI_MOUSE	P35441 mus musculus	1117	61.5	10.4	415	2	Q60N48_CAEER	Q60n48 caenorhabdi
1045	62	10.5	1170	2	Q71S83_RAT	Q71s83 rattus norv	1118	61.5	10.4	422	2	Q9K3H4_STRCO	Q9k3h4 streptomyce
1046	62	10.5	1170	2	Q3TR40_MOUSE	Q3tr40 mus musculus	1119	61.5	10.4	435	2	O505M6_XENLA	O505m6 xenopus lae
1047	62	10.5	1170	2	Q80YQ1_MOUSE	Q80yq1 mus musculus	1120	61.5	10.4	448	2	Q641C0_XENLA	Q641c0 xenopus lae
1048	62	10.5	1171	2	Q8CG82_MOUSE	Q8cg82 mus musculus	1121	61.5	10.4	452	2	O51SL2_MACFA	O51sl2 macaca fasc
1049	62	10.5	1171	2	Q8K0P6_MOUSE	Q8k0p6 mus musculus	1122	61.5	10.4	459	2	Q2TAW1_XENLA	Q2taw1 xenopus lae
1050	62	10.5	1205	2	Q59E39_HUMAN	Q59e39 homo sapien	1123	61.5	10.4	504	2	Q7QWR4_GIALA	Q7qwr4 giardia lam
1051	62	10.5	1225	2	Q4RGJ3_TETNG	Q4rgj3 tetraodon n	1124	61.5	10.4	587	2	Q2HGA7_CHAGB	Q2hga7 chaetomium
1052	62	10.5	1343	2	Q6PD18_MOUSE	Q6pd18 mus musculus	1125	61.5	10.4	587	2	O5C3P1_SCHJA	O5c3p1 schistosoma
1053	62	10.5	1361	2			1126	61.5	10.4	659	2	Q1Q4X4_9BACT	Q1q4x4 candidatus

1127	61.5	10.4	705	1	CTL2_CAVPO	Q810f1	cavia porce	1200	61	10.4	369	2	Q7QDZ6	ANOCA	Q7qdz6	anopheles g
1128	61.5	10.4	719	2	Q5XG79_HUMAN	Q5xg79	homo sapien	1201	61	10.4	398	2	Q21P42	SACD2	Q21p42	saccharoph
1129	61.5	10.4	735	2	Q498M5_RAT	Q498m5	rattus norv	1202	61	10.4	402	2	Q64WM1_BACFR		Q64wm1	bacteroides
1130	61.5	10.4	774	2	Q3SEM2_PART2	Q3sem2	paramecium	1203	61	10.4	402	2	Q5LGO5_BACFN		Q5lgo5	bacteroides
1131	61.5	10.4	774	2	Q3SEM3_PART2	Q3sem3	paramecium	1204	61	10.4	406	2	Q3FDG7_9BURK		Q3fdg7	burkholderi
1132	61.5	10.4	782	2	Q7PDS2_PLAYO	Q7pds2	plasmodium	1205	61	10.4	413	2	Q23015_CAEEL		Q23015	caenorhabdi
1133	61.5	10.4	816	2	Q5R449_PONPY	Q5r449	pongo pygma	1206	61	10.4	432	2	Q3BKP1_CAEEL		Q3bkp1	caenorhabdi
1134	61.5	10.4	818	2	Q6KF79_XENLA	Q6kf79	xenopus lae	1207	61	10.4	441	2	Q3PB67_PARDE		Q3pb67	paracoccus
1135	61.5	10.4	833	2	Q5R684_PONPY	Q5r684	pongo pygma	1208	61	10.4	447	2	Q4J3W1_AZOV1		Q4j3w1	azotobacter
1136	61.5	10.4	909	2	Q61GM2_CAEER	Q61gm2	caenorhabdi	1209	61	10.4	451	2	Q98173_MCV1		Q98173	molluscum c
1137	61.5	10.4	932	2	Q5Y4N8_RAT	Q5y4n8	rattus norv	1210	61	10.4	485	2	Q4H3Q6_CIOIN		Q4h3q6	ciona intes
1138	61.5	10.4	941	2	Q54YPO_DICDI	Q54yp0	dictyosteli	1211	61	10.4	506	2	Q8C7M2_MOUSE		Q8c7m2	mus musculus
1139	61.5	10.4	1124	2	Q23GM4_TETTH	Q23gm4	tetrahymena	1212	61	10.4	525	2	Q92162_BOMMO		P92162	bombyx mori
1140	61.5	10.4	1179	2	Q1S1Z0_MEDTR	Q1s1z0	medicago tr	1213	61	10.4	538	2	Q8CC86_MOUSE		Q8cc86	m adult mal
1141	61.5	10.4	1247	1	JAG2_MOUSE	Q9qye5	mus musculus	1214	61	10.4	563	2	Q7TP82_RAT		Q7tp82	rattus norv
1142	61.5	10.4	1267	2	Q2EG68_PONPY	Q2eg68	pongo pygma	1215	61	10.4	571	2	Q8C1E3_MOUSE		Q8c1e3	mus musculus
1143	61.5	10.4	1316	2	Q96JUT_HUMAN	Q96jut	homo sapien	1216	61	10.4	586	2	Q8KDS0_CHLTE		Q8kds0	chlorobium
1144	61.5	10.4	1373	2	Q75372_HUMAN	Q75372	homo sapien	1217	61	10.4	601	2	Q7M4J3_DICDI		Q7m4j3	dictyosteli
1145	61.5	10.4	1394	2	Q8MST1_DROME	Q8mst1	drosofila	1218	61	10.4	606	2	Q17LW1_AEDAE		Q17lw1	aedes aegypt
1146	61.5	10.4	1458	2	Q1ASU1_BRARE	Q1asu1	brachydanio	1219	61	10.4	610	2	Q4B0K0_9HURK		Q4b0k0	polaromonas
1147	61.5	10.4	1511	2	Q9VB21_DROME	Q9vb21	g sortilin-	1220	61	10.4	657	2	Q4T6N0_TETNG		Q4t6n0	tetradodon n
1148	61.5	10.4	1592	1	SORL_CHICK	Q98930	g sortilin-	1221	61	10.4	703	2	Q8C122_MOUSE		Q8c122	mus musculus
1149	61.5	10.4	1666	1	LTBP4_MOUSE	Q8k4g1	mus musculus	1222	61	10.4	715	2	Q9H0L5_HUMAN		Q9h0l5	homo sapien
1150	61.5	10.4	1702	2	Q6ZQAI_MOUSE	Q6zqa1	mus musculus	1223	61	10.4	735	2	Q8BZT2_MOUSE		Q8bzt2	mus musculus
1151	61.5	10.4	1721	2	Q614N6_CAEER	Q614n6	caenorhabdi	1224	61	10.4	745	2	Q8VCB2_MOUSE		Q8vcb2	mus musculus
1152	61.5	10.4	1761	2	Q17EM2_AEDAE	Q17ew2	aedes aegypt	1225	61	10.4	747	2	Q71SY5_HUMAN		Q71sy5	homo sapien
1153	61.5	10.4	1913	2	Q5SVA2_HUMAN	Q5sava2	homo sapien	1226	61	10.4	754	2	Q6P143_HUMAN		Q6p143	homo sapien
1154	61.5	10.4	2030	2	Q9VXV3_DROME	Q9vxxv3	drosofila	1227	61	10.4	754	2	Q707U4_HUMAN		Q707u4	homo sapien
1155	61.5	10.4	2045	1	AGRN_HUMAN	Q00468	homo sapien	1228	61	10.4	759	2	Q19UW4_9CAUD		Q19uw4	bacterioph
1156	61.5	10.4	2045	2	Q60FE1_HUMAN	Q60fel	homo sapien	1229	61	10.4	787	1	SNO_HUMAN		Q99835	homo sapien
1157	61.5	10.4	2224	2	Q44131_CAEEL	Q44131	caenorhabdi	1230	61	10.4	796	2	Q6QMH5_HUMAN		Q6qmh5	homo sapien
1158	61.5	10.4	2277	2	Q22QJ9_TETTH	Q22qj9	tetrahymena	1231	61	10.4	856	2	Q91LE1_WSSV		Q91le1	white spot
1159	61.5	10.4	2470	1	NOTC2_MOUSE	Q35516	mus musculus	1232	61	10.4	875	2	Q4CMA5_TRYCR		Q4cma5	trypanosoma
1160	61.5	10.4	2471	1	NOTC2_RAT	Q9qw30	rattus norv	1233	61	10.4	881	2	Q9W0A0_DROME		Q9w0a0	drosofila
1161	61.5	10.4	2570	1	STAB1_HUMAN	Q9ny15	homo sapien	1234	61	10.4	903	2	Q44397_TRITR		Q44397	trichuris t
1162	61.5	10.4	2843	2	Q89251_9FLAV	Q89251	gb virus c.	1235	61	10.4	915	2	Q4RSL5_TETNG		Q4rsl5	tetradodon n
1163	61.5	10.4	2873	2	Q69431_9FLAV	Q69431	gb virus c.	1236	61	10.4	937	2	Q9BLJ1_CIOIN		Q9blj1	ciona intes
1164	61.5	10.4	2966	2	Q4RMT7_TETNG	Q4rmt7	tetradodon n	1237	61	10.4	968	2	Q4SNB3_TETNG		Q4snb3	tetradodon n
1165	61.5	10.4	3126	2	Q3V514_MOUSE	Q3v514	mus musculus	1238	61	10.4	1027	2	Q22AD5_TETTH		Q22ad5	tetrahymena
1166	61.5	10.4	3333	1	LAMA3_MOUSE	Q61789	mus musculus	1239	61	10.4	1031	2	Q1EC80_DROME		Q1ec80	drosofila
1167	61.5	10.4	3457	2	Q4E0C7_TRYCR	Q4e0c7	trypanosoma	1240	61	10.4	1038	2	Q5A282_CANAL		Q5a282	candida alb
1168	61.5	10.4	3548	2	Q5VTE4_HUMAN	Q5vte4	homo sapien	1241	61	10.4	1062	2	Q60789_MOUSE		Q60789	mus musculus
1169	61.5	10.4	3574	2	Q4LDE5_HUMAN	Q4ldes5	homo sapien	1242	61	10.4	1111	2	Q80YN4_RAT		Q80yn4	rattus norv
1170	61.5	10.4	3834	2	Q29DL3_DROPS	Q29dl3	drosofila	1243	61	10.4	1123	2	Q5RD15_PONPY		Q5rd15	pongo pygma
1171	61.5	10.4	4006	2	Q35452_MOUSE	Q35452	mus musculus	1244	61	10.4	1128	2	Q4S6G8_TETNG		Q4s6g8	tetradodon n
1172	61.5	10.4	4114	2	Q54796_MOUSE	Q54796	mus musculus	1245	61	10.4	1134	2	Q2GRE7_CHAGB		Q2gre7	chaetomium
1173	61	10.4	93	2	Q4HA1_ORISA	Q4ha1	oryza sativ	1246	61	10.4	1170	1	TSP1_BOVIN		Q28178	bos taurus
1174	61	10.4	95	2	Q9ZGV4_ECO57	Q9zgv4	escherichia	1247	61	10.4	1202	1	JAG2_RAT		P97607	rattus norv
1175	61	10.4	111	1	COL_MYOCCO	Q92gv4	myocastor c	1248	61	10.4	1213	1	JAG1B_BRARE		Q90y54	brachydanio
1176	61	10.4	115	1	MERT_SHEPU	Q54462	shewanella	1249	61	10.4	1270	2	Q9GPN0_CAEER		Q9gpn0	caenorhabdi
1177	61	10.4	116	2	Q5T6Z9_HUMAN	Q5t6z9	homo sapien	1250	61	10.4	1382	2	Q4CPN1_TRYCR		Q4cpn1	trypanosoma
1178	61	10.4	156	2	Q29FD2_DROPS	Q29fd2	drosofila	1251	61	10.4	1385	2	Q613Q0_CAEER		Q613q0	caenorhabdi
1179	61	10.4	177	2	Q6SG20_9BACT	Q6sg20	uncultured	1252	61	10.4	1396	2	Q4RPY1_TETNG		Q4rpy1	tetradodon n
1180	61	10.4	178	2	Q5TPK8_ANOGA	Q5tpk8	anopheles g	1253	61	10.4	1418	2	Q93457_SCOMX		Q93457	scophthalmu
1181	61	10.4	190	2	Q93518_AGKHB	Q93518	agkistrodon	1254	61	10.4	1476	2	Q90285_CARAU		Q90285	carassius a
1182	61	10.4	205	2	Q5T700_HUMAN	Q5t700	homo sapien	1255	61	10.4	1477	2	Q4H3A4_CIOIN		Q4h3a4	ciona intes
1183	61	10.4	212	2	Q90Y44_AGKHP	Q90y44	agkistrodon	1256	61	10.4	1506	2	Q54U77_DICDI		Q54u77	dictyosteli
1184	61	10.4	214	2	Q4RG67_TETNG	Q4rg67	tetradodon n	1257	61	10.4	1525	2	Q4D8M2_TRYCR		Q4d8m2	trypanosoma
1185	61	10.4	227	2	Q1AVJ4_9ACTN	Q1avj4	rubrobacter	1258	61	10.4	1747	2	Q4CQV8_TRYCR		Q4cq8	trypanosoma
1186	61	10.4	249	2	Q5CK70_CRYHO	Q5ck70	cryptospori	1259	61	10.4	1827	2	Q4CQ44_TRYCR		Q4cq44	trypanosoma
1187	61	10.4	254	2	Q2U3M4_ASPOR	Q2u3m4	aspergillus	1260	61	10.4	1834	2	Q4C057_TRYCR		Q4cq57	trypanosoma
1188	61	10.4	260	2	Q3PB20_PARDE	Q3pb20	paracoccus	1261	61	10.4	1955	1	AGRN_CHICK		P31696	gallus gall
1189	61	10.4	269	2	Q9U2B8_CAEEL	Q9u2b8	caenorhabdi	1262	61	10.4	2262	2	Q4CXH5_TRYCR		Q4cxh5	trypanosoma
1190	61	10.4	289	2	Q1PG20_HYDSY	Q1pg20	hydractinia	1263	61	10.4	2345	2	Q4CX92_TRYCR		Q4cx92	trypanosoma
1191	61	10.4	289	2	Q1PG09_HYDSY	Q1pg09	hydractinia	1264	61	10.4	2450	2	Q9P273_HUMAN		Q9p273	homo sapien
1192	61	10.4	289	2	Q1PG19_HYDSY	Q1pg19	hydractinia	1265	61	10.4	2476	1	ZAN_PIG		Q28983	sus scrofa
1193	61	10.4	289	2	Q1PG18_HYDSY	Q1pg18	hydractinia	1266	61	10.4	2520	2	Q5SVC7_MOUSE		Q5svc7	mus musculus
1194	61	10.4	289	2	Q1PG17_HYDSY	Q1pg17	hydractinia	1267	61	10.4	2806	2	Q4DH79_TRYCR		Q4dh79	trypanosoma
1195	61	10.4	307	2	Q4C965_CROWT	Q4c965	crocosphaer	1268	61	10.4	2857	2	Q29L36_DROPS		Q29l36	drosofila
1196	61	10.4	309	2	Q69525_MYCLE	Q69525	mycobacteri	1269	61	10.4	3450	2	Q4D801_TRYCR		Q4d801	trypanosoma
1197	61	10.4	320	2	Q8QQY4_WSSV	Q8qqy4	white spot	1270	61	10.4	3452	2	Q4D134_TRYCR		Q4d134	trypanosoma
1198	61	10.4	339	2	Q4CKA1_TRYCR	Q4ckal	trypanosoma	1271	61	10.4	3467	2	Q4D6V4_TRYCR		Q4d6v4	trypanosoma
1199	61	10.4	352	2	Q20WV9_RHOPB	Q20wv9	rhodospseudo	1272	61	10.4	3473	2	Q4DAR6_TRYCR		Q4dar6	trypanosoma

1273	61	10.4	3476	2	Q4DS00_TRYCR	Q4ds00 trypanosoma	1346	60.5	10.3	700	2	Q5SW66_HUMAN	Q5sw66 homo sapien
1274	61	10.4	3480	2	Q4DH83_TRYCR	Q4dh83 trypanosoma	1347	60.5	10.3	723	1	DL11_HUMAN	DL11 homo sapien
1275	61	10.4	3483	2	Q4DRP9_TRYCR	Q4drp9 trypanosoma	1348	60.5	10.3	737	2	Q8NFT8_HUMAN	Q8nft8 homo sapien
1276	61	10.4	3487	2	Q4DL83_TRYCR	Q4dl83 trypanosoma	1349	60.5	10.3	737	2	Q8IYTO_HUMAN	Q8iyto homo sapien
1277	61	10.4	5429	2	Q16KQ8_AEDAE	Q16kq8 aedes aegypt	1350	60.5	10.3	738	2	Q90245_CHICK	Q90245 gallus gall
1278	60.5	10.3	64	1	CX12_CONIM	Pe9496 conus imper	1351	60.5	10.3	754	2	Q5TNY8_ANOGA	Q5tny8 anopheles g
1279	60.5	10.3	64	2	Q59AAB_CONIM	Q59aa8 conus imper	1352	60.5	10.3	787	1	ITB3_MOUSE	ITB3 mus musculus
1280	60.5	10.3	81	2	Q5RLQ5_PIG	Q5rlq5 sus scrofa	1353	60.5	10.3	787	1	Q3TZC6_MOUSE	Q3tzc6 mus musculus
1281	60.5	10.3	88	2	Q6UXU7_HUMAN	Q6uxu7 homo sapien	1354	60.5	10.3	790	2	Q4R728_MACFA	Q4r728 macaca fasc
1282	60.5	10.3	92	2	Q8GX19_ARATH	Q8gxy9 arabidopsis	1355	60.5	10.3	833	2	Q5AB17_CANAL	Q5ab17 candida alb
1283	60.5	10.3	96	2	Q9CJ11_LACLA	Q9cjl1 lactococcus	1356	60.5	10.3	834	2	Q5AAS8_CANAL	Q5aas8 candida alb
1284	60.5	10.3	99	1	GASA3_ARATH	P46687 arabidopsis	1357	60.5	10.3	836	2	Q19057_PONPY	Q19057 pongo pygma
1285	60.5	10.3	99	2	Q9D638_MOUSE	Q9d638 mus musculus	1358	60.5	10.3	864	2	Q6KFB0_XENLA	Q6kfb0 xenopus lae
1286	60.5	10.3	115	2	Q19VG5_MAIZE	Q19vg5 zea mays	1359	60.5	10.3	871	2	Q4SCX8_TETNG	Q4scx8 tetraodon n
1287	60.5	10.3	117	2	Q53TQ4_HUMAN	Q53tq4 homo sapien	1360	60.5	10.3	883	2	Q9VBN1_DROME	Q9vbn1 drosophila
1288	60.5	10.3	126	2	Q6FAF7_TRISC	Q6faf7 triakis scy	1361	60.5	10.3	917	2	Q7VE20_DROME	Q7ve20 drosophila
1289	60.5	10.3	129	2	Q9YCE5_AERPE	Q9yce5 aeropyrum p	1362	60.5	10.3	926	2	Q7LXB6_HUMAN	Q7lxb6 homo sapien
1290	60.5	10.3	129	2	Q8H7V2_ORYSA	Q8h7v2 oryza sativ	1363	60.5	10.3	931	2	Q7Z3T9_HUMAN	Q7z3t9 homo sapien
1291	60.5	10.3	131	2	Q9YZW6_FFLAV	Q9yzw6 gb virus c.	1364	60.5	10.3	931	2	Q7LXB7_HUMAN	Q7lxb7 homo sapien
1292	60.5	10.3	131	2	Q9YZW4_FFLAV	Q9yzw4 gb virus c.	1366	60.5	10.3	978	1	MCR_MOUSE	MCR mus musculus
1293	60.5	10.3	131	2	Q9YZW5_FFLAV	Q9yzw5 gb virus c.	1367	60.5	10.3	1024	2	Q9BX11_HUMAN	Q9bx11 homo sapien
1294	60.5	10.3	131	2	Q9YUN0_FFLAV	Q9yun0 gb virus c.	1368	60.5	10.3	1030	2	Q22D69_TERTH	Q22d69 tetrahymena
1295	60.5	10.3	135	2	Q9YUN0_FFLAV	Q9yun0 gb virus c.	1369	60.5	10.3	1031	2	Q9VBN0_DROME	Q9vbn0 drosophila
1296	60.5	10.3	155	2	Q21GR8_SACD2	Q21gr8 saccharoph	1370	60.5	10.3	1037	2	Q6NPP6_DROME	Q6np66 drosophila
1297	60.5	10.3	161	2	Q35KP7_9BRAD	Q35kp7 bradyrhizob	1371	60.5	10.3	1071	2	Q4RTI6_TETNG	Q4rti6 tetraodon n
1298	60.5	10.3	168	1	WFDCC2_RAT	Q8chn3 rattus norv	1372	60.5	10.3	1087	2	Q23H08_TERTH	Q23h08 tetrahymena
1299	60.5	10.3	173	2	Q3NQL2_SHEPR	Q3nql2 shewanella	1373	60.5	10.3	1101	2	Q1SA17_MEDTR	Q1sa17 medicago tr
1300	60.5	10.3	181	2	Q3F736_9BURK	Q3f736 burkholderi	1374	60.5	10.3	1104	1	NFX1_HUMAN	NFX1 homo sapien
1301	60.5	10.3	181	2	Q872V4_NEUCR	Q872v4 neurospora	1375	60.5	10.3	1116	2	Q55A31_DICDI	Q55a31 dictyosteli
1302	60.5	10.3	214	2	Q7NEW7_GLOVI	Q7new7 gloeobacter	1376	60.5	10.3	1117	2	Q86KY4_DICDI	Q86ky4 dictyosteli
1303	60.5	10.3	234	2	Q5C033_SCHJA	Q5c033 schistosoma	1377	60.5	10.3	1120	2	Q96EL5_HUMAN	Q96el5 mus musculus
1304	60.5	10.3	249	2	Q14VV4_SHERP	Q14vv4 anelid herpe	1378	60.5	10.3	1389	1	LTB1S_MOUSE	LTB1S mus musculus
1305	60.5	10.3	251	2	Q2EFY6_ATEGE	Q2efy6 atelea geof	1379	60.5	10.3	1394	2	Q505C9_MOUSE	Q505c9 mus musculus
1306	60.5	10.3	252	2	Q2GLX9_CHAGB	Q2glx9 chaetomium	1380	60.5	10.3	1577	2	Q9VSR9_DROME	Q9vsr9 drosophila
1307	60.5	10.3	252	2	Q2EG79_LAGLA	Q2eg79 lagotrrix l	1381	60.5	10.3	1622	2	Q3ZTN4_SAISC	Q3ztn4 saimir sci
1308	60.5	10.3	288	2	Q4TT94_CAEEL	Q4tt94 caenorhabdi	1382	60.5	10.3	1674	2	Q80Z18_MOUSE	Q80z18 mus musculus
1309	60.5	10.3	289	1	F1P26_ARATH	Q9zv07 arabidopsis	1383	60.5	10.3	1713	1	LTB1L_MOUSE	LTB1L mus musculus
1310	60.5	10.3	290	2	Q9DAU5_MOUSE	Q9daus5 mus musculus	1384	60.5	10.3	1914	2	Q4WHJ5_ASPFU	Q4whj5 aspergillus
1311	60.5	10.3	291	2	Q9UDM2_HUMAN	Q9udm2 homo sapien	1385	60.5	10.3	2038	2	Q7QFS2_ANOGA	Q7qfs2 anopheles g
1312	60.5	10.3	296	2	Q5M8H8_XENTR	Q5m8h8 xenopus tro	1386	60.5	10.3	2516	2	Q7TQ52_MOUSE	Q7tq52 mus musculus
1313	60.5	10.3	307	2	Q7R3F7_GIALA	Q7r3f7 giardia lam	1387	60.5	10.3	2526	2	Q7TQ51_MOUSE	Q7tq51 mus musculus
1314	60.5	10.3	313	2	Q8K3U2_MOUSE	Q8k3u2 mus musculus	1388	60.5	10.3	2531	1	NOTC1_MOUSE	NOTC1 mus musculus
1315	60.5	10.3	316	1	1BP2_PIG	P24853 sus scrofa	1389	60.5	10.3	2531	2	Q7TQ50_MOUSE	Q7tq50 mus musculus
1316	60.5	10.3	324	1	CH12_TOBAC	P24091 nicotiana t	1390	60.5	10.3	2531	2	NOTCH_MOUSE	NOTCH drosophila
1317	60.5	10.3	324	1	Q9FEW1_NICSY	Q9few1 nicotiana s	1391	60.5	10.3	2703	1	Q7Q509_BRARE	Q7q509 brachydanio
1318	60.5	10.3	335	2	Q4UBZ5_THEAN	Q4ubz5 theileria a	1392	60.5	10.3	2783	2	Q36178_9FLAV	Q36178 gb virus c.
1319	60.5	10.3	349	1	CTGF_HUMAN	P29279 homo sapien	1393	60.5	10.3	2842	2	Q09804_9FLAV	Q09804 gb virus c.
1320	60.5	10.3	349	2	Q6FHL8_HUMAN	Q6fhl8 homo sapien	1394	60.5	10.3	2842	2	Q80T03_MOUSE	Q80t03 mus musculus
1321	60.5	10.3	349	2	Q5M8Y4_HUMAN	Q5m8t4 homo sapien	1395	60.5	10.3	2850	2	P89967_9FLAV	P89967 gb virus c.
1322	60.5	10.3	370	2	Q1CIM2_YERPE	Q1cim2 yersinia pe	1396	60.5	10.3	2873	2	Q93070_9FLAV	Q93070 gb virus c.
1323	60.5	10.3	370	2	Q1C788_YERPE	Q1c788 yersinia pe	1397	60.5	10.3	2873	2	Q90481_9FLAV	Q90481 gb virus c.
1324	60.5	10.3	370	2	Q66A46_YERPS	Q66a46 yersinia ps	1398	60.5	10.3	2910	2	Q9WGY8_9FLAV	Q9wgy8 gb virus c.
1325	60.5	10.3	370	2	Q8ZE17_YERPE	Q8ze17 yersinia pe	1399	60.5	10.3	2933	2	Q09803_9FLAV	Q09803 gb virus c.
1326	60.5	10.3	384	2	Q8D0L6_YERPE	Q8d0l6 yersinia pe	1400	60.5	10.3	3480	2	Q4E492_TRYCR	Q4e492 trypanosoma
1327	60.5	10.3	385	1	DLK_MOUSE	Q99163 mus musculus	1401	60.5	10.3	3486	2	Q4DGM4_TRYCR	Q4dgm4 trypanosoma
1328	60.5	10.3	385	2	Q925U3_MOUSE	Q925u3 m dlk (gelt	1402	60.5	10.3	4071	1	Q6KZL1_CHICK	Q6kz1 gallus gall
1329	60.5	10.3	386	2	Q53L82_ORYSA	Q53l82 oryza sativ	1403	60.5	10.3	4544	1	LRP1_HUMAN	LRP1 mus sapien
1330	60.5	10.3	394	2	Q6Z434_ORYSA	Q6z434 oryza sativ	1404	60.5	10.3	5193	1	USH2A_MOUSE	USH2A mus musculus
1331	60.5	10.3	401	2	Q811K6_MOUSE	Q811k6 mus musculus	1405	60.5	10.3	5703	1	MUC5B_HUMAN	MUC5B homo sapien
1332	60.5	10.3	401	2	Q811K6_MOUSE	Q811k6 mus musculus	1406	60.5	10.3	5703	1	Q1JSM5_TOXGO	Q1jms5 toxoplasma
1333	60.5	10.3	452	1	ZN672_HUMAN	Q96113 drosophila	1407	60.5	10.3	1269	2	Q1JSM5_TOXGO	Q1jms5 toxoplasma
1334	60.5	10.3	454	2	Q8B714_HUMAN	Q8b714 homo sapien	1408	60	10.2	84	2	Q8MNZ3_SCHMA	Q8mnz8 schistosoma
1335	60.5	10.3	499	2	Q88714_MOUSE	Q88714 mus musculus	1409	60	10.2	93	2	Q6J0U3_BRACH	Q6j0u3 brachioosto
1336	60.5	10.3	515	1	NAGPA_HUMAN	Q9uk23 homo sapien	1410	60	10.2	97	2	Q3E715_ARATH	Q3e715 arabidopsis
1337	60.5	10.3	533	2	Q66HB8_RAT	Q66hb8 rattus norv	1411	60	10.2	102	1	108_LYCES	108 lycos
1338	60.5	10.3	551	2	Q99967_CAEEL	Q99967 caenorhabdi	1412	60	10.2	102	2	Q8TBR8_HUMAN	Q8tbr8 homo sapien
1339	60.5	10.3	556	2	Q5VXW6_HUMAN	Q5vwx6 homo sapien	1413	60	10.2	116	2	Q7YX03_CAEEL	Q7yx03 caenorhabdi
1340	60.5	10.3	562	2	Q10703_9FLAV	Q10703 gb virus c.	1414	60	10.2	118	2	Q21ZP4_RHOP2	Q21zpf4 rhodopeudo
1341	60.5	10.3	569	2	Q7PMF9_ANOGA	Q7pmf9 anopheles g	1415	60	10.2	121	2	Q6ZNN7_HUMAN	Q6znn7 homo sapien
1342	60.5	10.3	591	2	Q6LBN5_HUMAN	Q6lbn5 homo sapien	1416	60	10.2	125	2	Q4WZP5_ASPFU	Q4wzps aspergillus
1343	60.5	10.3	637	2	Q7PFQ7_ANOGA	Q7pfq7 anopheles g	1417	60	10.2	126	2	Q8T5W4_CAEER	Q8t5w4 caenorhabdi
1344	60.5	10.3	664	1	DL1C_BRARE	Q9iat6 brachydanio	1418	60	10.2	127	2	Q8T5X2_CAEER	Q8t5x2 caenorhabdi
1345	60.5	10.3	680	2	Q9QW15_9MURI	Q9qw15 mus sp. bet							

RL Protein Sci. 13:2819-2824(2004).
CC -1- FUNCTION: Potently contract gastrointestinal (GI) smooth muscle.
CC Induces proliferation, migration and fenestration (the formation
CC of membrane discontinuities) in capillary endothelial cells
CC derived from endocrine glands. Has little or no effect on a
CC variety of other endothelial and non-endothelial cell types.
CC -1- SUBCELLULAR LOCATION: Secreted protein.
CC -1- TISSUE SPECIFICITY: Expressed in the steroidogenic glands, ovary,
CC testis, adrenal and placenta.
CC -1- SIMILARITY: Belongs to the prokinectin family.
CC
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL; AF333024; AAK49918.1; -; mRNA.
CC EMBL; AY029225; AAK33111.1; -; mRNA.
CC EMBL; AY358683; AAK89046.1; -; mRNA.
CC UniGene; Hs.514793; -;
CC HSP; P25687; 1MT
CC Ensembl; ENSG00000143125; Homo sapiens.
CC H-InvDB; HIX0000868; -;
CC HGNC; HGNC:18454; PROK1.
CC MIM; 606233; Gene.
CC RZPD-ProtExp; IOH11285; -;
CC RZPD-ProtExp; RZPD0839A10127; -;
CC RZPD-ProtExp; RZPD0839A10128; -;
CC RZPD-ProtExp; W1161; -;
CC InterPro; IPR009523; Prokinectin.
CC PANTHER; PTHR18821; Prokinectin; 1.
CC Pfam; PF06607; Prokinectin; 1.
CC Direct protein sequencing; Growth factor; Mitogen; Signal.
FT SIGNAL 1 19
FT CHAIN 20 105
FT FT Prokinectin-1.
FT FT /FTID=PRO_0000025807.
FT FT
FT DISULFID 26 38
FT By similarity.
FT DISULFID 32 50
FT By similarity.
FT DISULFID 37 78
FT By similarity.
FT DISULFID 60 86
FT By similarity.
FT DISULFID 80 96
FT By similarity.
FT SEQUENCE 105 AA; 11715 MW; C7E3FDE30EFPB416A CRC64;
SQ
Query Match 100.0%; Score 589; DB 1; Length 105;
Best Local Similarity 100.0%; Pred. No. 8.6e-55;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRGATRVSIMLLVTVDCAVITGACERDVCGAGTCCCAISLWLRGLMCTPLGREGSEC 60
DB 1 MRGATRVSIMLLVTVDCAVITGACERDVCGAGTCCCAISLWLRGLMCTPLGREGSEC 60
QY 61 HPGSHKVPFFRRKRKHTCPCLPNLLCSRFDPGRYRCSDMLKNINF 105
DB 61 HPGSHKVPFFRRKRKHTCPCLPNLLCSRFDPGRYRCSDMLKNINF 105
RESULT 2
ID Q5VWD4 HUMAN PRELIMINARY; PRT; 105 AA.
AC Q5VWD4
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DT 13-JUN-2006, entry version 9.
DE Prokinectin 1.
DE Name=PROK1; ORFNames=RP11-470L19.1-001;
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN
RP NUCLEOTIDE SEQUENCE.
RA Hall R.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
RN [2]

RP NUCLEOTIDE SEQUENCE.
RA Wallis J.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL; AL390797; CAH71489.1; -; Genomic DNA.
CC EMBL; AL358215; CAH71489.1; JOINED; Genomic DNA.
CC EMBL; AL358215; CAH71402.1; -; Genomic DNA.
CC EMBL; AL390797; CAH71402.1; JOINED; Genomic DNA.
CC UniGene; Hs.514793; -;
CC Ensembl; ENSG00000143125; Homo sapiens.
CC RZPD-ProtExp; IOH11285; -;
CC RZPD-ProtExp; RZPD0839A10127; -;
CC RZPD-ProtExp; RZPD0839A10128; -;
CC RZPD-ProtExp; W1161; -;
CC InterPro; IPR009523; Prokinectin.
CC PANTHER; PTHR18821; Prokinectin; 1.
CC Pfam; PF06607; Prokinectin; 1.
CC SEQUENCE 105 AA; 11715 MW; C7E3FDE30EFPB416A CRC64;
SQ
Query Match 100.0%; Score 589; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 8.6e-55;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRGATRVSIMLLVTVDCAVITGACERDVCGAGTCCCAISLWLRGLMCTPLGREGSEC 60
DB 1 MRGATRVSIMLLVTVDCAVITGACERDVCGAGTCCCAISLWLRGLMCTPLGREGSEC 60
QY 61 HPGSHKVPFFRRKRKHTCPCLPNLLCSRFDPGRYRCSDMLKNINF 105
DB 61 HPGSHKVPFFRRKRKHTCPCLPNLLCSRFDPGRYRCSDMLKNINF 105
RESULT 3
ID Q8TC69 HUMAN PRELIMINARY; PRT; 105 AA.
AC Q8TC69;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 13-JUN-2006, entry version 1.
DE Prokinectin 1.
DE Name=PROK1;
DE OS Homo sapiens (Human).
DE OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DE OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
DE OC Catarrhini; Hominidae; Homo.
DE NCBI_TaxID=9606;
DE [1]
RN
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Wozley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Smallos D.E.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Testis;
 RG NIH MGC Project;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
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 CC -----
 DR EMBL; BC025399; AAH25399.1; -, mRNA.
 DR HSSP; P25687; 1IMT.
 DR Ensembl; ENSG00000143125; Homo sapiens.
 DR RZPD-ProExp; IOH11285; -.
 DR RZPD-ProExp; RZPD0839A10127; -.
 DR RZPD-ProExp; RZPD0839A10128; -.
 DR RZPD-ProExp; W161; -.
 DR InterPro; IPR009523; Prokineticin.
 DR PANTHER; PTHR18821; Prokineticin; 1.
 DR Pfam; PF06607; Prokineticin; 1.
 SQ SEQUENCE 105 AA; 11729 MW; E570FDE30EFB52D2 CRC64;

 Query Match 99.8%; Score 588; DB 2; Length 105;
 Best Local Similarity 99.0%; Pred. No. 1.1e-54;
 Matches 104; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 QY 1 MRGATRVSIMLLLVTSDCAVITGACERDVOCGAGTCCCAISLWRLGLMCTPLRGEGEC 60
 DB 1 MRGATRVSIMLLLVTSDCAVITGACERDVOCGAGTCCCAISLWRLGLMCTPLRGEGEC 60

 QY 61 HPGSHKVPFFKRKHHTCPCLPNTLLCSFPDGRYRCSDMLKNINF 105
 DB 61 HPGSHKVPFFKRKHHTCPCLPNTLLCSFPDGRYRCSDMLKNINF 105

 RESULT 4
 PROK1_RAT
 ID PROK1_RAT STANDARD; PRT; 105 AA.
 AC Q8R414;
 DT 19-JUL-2003, integrated into UniProtKB/Swiss-Prot.
 DT 01-JUN-2002, sequence version 1.
 DT 18-APR-2006, entry version 25.
 DE Prokineticin-1 precursor (Endocrine-gland-derived vascular endothelial growth factor) (EG-VEGF).
 GN Name=Proki;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=22050031; PubMed=12054613; DOI=10.1016/S0006-291X(02)00239-5;
 RA Masuda Y., Takatsu Y., Terao Y., Kumano S., Ishibashi Y., Suenaga M., Abe M., Fukusumi S., Watanabe T., Shintani Y., Yamada T., Hinuma S., Inatomi N., Ohtaki T., Onda H., Fujino M.;
 RT "Isolation and identification of EG-VEGF/prokineticins as cognate ligands for two orphan G-protein-coupled receptors.";
 RL Biochem. Biophys. Res. Commun. 293:396-402(2002).
 CC -1- FUNCTION: Potently contract gastrointestinal (GI) smooth muscle. Induces proliferation, migration and fenestration (the formation of membrane discontinuities) in capillary endothelial cells derived from endocrine glands. Has little or no effect on a variety of other endothelial and non-endothelial cell types (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted protein (By similarity).
 CC -1- SIMILARITY: Belongs to the prokineticin family.
 CC -----
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 CC -----
 DR EMBL; AY089983; AA09104.1; -, mRNA.
 DR UniGene; Rn.82757; -.

DR HSSP; P25687; 1IMT.
 DR Ensembl; ENSRNOG0000018201; Rattus norvegicus.
 DR RGD; 620898; Proki.
 DR GO; GO:0008283; P:cell proliferation; TAS.
 DR GO; GO:0045765; P:regulation of angiogenesis; NAS.
 DR InterPro; IPR009523; Prokineticin.
 DR PANTHER; PTHR18821; Prokineticin; 1.
 DR Pfam; PF06607; Prokineticin; 1.
 KW Growth factor; Mitogen; Signal.
 FT SIGNAL 1 19 Potential.
 FT CHAIN 20 105 Prokineticin-1.
 FT FTID=PRO 0000025808.
 FT DISULFID 26 38 By similarity.
 FT DISULFID 32 50 By similarity.
 FT DISULFID 37 78 By similarity.
 FT DISULFID 80 86 By similarity.
 FT DISULFID 96 By similarity.
 SQ SEQUENCE 105 AA; 11643 MW; 8DF0C42122B1C5B6 CRC64;

 Query Match 92.5%; Score 545; DB 1; Length 105;
 Best Local Similarity 89.5%; Pred. No. 4.2e-50;
 Matches 94; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

 QY 1 MRGATRVSIMLLLVTSDCAVITGACERDVOCGAGTCCCAISLWRLGLMCTPLRGEGEC 60
 DB 1 MRGATRVSIMLLLVTSDCAVITGACERDVOCGAGTCCCAISLWRLGLMCTPLRGEGEC 60

 QY 61 HPGSHKVPFFKRKHHTCPCLPNTLLCSFPDGRYRCSDMLKNINF 105
 DB 61 HPGSHKVPFFKRKHHTCPCLPNTLLCSFPDGRYRCSDMLKNINF 105

 RESULT 5
 Q8K457_MOUSE
 ID Q8K457_MOUSE PRELIMINARY; PRT; 81 AA.
 AC Q8K457;
 DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
 DT 01-OCT-2002, sequence version 1.
 DT 07-FEB-2006, entry version 12.
 DE Prokineticin 1 (Fragment).
 GN Name=Proki; Synonyms=PK1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6;
 RX MEDLINE=22022134; PubMed=12024206; DOI=10.1038/417405a;
 RA Cheng M.Y., Bullock C.M., Li C., Lee A.G., Bermak J.C., Belluzzi J., Weaver D.R., Leslie F.M., Zhou Q.-Y.;
 RT "Prokineticin 2 transmits the behavioural circadian rhythm of the suprachiasmatic nucleus.";
 RL Nature 417:405-410(2002).
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 DR EMBL; AF487281; AAM49573.1; -, mRNA.
 DR HSSP; P25687; 1IMT.
 DR Ensembl; ENSMUSG00000046213; Mus musculus.
 DR MGI; MGI:2180370; Proki.
 DR GO; GO:0005576; C:extracellular region; IDA.
 DR GO; GO:0000187; P:activation of MAPK activity; IDA.
 DR GO; GO:0007623; P:circadian rhythm; TAS.
 DR GO; GO:0008284; P:positive regulation of cell proliferation; IDA.
 DR GO; GO:0045765; P:regulation of angiogenesis; IDA.
 DR InterPro; IPR009523; Prokineticin.
 DR PANTHER; PTHR18821; Prokineticin; 1.
 DR Pfam; PF06607; Prokineticin; 1.
 FT NON_TER 1 1
 SQ SEQUENCE 81 AA; 9192 MW; 7BBE3EC6B16A8011 CRC64;


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Query Match 73.3%; Score 432; DB 2; Length 81;
Best Local Similarity 87.7%; Pred. No. 3.6e-36;
Matches 71; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 25 ACERDVQCGAGTCCATSLWLRGLMCTPLGREGECHPGSHKVPFFFRKRKHHTCPCLPNL 84
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 ACERDVQCGAGTCCATSLWLRGLMCTPLGREGECHPGSHKVPFFFRKRKHHTCPCLPNL 60

QY 85 LCSRFPDGRYRCMDLKNINF 105
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 LCSRFPDGRYRCMDLKNANF 81

RESULT 6
Q3ZF12_BOVIN PRELIMINARY; PRT; 81 AA.
AC Q3ZF12_BOVIN PRELIMINARY; PRT; 81 AA.
DT 27-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 27-SEP-2005, sequence version 1.
DT 18-APR-2006, entry version 4.
DE Prokineticin-1 (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15932929; DOI=10.1210/en.2005-0297;
RA Kisilouk T., Podlowski H., Spaniel-Sorowski K., Ovadia O., Zhou Q.Y.,
RA Meidan R.;
RT "Prokineticins (endocrine gland-derived vascular endothelial growth
RT factor and bFGF) in the bovine ovary: expression and role as mitogens
RT and survival factors for corpus luteum-derived endothelial cells.";
RL Endocrinology 146:3950-3958(2005).
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CC -----
CC EMBL; AY877432; ANX81517.1; -; mRNA.
DR InterPro; IPR009523; Prokineticin.
DR PANTHER; PTHR18821; Prokineticin; 1.
DR Pfam; PF06607; Prokineticin; 1.
FT NON TER 1
SQ SEQUENCE 81 AA; 9086 MW; 228634A7B83BA536 CRC64;

Query Match 70.8%; Score 417; DB 2; Length 81;
Best Local Similarity 87.7%; Pred. No. 1.4e-36;
Matches 71; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 25 ACERDVQCGAGTCCATSLWLRGLMCTPLGREGECHPGSHKVPFFFRKRKHHTCPCLPNL 84
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 ACERDVQCGAGTCCATSLWLRGLMCTPLGREGECHPGSHKVPFFFRKRKHHTCPCLPNL 60

QY 85 LCSRFPDGRYRCMDLKNINF 105
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 LCSRGLDGRYRCSTNLKNINF 81

RESULT 7
Q2XXR8_VARVA PRELIMINARY; PRT; 104 AA.
ID Q2XXR8_VARVA PRELIMINARY; PRT; 104 AA.
AC Q2XXR8;
DT 20-DEC-2005, integrated into UniProtKB/TrEMBL.
DT 20-DEC-2005, sequence version 1.
DT 18-APR-2006, entry version 5.
DE AVIToxin-VAR1 precursor.
OS Varanus varius (Lace monitor).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Lepidodactylia; Squamata; Scieroglossa; Anguimorpha; Varanidae; Varanus.
OX NCBI_TaxID=8559;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=16292255; DOI=10.1038/nature04328;
RA Fry B.G., Vidal N., Norman J.A., Vonk F.J., Scheib H., Ramjan S.F.,
RA Kuruppu S., Fung K., Blair Hedges S., Richardson M.K., Hodgson W.C.,
RA Ignjatovic V., Summerhayes R., Kochva E.;
RT "Early evolution of the venom system in lizards and snakes.";
RL Nature 439:584-588(2006).
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CC -----
CC EMBL; DQ139878; AAZ75584.1; -; mRNA.
DR SMR; Q2XXR7; 20-97.
DR InterPro; IPR009523; Prokineticin.
DR PANTHER; PTHR18821; Prokineticin; 1.
DR Pfam; PF06607; Prokineticin; 1.
KW Signal.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 104 AVIToxin-VAR2.
SQ SEQUENCE 104 AA; 11191 MW; C25A83A6B59D3AA3 CRC64;

Query Match 61.6%; Score 363; DB 2; Length 104;
Best Local Similarity 56.3%; Pred. No. 1e-30;
Matches 58; Conservative 21; Mismatches 24; Indels 0; Gaps 0;
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RP NUCLEOTIDE SEQUENCE.
RX TISSUE=Compound mandibular venom gland;
RX PubMed=16292255; DOI=10.1038/nature04328;
RA Fry B.G., Vidal N., Norman J.A., Vonk F.J., Scheib H., Ramjan S.F.,
RA Kuruppu S., Fung K., Blair Hedges S., Richardson M.K., Hodgson W.C.,
RA Ignjatovic V., Summerhayes R., Kochva E.;
RT "Early evolution of the venom system in lizards and snakes.";
RL Nature 439:584-588(2006).
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CC -----
CC EMBL; DQ139877; AAZ75583.1; -; mRNA.
DR SMR; Q2XXR8; 20-97.
DR InterPro; IPR009523; Prokineticin.
DR PANTHER; PTHR18821; Prokineticin; 1.
DR Pfam; PF06607; Prokineticin; 1.
KW Signal.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 104 AVIToxin-VAR1.
SQ SEQUENCE 104 AA; 11217 MW; C25A96B3B59D3AA3 CRC64;

Query Match 62.5%; Score 368; DB 2; Length 104;
Best Local Similarity 57.3%; Pred. No. 3e-31;
Matches 59; Conservative 20; Mismatches 24; Indels 0; Gaps 0;

QY 1 MRCATRVSIMLLVTVSDCAVITGACERDVQCGAGTCCATSLWLRGLMCTPLGREGECH 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MRSLLCAPLILLLLSAGESAVITGACDKDLCQCGMGCCAVSLWIRSTRICTPGLSSGDC 60

QY 61 HPQSHKVPFFFRKRKHHTCPCLPNLLCSRFDPDGRYRCMDLKN1 103
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 HPLSHKVPFDGQRKHHTCPCLPNLVCGQTSPGKYKCLPEFKNV 103

RESULT 8
Q2XXR7_VARVA PRELIMINARY; PRT; 104 AA.
ID Q2XXR7_VARVA PRELIMINARY; PRT; 104 AA.
AC Q2XXR7;
DT 20-DEC-2005, integrated into UniProtKB/TrEMBL.
DT 20-DEC-2005, sequence version 1.
DT 18-APR-2006, entry version 5.
DE AVIToxin-VAR2 precursor.
OS Varanus varius (Lace monitor).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Lepidodactylia; Squamata; Scieroglossa; Anguimorpha; Varanidae; Varanus.
OX NCBI_TaxID=8559;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX TISSUE=Compound mandibular venom gland;
RX PubMed=16292255; DOI=10.1038/nature04328;
RA Fry B.G., Vidal N., Norman J.A., Vonk F.J., Scheib H., Ramjan S.F.,
RA Kuruppu S., Fung K., Blair Hedges S., Richardson M.K., Hodgson W.C.,
RA Ignjatovic V., Summerhayes R., Kochva E.;
RT "Early evolution of the venom system in lizards and snakes.";
RL Nature 439:584-588(2006).
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CC -----
CC EMBL; DQ139878; AAZ75584.1; -; mRNA.
DR SMR; Q2XXR7; 20-97.
DR InterPro; IPR009523; Prokineticin.
DR PANTHER; PTHR18821; Prokineticin; 1.
DR Pfam; PF06607; Prokineticin; 1.
KW Signal.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 104 AVIToxin-VAR2.
SQ SEQUENCE 104 AA; 11191 MW; C25A83A6B59D3AA3 CRC64;

Query Match 61.6%; Score 363; DB 2; Length 104;
Best Local Similarity 56.3%; Pred. No. 1e-30;
Matches 58; Conservative 21; Mismatches 24; Indels 0; Gaps 0;
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QY 1 MRGATRVSIMLLVTVSDCAVITGACERDVOCGAGTCCCAISLWRLGRLMCTPLRGREGEC 60
Db 1 MRSLLCAPLILLVLSAGSVAITGACDLOQEGGMCVAVLSIRICTPLSGSGEDC 60

QY 61 HPGSHKVPFFRRKHHTCPCLPNLLCSRFPPDGRYRCSDMLKNI 103
Db 61 HPLSHKVPFFDQGRKHHTCPCLPNLVCGTSPGKHKLPEFKNV 103

RESULT 9
Q4RVU3 TETNG
ID Q4RVU3 TETNG PRELIMINARY; PRT; 106 AA.
AC Q4RVU3
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Chromosome 9 SCAP14991, whole genome shotgun sequence. (Fragment).
GN ORFNames=GSTENG00028169001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15496914; DOI=10.1038/nature03025;
RA Jallion O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anhouard V., Jubin C., Cattolico L., Poullain J., De Berardinis V.,
RA Biemont C., Skalli Z., Cattolico L., Katinka M., Vacherie B.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
RA Parra G., Lardier G., Chappell C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier P., Saurin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissbach J., Roest Crollius H.
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype."
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBSJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBSJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; CAAB01014991; CAG07489.1; -; Genomic_DNA.
DR InterPro; IPR009523; Prokineticin.
DR PANTHER; PTHR18821; Prokineticin; 1.
DR Pfam; PF06607; Prokineticin; 1.
FT NON_TER 106
SQ SEQUENCE 106 AA; 12098 MW; 8DA4DC1B388B3052 CRC64;

Query Match 54.5%; Score 321; DB 2; Length 106;
Best Local Similarity 56.4%; Pred. No. 3.2e-26;
Matches 57; Conservative 20; Mismatches 24; Indels 0; Gaps 0;

QY 4 ATRVSIIMLLVTVSDCAVITGACERDVOCGAGTCCCAISLWRLGRLMCTPLRGREGCHPG 63
Db 5 AVLLSFLVLSWSRGAVITGAREKHMCGGLFCSVLLRLGRLMCAPRGLEGDECYFP 64

QY 64 SHKVPFFRRKHHTCPCLPNLLCSRFPPDGRYRCSDMLKNI 104
Db 65 SHKVPYFGKQHQHTCPCLPHLMCTRFEDSKYRCRTDFFKNVD 105

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RESULT 10
Q863H4 BOVIN
ID Q863H4 BOVIN PRELIMINARY; PRT; 108 AA.
AC Q863H4
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Bv8/prokineticin 2-like protein splice variant.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RX MEDLINE=22612805; PubMed=12728244; DOI=10.1038/sj.embor.embor830;
RA Kaser A., Winklmayr M., Lepperding G., Krell G.;
RT "The AVIT protein family.";
RL EMBO Rep. 4:469-473(2003).
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CC -----
DR EMBL; AY192558; AAP31907.1; -; mRNA.
DR HSSP; P25687; 1MT.
DR Ensembl; ENSBTAG00000019330; Bos taurus.
DR InterPro; IPR009523; Prokineticin.
DR PANTHER; PTHR18821; Prokineticin; 1.
DR Pfam; PF06607; Prokineticin; 1.
SQ SEQUENCE 108 AA; 11672 MW; C00410399A9B215E CRC64;

Query Match 54.0%; Score 318; DB 2; Length 108;
Best Local Similarity 51.9%; Pred. No. 6.7e-26;
Matches 54; Conservative 15; Mismatches 27; Indels 8; Gaps 1;

QY 1 MRGATRVSIMLLV-----TVSDCAVITGACERDVOCGAGTCCCAISLWRLGRLMCTP 52
Db 1 MESSRCARILLVLLPPLLLTPAGDAVITGACDRDPQCGGGMCAVLSWKSIRICTP 60

QY 53 LGREGEECHPGSHKVPFFRRKHHTCPCLPNLLCSRFPPDGRYRC 96
Db 61 MGKVGDSCHPMTKRVFFLGRMHHTCPCLPLGLACRTSFNRYTC 104

RESULT 11
VPRA DENPO
ID VPRA DENPO STANDARD; PRT; 81 AA.
AC P25687;
DT 01-MAY-1992, integrated into UniProtKB/Swiss-Prot.
DT 19-JUL-2005, sequence version 3.
DT 30-MAY-2006, entry version 38.
DE Intestinal toxin 1 (Mamba intestinal toxin 1) (MIT1) (Venom protein A).
OS Dendroaspis polylepis polylepis (Black mamba).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Elapinae; Dendroaspis.
OX NCBI_TaxID=8620;
RN [1]
RP PROTEIN SEQUENCE OF 1-80.
RC TISSUE=Venom;
RX MEDLINE=81115818; PubMed=7461607;
RA Joubert F.J., Strydom D.J.;
RT "Snake venom. The amino acid sequence of protein A from Dendroaspis polylepis polylepis (black mamba) venom.";
RL Hoppe-Seyler's Z. Physiol. Chem. 361:1787-1794(1980).
RN [2]
RP PROTEIN SEQUENCE, AND CHARACTERIZATION.
RC TISSUE=Venom;
RX MEDLINE=20036442; PubMed=10567694; DOI=10.1016/S0014-5793(99)01459-3;
RA Schweitz H., Pascaud P., Diocot S., Moirier D., Lazdunski M.;

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RT "MT1, a black mamba toxin with a new and highly potent activity on
 RT intestinal contraction."
 RL FEBS Lett. 461:183-188(1998).
 RN [3]
 RP STRUCTURE BY NMR OF 1-81, AND DISULFIDE BONDS.
 RC TISSUE=Venom;
 RX MEDLINE=98437381; PubMed=9761684; DOI=10.1006/jmbi.1998.2057;
 RA Boishovier J., Albrand J.-P., Blackledge M., Jaquined M.,
 RA Schweitz H., Lazdunski M., Marion D.;
 RT "A structural homologue of colipase in black mamba venom revealed by
 RT NMR floating disulphide bridge analysis.";
 RL J. Mol. Biol. 283:205-219(1998).
 CC -1- FUNCTION: Potently contracts gastrointestinal (GI) smooth muscle.
 CC May act on potassium channels, but not on Kv1.1, Kv1.2, Kv1.3,
 CC Kv1.4, Kv1.5, IRK2.1, Kv3.4, Kv4.2, TREK-1, HERG, KCNQ1, KCNQ2,
 CC KCNQ3, IRK1, IRK2, ROMK1, GIRK1.2 and GIRK1.4.
 CC -1- SUBCELLULAR LOCATION: Secreted protein.
 CC -1- SIMILARITY: Belongs to the prokineticin family.
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 CC -----
 CC PDB; 1MT1; NMR; @=1-80.
 DR InterPro; IPR009523; Prokineticin.
 DR Pfam; PF06607; Prokineticin; 1.
 KW 3D-structure; Direct protein sequencing; Toxin.
 FT CHAIN 1 81
 FT /FTID=PRO_0000165469.
 FT
 FT DISULFID 7 19
 FT DISULFID 13 31
 FT DISULFID 18 59
 FT DISULFID 41 67
 FT DISULFID 61 77
 FT VARIANT 72 18
 FT CONFLICT 18 18
 FT CONFLICT 22 22
 FT CONFLICT 54 54
 FT STRAND 5 6
 FT STRAND 8 9
 FT HELIX 10 12
 FT TURN 13 13
 FT TURN 15 16
 FT TURN 17 21
 FT STRAND 23 24
 FT TURN 26 27
 FT STRAND 29 33
 FT STRAND 35 35
 FT TURN 37 38
 FT STRAND 40 41
 FT TURN 43 44
 FT STRAND 48 49
 FT STRAND 52 52
 FT STRAND 57 58
 FT STRAND 62 62
 FT TURN 64 65
 FT TURN 67 72
 FT TURN 73 74
 FT TURN 75 79
 SQ SEQUENCE 81 AA; 8604 MW; 5F6B70343338B03 CRC64;
 Query Match 53.5%; Score 315; DB 1; Length 81;
 Best Local Similarity 62.3%; Pred. No. 1.1e-25;
 Matches 48; Conservative 14; Mismatches 15; Indels 0; Gaps 0;
 QY 20 AVITGACERDVQCGAGTCCATSLWLRGLRMCTPLGREGEGCHPGSHKVPFFKRKHHTCP 79
 DB 1 AVITGACERDVQCGAGTCCATSLWLRGLRMCTPLGREGEGCHPGSHKVPFFKRKHHTCP 60
 QY 80 CLPNLLCSRFPDGRYRC 96
 DB 61 CAPNLACVQTSPPKPKC 77

RESULT 12
 Q6ISRO HUMAN PRELIMINARY; PRT; 108 AA.
 AC Q6ISRO;
 DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
 DT 10-MAY-2005, sequence version 1.
 DT 25-JUL-2006, entry version 10.
 DE Prokineticin 2.
 GN Name=PROK2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 OC Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=PCR rescued clones;
 RX MEDLINE=2238625; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins L., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=PCR rescued clones;
 RA Strausberg R.;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=PCR rescued clones;
 RG NIH MGC Project;
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=PCR rescued clones;
 RG NIH MGC Project;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
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 CC -----
 CC EMBL; BC069395; AAH69395.1; -; mRNA.
 CC EMBL; BC098110; AAH98110.1; -; mRNA.
 CC EMBL; BC096695; AAH96695.1; -; mRNA.
 CC UniGene; Hs.528665; -;
 CC Ensembl; ENSG00000163421; Homo sapiens.
 CC RZPD-ProExp; W1162; -;
 CC InterPro; IPR009523; Prokineticin.
 CC PANTHER; PTHR18821; Prokineticin; 1.
 CC Pfam; PF06607; Prokineticin; 1.
 SQ SEQUENCE 108 AA; 11659 MW; D7AF89D8551A97FC CRC64;
 Query Match 51.4%; Score 303; DB 2; Length 108;
 Best Local Similarity 55.2%; Pred. No. 2.7e-24;
 Matches 48; Conservative 15; Mismatches 24; Indels 0; Gaps 0;
 QY 10 MLLLVTVSDCAVITGACERDVQCGAGTCCATSLWLRGLRMCTPLGREGEGCHPGSHKVPF 69

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Db 18 LLLTPRAGDAVITGADKDSQCGGMCCAVSIWKSIRICTPMKLGDSCHPTTRKVPF 77
QY 70 FRKPKHHTCPLNLLSRPDPGRYCS 96
Db 78 FGRMHHTCPLCLGLACLTSTFNRFIC 104

RESULT 13
Q8JFQO_BOMMX
ID Q8JFQO_BOMMX PRELIMINARY; PRT; 96 AA.
AC Q8JFQO;
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DE Bv8 protein homolog 2.
OS Bombina maxima (Giant fire-bellied toad) (Chinese red belly toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCBI_TaxID=161274;
RN 13
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skin secretions;
RX MEDLINE=22515712; PubMed=12628381; DOI=10.1016/S1096-4959(02)00294-4;
RA Lai R., Liu H., Lee W.H., Zhang Y.;
RT "Two novel Bv8-like peptides from skin secretions of the toad Bombina maxima.";
RL Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 134:509-514 (2003).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AF411091; AAM03822.1; -; mRNA.
DR HSSP; P25687; 11MT.
DR InterPro; IPR009523; Prokineticin.
DR PANTHER; PTHR18821; Prokineticin; 1.
DR Pfam; PF06607; Prokineticin; 1.
SQ SEQUENCE 96 AA; 10198 MW; EC4EAA5EFB49B2F0 CRC64;

Query Match 50.7%; Score 298.5; DB 2; Length 96;
Best Local Similarity 53.6%; Pred. No. 7.2e-24;
Matches 52; Conservative 16; Mismatches 28; Indels 1; Gaps 1;

QY 1 MRGATRVSIIMLLVTVDCAVITGACERDVCGAGTCACISLWLRLMCTPLRGEGEC 60
Db 1 MKCFAQIVLLVITAFSHGAVITGACERDVCGAGTCACISLWLRLMCTPLRGEGEC 60
QY 61 HPGSHKVPFFRRKHHTCPLNLLSRPDPGRYCS 97
Db 61 HPASHKVPYNGKRLSLCPCKSGLTCSKSGE-KFQCS 96

RESULT 14
Q4SR12_TETNG
ID Q4SR12_TETNG PRELIMINARY; PRT; 102 AA.
AC Q4SR12;
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.
DE Chromosome 11 SCAF14528, whole genome shotgun sequence. (Fragment).
GN ORFNames=GSTENG0014129001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN 14
RP NUCLEOTIDE SEQUENCE.
RC PubMed=15496914; DOI=10.1038/nature03025;
RA Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,

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RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Aumont V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulin J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN 12
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; CAAS01014528; CAF96920.1; -; Genomic DNA.
DR InterPro; IPR009523; Prokineticin.
DR PANTHER; PTHR18821; Prokineticin; 1.
DR Pfam; PF06607; Prokineticin; 1.
FT NON TER 102 102
SQ SEQUENCE 102 AA; 11062 MW; 470A2CDF2D069043 CRC64;

Query Match 50.6%; Score 298; DB 2; Length 102;
Best Local Similarity 57.8%; Pred. No. 8.6e-24;
Matches 52; Conservative 9; Mismatches 15; Indels 14; Gaps 1;

QY 11 LLLVTVDCAVITGACERDVCGAGTCACISLWLRLMCTPLRGEGECBP----- 62
Db 11 LLLVSRGSSAVITGACERDSCGGGLCCAVSLWIRSLRLCMPGAEGDCHPMQATSYL 70
QY 63 -----GSHKVPFFRRKHHTCPLNLLC 86
Db 71 VEQSSSSSFQVFFFGKRLHHTCPLNLLSC 100

RESULT 15
PROK2_RAT
ID PROK2_RAT STANDARD; PRT; 107 AA.
AC Q8R413;
DT 02-AUG-2002, integrated into UniProtKB/Swiss-Prot.
DT 01-JUN-2002, sequence version 1.
DT 18-APR-2006, entry version 26.
DE Prokineticin-2 precursor (PK2).
GN Name=Prok2; Synonyms=Bv8;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN 15
RP NUCLEOTIDE SEQUENCE [MRNA].
RC STRAIN=Sprague-Dawley;
RX MEDLINE=22050031; PubMed=12054613; DOI=10.1016/S0006-291X(02)00239-5;
RA Masuda Y., Takatsu Y., Terao Y., Kumano S., Ishibashi Y., Suenaga M.,
RA Abe M., Fukusumi S., Watanabe T., Shintani Y., Yamada T., Hinuma S.,
RA Inatomi N., Ohtaki T., Onda H., Fujino M.;
RT "Isolation and identification of EG-VEGF/prokineticins as cognate
RT ligands for two orphan G-protein-coupled receptors.";
RL Biochem. Biophys. Res. Commun. 293:396-402(2002).
RN 16
RP EFFECT ON CIRCADIAN LOCOMOTOR ACTIVITY.
RX MEDLINE=22022134; PubMed=12024206; DOI=10.1038/417405a;
RA Cheng M.Y., Bullock C.M., Li C., Lee A.G., Bermak J.C., Belluzzi J.,
RA Weaver D.R., Leslie F.M., Zhou Q.-Y.;
RT "Prokineticin 2 transmits the behavioural circadian rhythm of the

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RT suprachiasmatic nucleus.";
RL Nature 417:405-410(2002).
CC -|- FUNCTION: May function as an output molecule from the
CC suprachiasmatic nucleus (SCN) that transmits behavioral circadian
CC rhythm. May also function locally within the SCN to synchronize
CC output. Potentially contracts gastrointestinal (GI) smooth muscle (By
CC similarity).
CC -|- SUBCELLULAR LOCATION: Secreted protein (By similarity).
CC -|- TISSUE SPECIFICITY: Expressed at high levels in testis and at
CC lower levels in brain, lung, ovary, spleen, thymus and uterus.
CC -|- INDUCTION: Activated by CLOCK and BMAL1 heterodimers and light;
CC inhibited by period genes (PER1, PER2 and PER3) and cryptochrome
CC genes (CRY1 and CRY2) (Probable).
CC -|- SIMILARITY: Belongs to the prokineticin family.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR ENBL; AY089984; AAM09105.1; -; mRNA.
DR UniGene; Rn.82766; -.
DR HSSP; P25687; IIMT.
DR Ensembl; ENSRNOG0000010898; Rattus norvegicus.
DR RGD; 620280; Prok2.
DR GO; GO:0001664; F:G-protein-coupled receptor binding; IDA.
DR InterPro; IPR009523; Prokineticin; 1.
DR PANTHER; PTHR18821; Prokineticin; 1.
DR Pfam; PF06607; Prokineticin; 1.
KW Biological rhythms; Neuropeptide; Signal.
FT SIGNAL 1 26 Potential.
FT CHAIN 27 107 Prokineticin-2.
FT FTID=PRO_0000025811.
FT DISULFID 33 45 By similarity.
FT DISULFID 39 57 By similarity.
FT DISULFID 44 85 By similarity.
FT DISULFID 67 93 By similarity.
FT DISULFID 87 103 By similarity.
SQ SEQUENCE 107 AA; 11594 MW; BDFP316CDCB5FED0 CRC64;

Query Match 50.6%; Score 298; DB 1; Length 107;
Best Local Similarity 54.0%; Pred. No. 9e-24;
Matches 47; Conservative 16; Mismatches 24; Indels 0; Gaps 0;

Qy 10 MLLLVTVSDCAVITGACERDVOCAGTCCALSLWLRGRLMCTPLGREGECHGSHKVPF 69
Db 17 LLLTPPAGDAAVITGACDKDSQCGGMCACVSIWKSIRICTPMGQVGDSCPLTRKVPF 76

Qy 70 FRKEKHHTCPCLNLCRPPDGRYC 96
Db 77 WGRMHHTCPCLPLGLCLRTSFRNIC 103

Search completed: November 29, 2007, 17:25:53
Job time : 227.555 secs

GenCore version 6.2.1
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OM protein - protein search, using sw model

Run on: November 29, 2007, 17:18:33 ; Search time 15 Seconds

(without alignments)
656.336 Million cell updates/sec

Title: US-10-692-299-2

Perfect score: 589

Sequence: 1 MRGNTRVSIMLLLVTSDC.....CSRFPDGRYRCMDLKNINF 105

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

1: PIR.80.*

2: PIR1.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100.5	17.1	350	2	JC7188
2	88.5	15.0	640	2	T08179
3	83	14.1	1101	2	T16840
4	81	13.8	1964	2	T09059
5	79	13.4	112	1	XLHU
6	77.5	13.2	473	2	A56175
7	77	13.1	251	2	A55035
8	75.5	12.8	1574	2	T13954
9	75	12.7	734	2	JC4861
10	75	12.7	2318	2	A53306
11	75	12.7	2531	2	T31070
12	74	12.6	112	2	I51909
13	74	12.6	1620	2	T27283
14	73	12.4	461	1	A35356
15	73	12.4	3075	2	SI4458
16	72.5	12.3	643	2	T25473
17	72.5	12.3	2871	2	A55567
18	72.5	12.3	3002	2	A47221
19	72	12.2	1639	1	MMFFB2
20	71.5	12.1	591	2	I48141
21	71.5	12.1	601	2	B36346
22	71.5	12.1	683	2	C36346
23	71.5	12.1	1178	1	A39804
24	71.5	12.1	1854	2	T13576
25	71	12.1	286	2	S34665
26	71	12.1	593	1	GRHU
27	70.5	12.0	1847	2	T18308
28	70.5	12.0	2871	2	A55624
29	69.5	11.8	802	2	T24293

30	69.5	11.8	949	2	T24294
31	69.5	11.8	2352	2	T30201
32	69.5	11.8	4545	1	S25111
33	69	11.7	2918	2	A54105
34	69	11.7	3133	2	S52093
35	69	11.7	3712	2	S18253
36	68.5	11.6	728	2	I50719
37	68.5	11.6	850	2	T14450
38	68.5	11.6	884	2	T18649
39	68.5	11.6	1172	2	A42587
40	68.5	11.6	1376	2	G00043
41	68	11.5	112	2	A46717
42	68	11.5	345	2	T25138
43	68	11.5	358	2	T25137
44	68	11.5	427	1	GQHUN
45	68	11.5	547	2	A33901
46	68	11.5	586	1	WMBEDE
47	68	11.5	1119	2	A88481
48	68	11.5	1150	2	A41641
49	68	11.5	2215	2	T00348
50	68	11.5	5147	1	IJFTM
51	67.5	11.5	108	2	C88450
52	67.5	11.5	895	2	T49010
53	67.5	11.5	1184	2	A55184
54	67.5	11.5	1469	2	B36665
55	67.5	11.5	1480	2	A36665
56	67.5	11.5	1687	2	T30176
57	67	11.4	237	2	S45463
58	67	11.4	993	2	I48653
59	67	11.4	1172	1	TSHUP2
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61	67	11.4	1722	2	E89753
62	67	11.4	2321	2	S78549
63	67	11.4	2437	2	S42612
64	67	11.4	2825	2	T14271
65	67	11.4	2907	2	A57278
66	66.5	11.3	589	2	C38128
67	66.5	11.3	589	2	B38128
68	66.5	11.3	1111	2	T26972
69	66.5	11.3	1221	2	A49457
70	66.5	11.3	3020	2	A43932
71	66	11.2	1327	2	D70759
72	66	11.2	1743	2	T26859
73	65.5	11.1	459	2	I48854
74	65.5	11.1	722	2	I48324
75	65.5	11.1	2555	2	A40043
76	65.5	11.1	3635	2	T10053
77	65	11.0	143	2	B21761
78	65	11.0	302	2	S65021
79	65	11.0	328	2	S42152
80	65	11.0	329	2	T07000
81	65	11.0	329	2	T06999
82	65	11.0	1295	2	A32901
83	65	11.0	2139	2	A35672
84	64.5	11.0	191	2	H71370
85	64.5	11.0	823	2	S18968
86	64.5	11.0	1790	1	MMFFB1
87	64	10.9	117	2	H72706
88	64	10.9	130	1	KRSHJA
89	64	10.9	178	2	A23219
90	64	10.9	217	2	A98196
91	64	10.9	225	2	A86043
92	64	10.9	325	2	B43692
93	64	10.9	425	1	A26431
94	64	10.9	587	1	WMBETE
95	64	10.9	723	2	PN0509
96	64	10.9	1143	2	T22952
97	64	10.9	1984	2	T13171
98	63.5	10.8	682	2	A69170
99	63.5	10.8	782	2	A61625
100	63.5	10.8	905	2	T23229
101	63.5	10.8	3707	2	S18252
102	63.5	10.8	5376	2	T42215

hypothetical prote
Notch homolog prot
alpha-2-macroglobu
fibrillin-2 precu
hemocytin - silkw
laminin alpha-1 ch
C-Delta-1 - chicke
serine/threonine k
hypothetical prote
thrombospondin 2 p
osteonidogen - hum
colipase precursor
hypothetical prote
hypothetical prote
nerve growth facto
mannosyl-oligosacc
65K early nonstruc
protein C16A3.6 [i
mannosyl-oligosacc
LR11 protein - mou
cadherin-related t
protein F21H1.4 [i
hypothetical prote
fibulin-2 precursor
slit protein 2 pre
slit protein 1 pre
EGF repeat transme
probable membrane
mouse developmenta
thrombospondin 2 p
jagged protein pre
protein F11C7.4 [i
notch3 protein - h
transmembrane prot
Doc4 protein, stre
fibrillin-2 precu
epithelin/granulin
epithelin/granulin
hypothetical prote
fibulin-2 precursor
mucin 2 precursor,
probable otstB prot
hypothetical prote
gene murine tumour
DELTA-like 1 - mou
notch protein homo
laminin alpha 5 ch
high cysteine chor
chitinase (EC 3.2.
chitinase (EC 3.2.
urinary plasminoge
chitinase (EC 3.2.
glp1 protein precu
crumbs protein - f
hypothetical prote
hypocytetinal prote
laminin beta-1 cha
hypothetical prote
keratin high-sulfu
high-cysteine chor
hypothetical prote
probable transposa
T2 protein - rabbi
nerve growth facto
65K early nonstruc
integrin beta-3 ch
hypothetical prote
probable vitellog
UDP-N-acetylmuram
tenascin-like prot
hypothetical prote
heparan sulfate pr
zonadhesin - mouse

103	63	10.7	95	1	XLPG2	colipase II precu	176	60	10.2	351	2	S20078	NOV protein - chic
104	63	10.7	350	2	T37511	probable phosphor	177	60	10.2	419	2	S41607	atrolysin A (EC 3.
105	63	10.7	389	1	B64921	conserved hypotet	178	60	10.2	419	2	A59414	metalloproteinase
106	63	10.7	369	2	A85771	hypothetical prote	179	60	10.2	589	2	T43210	fibulin-ID precurs
107	63	10.7	369	2	E90922	hypothetical prote	180	60	10.2	837	1	A29512	LDL receptor precu
108	63	10.7	689	2	T42760	fibulin, splice fo	181	60	10.2	869	1	JC4858	VLDL receptor prec
109	63	10.7	712	2	T42990	fibulin 1, splice	182	60	10.2	905	2	T02205	Lu-ECM-1 protein
110	63	10.7	735	2	G02937	fertilin beta - cr	183	60	10.2	996	2	JE0237	apolipoprotein E r
111	62.5	10.6	308	2	JC7125	epidermal growth f	184	60	10.2	1142	2	T30272	hypothetical prote
112	62.5	10.6	360	2	AH2272	fructose-bisphosph	185	60	10.2	1203	2	A49175	Motch B protein -
113	62.5	10.6	645	2	T22178	hypothetical prote	186	60	10.2	1357	2	T16860	hypothetical prote
114	62.5	10.6	685	2	S78040	fibulin, splice fo	187	60	10.2	1547	2	JQ0096	hypothetical 175K
115	62.5	10.6	705	2	S34968	fibulin, splice fo	188	60	10.2	1607	2	T43212	insulin-like growt
116	62.5	10.6	895	1	LUXLCP	EP-cadherin precu	189	60	10.2	1680	2	A43434	furin (EC 3.4.21.7
117	62.5	10.6	907	2	T27317	hypothetical prote	190	59.5	10.1	128	2	S32936	sporulation initia
118	62.5	10.6	4135	2	T42629	tenascin-X - bovin	191	59.5	10.1	186	2	T32656	hypothetical prote
119	62	10.5	92	1	S36658	proteinase inhibit	192	59.5	10.1	886	2	A57172	probable hormone r
120	62	10.5	491	2	T21421	hypothetical prote	193	59.5	10.1	925	2	T37475	lipoprotein recept
121	62	10.5	998	2	S37627	protein-tyrosine k	194	59.5	10.1	952	2	T18900	disintegrin and me
122	62	10.5	1113	2	JE0315	low-density lipopr	195	59.5	10.1	1245	1	MMMSND	nidogen precursor
123	62	10.5	1170	1	TSHP1	thrombospondin 1 p	196	59.5	10.1	2823	2	F87908	protein T22A3.8 [i
124	62	10.5	1170	2	H83380	thrombospondin 1 p	197	59.5	10.1	2823	2	T23064	hypothetical prote
125	62	10.5	1522	2	T13953	MEGF5 protein - ra	198	59.5	10.1	3102	2	T43291	laminin alpha chai
126	62	10.5	1523	2	T13953	MEGF5 protein - ra	199	59	10.0	96	2	SI4018	hypothetical prote
127	62	10.5	1599	2	T16210	hypothetical prote	200	59	10.0	131	1	KRSHA3	keratin high-sulfu
128	62	10.5	2195	2	T34264	hypothetical prote	201	59	10.0	132	1	KRG73J	keratin high-sulfu
129	61.5	10.4	83	2	T26545	hypothetical prote	202	59	10.0	141	2	S54236	Ig mu heavy chain
130	61.5	10.4	220	2	A95956	hypothetical prote	203	59	10.0	186	2	A28401	agglutinin isolect
131	61.5	10.4	272	2	T37552	hypothetical prote	204	59	10.0	315	2	B84654	probable CCH-type
132	61.5	10.4	322	1	S37344	OX40 homolog - hum	205	59	10.0	319	2	A53502	folistatin - Afri
133	61.5	10.4	373	2	T34126	hypothetical prote	206	59	10.0	474	2	B38634	tumor necrosis fac
134	61.5	10.4	1373	2	JE0095	gastric mucin MUC5	207	59	10.0	616	2	T29234	fibroin-3 related
135	61.5	10.4	2150	2	T32497	hypothetical prote	208	59	10.0	670	2	T49510	RNA-2 polyprotein
136	61.5	10.4	2471	2	A49128	cell-fate determin	209	59	10.0	930	2	T34334	hypothetical prote
137	61.5	10.4	2946	2	T15840	hypothetical prote	210	59	10.0	1106	2	T18739	hypothetical prote
138	61.5	10.4	4006	2	T09070	probable tenascin	211	59	10.0	1170	2	A53612	laminin B1k chain
139	61	10.4	93	2	JE0159	gibberellin-stimul	212	59	10.0	1360	2	F96596	gene serrate prote
140	61	10.4	95	2	S53510	pancreatic colipas	213	59	10.0	1408	2	S16148	homeotic protein 1
141	61	10.4	141	95	T42112	colipase - nutria	214	59	10.0	1429	2	S06434	nudel protein prec
142	61	10.4	111	2	I48204	hypothetical prote	215	59	10.0	2616	2	A57096	laminin alpha-1 ch
143	61	10.4	269	2	T26957	hypothetical prote	216	59	10.0	3084	1	MMMSA	hypothetical prote
144	61	10.4	283	2	B88597	protein Y47D3B.6 [217	59	10.0	220	2	T21730	hypothetical prote
145	61	10.4	309	2	B86937	conserved hypotet	218	58.5	9.9	236	2	T05695	pathogenesis-relat
146	61	10.4	383	2	D88633	protein F56B3.2 [i	219	58.5	9.9	287	1	S75925	DNA-formamidopyrim
147	61	10.4	451	2	T30603	perlecan homolog 2	220	58.5	9.9	297	2	H69609	hypothetical prote
148	61	10.4	593	1	S25062	triacylglycerol li	221	58.5	9.9	316	2	S65020	chitinase (EC 3.2.
149	61	10.4	601	2	A37020	DIF-induced preta	222	58.5	9.9	329	2	S08627	chitinase (EC 3.2.
150	61	10.4	738	2	S40992	hypothetical prote	223	58.5	9.9	358	2	T34128	hypothetical prote
151	61	10.4	739	2	B88553	protein K04H4.2b [224	58.5	9.9	455	1	G0HUT1	tumor necrosis fac
152	61	10.4	1192	2	S69000	laminin gamma 2 ch	225	58.5	9.9	496	2	S51668	tyrosine kinase -
153	61	10.4	1251	2	A57293	latent transformin	226	58.5	9.9	503	2	A49431	activin/TGF-beta-1
154	61	10.4	1955	1	AGCH	agrin precursor -	227	58.5	9.9	601	2	D89711	protein F40E10.4 [
155	61	10.4	2476	2	T34022	zonadhesin - pig	228	58.5	9.9	601	2	T22025	hypothetical prote
156	60.5	10.3	90	2	S69487	bombaxin B-7 precu	229	58.5	9.9	717	2	S12100	transferrin precu
157	60.5	10.3	96	2	C86649	hypothetical prote	230	58.5	9.9	772	2	S32659	integrin beta 2 ch
158	60.5	10.3	99	2	S60231	gibberellin-regula	231	58.5	9.9	962	1	TVBE14	106.6K protein kin
159	60.5	10.3	129	2	A72606	hypothetical prote	232	58.5	9.9	1193	2	A44018	laminin B2t chain
160	60.5	10.3	289	2	A84812	probable aquaporin	233	58.5	9.9	1297	2	T30274	proteoliasin - se
161	60.5	10.3	324	2	S20981	chitinase (EC 3.2.	234	58.5	9.9	1712	1	CGHU2B	collagen alpha 2(I
162	60.5	10.3	349	2	A40551	connective tissue	235	58.5	9.9	1712	1	A38261	masking protein pr
163	60.5	10.3	370	2	A80289	conserved hypotet	236	58.5	9.9	3507	2	T34513	hypothetical prote
164	60.5	10.3	385	2	S33718	homeotic protein d	237	58.5	9.9	3566	1	A40701	tenascin-X precurs
165	60.5	10.3	385	2	A54785	preadipocyte facto	238	58.5	9.9	4391	2	A38096	perlecan precursor
166	60.5	10.3	387	2	B49175	Motch A protein -	239	58.5	9.9	46	2	A44794	antimicrobial pept
167	60.5	10.3	574	2	B88465	protein B0244.8 [i	240	58	9.8	170	2	H83404	probable ferredoxi
168	60.5	10.3	680	2	PN0510	integrin beta-3 ch	241	58	9.8	234	2	T44731	hypothetical prote
169	60.5	10.3	1104	2	I38869	transcription fact	242	58	9.8	268	2	A50195	4-amino-4-deoxycho
170	60.5	10.3	2531	2	A46019	notch-1 protein -	243	58	9.8	354	2	T22274	hypothetical prote
171	60.5	10.3	2703	1	A24420	notch protein - fr	244	58	9.8	383	2	S53716	delta-like homeoti
172	60.5	10.3	4544	1	S02392	alpha-2-macroglobu	245	58	9.8	755	2	A44315	cartilage oligomer
173	60	10.2	102	2	S26409	protein 108 precu	246	58	9.8	798	2	T22793	hypothetical prote
174	60	10.2	233	2	S46639	hypothetical prote	247	58	9.8	891	2	H86306	F20D23.20 protein
175	60	10.2	263	2	T27641	hypothetical prote	248	58	9.8				

NOV protein - chic
atrolysin A (EC 3.
metalloproteinase
fibulin-ID precurs
LDL receptor precu
VLDL receptor prec
Lu-ECM-1 protein
apolipoprotein E r
hypothetical prote
Motch B protein -
hypothetical prote
hypothetical 175K
insulin-like growt
furin (EC 3.4.21.7
sporulation initia
hypothetical prote
probable hormone r
lipoprotein recept
disintegrin and me
nidogen precursor
protein T22A3.8 [i
hypothetical prote
laminin alpha chai
hypothetical prote
keratin high-sulfu
keratin high-sulfu
Ig mu heavy chain
agglutinin isolect
probable CCH-type
folistatin - Afri
tumor necrosis fac
fibroin-3 related
RNA-2 polyprotein
hypothetical prote
hypothetical prote
laminin B1k chain
hypothetical prote
gene serrate prote
homeotic protein 1
nudel protein prec
laminin alpha-1 ch
hypothetical prote
pathogenesis-relat
DNA-formamidopyrim
hypothetical prote
chitinase (EC 3.2.
chitinase (EC 3.2.
hypothetical prote
tumor necrosis fac
tyrosine kinase -
activin/TGF-beta-1
protein F40E10.4 [i
hypothetical prote
transferrin precu
integrin beta 2 ch
106.6K protein kin
laminin B2t chain
proteoliasin - se
collagen alpha 2(I
masking protein pr
tenascin-X precurs
perlecan precursor
antimicrobial pept
probable ferredoxi
hypothetical prote
4-amino-4-deoxycho
hypothetical prote
delta-like homeoti
cartilage oligomer
hypothetical prote
F20D23.20 protein

249	58	9.8	898	2	T14764	hypothetical prote	322	56.5	9.6	1622	2	J50378	DNA (cytosine-5-) -
250	58	9.8	984	2	T00326	hypothetical prote	323	56.5	9.6	3623	2	T08618	intrinsic factor-B
251	58	9.8	1194	2	T03818	apoptotic proteina	324	56.5	9.6	4753	1	A47437	IDL-receptor-relat
252	58	9.8	1217	1	EGMSMG	epidermal growth f	325	56	9.5	254	2	I48603	insulin-like growt
253	58	9.8	1292	2	T09229	galactose binding	326	56	9.5	264	2	T52104	GATA-binding trans
254	58	9.8	1311	2	T33757	hypothetical prote	327	56	9.5	265	2	H84867	probable endochiti
255	58	9.8	1428	2	T08852	lustrin A - Califo	328	56	9.5	320	2	T14624	hypothetical prote
256	58	9.8	1522	2	T00038	brain-specific ang	329	56	9.5	335	2	S03212	hypothetical prote
257	57.5	9.8	196	2	T26943	hypothetical prote	330	56	9.5	377	2	T52606	squamosa promoter
258	57.5	9.8	279	2	C70458	diaminopimelate ep	331	56	9.5	391	2	C86347	F24J8.6 protein -
259	57.5	9.8	306	2	S51361	foliostat-in-relate	332	56	9.5	434	1	A35005	u-plasminogen acti
260	57.5	9.8	375	1	S66272	alcohol dehydrogen	333	56	9.5	442	1	UXPG	gene Tt52 protein
261	57.5	9.8	458	2	AF0631	probable 4-hydroxy	334	56	9.5	478	2	S47040	disintegrin (EC 3.
262	57.5	9.8	568	2	F86231	hypothetical prote	335	56	9.5	491	2	S52920	hypothetical prote
263	57.5	9.8	686	2	S43562	K08E5.3 protein -	336	56	9.5	548	2	T16642	squamosa promoter
264	57.5	9.8	710	2	T46589	ropy-2 protein (im	337	56	9.5	801	2	T52605	S-receptor kinase
265	57.5	9.8	810	2	T10756	Nel-homolog protei	338	56	9.5	849	1	T05181	complement C6 prec
266	57.5	9.8	1036	2	T17405	scavenger receptor	339	56	9.5	934	1	A34372	protein-tyrosine K
267	57.5	9.8	1046	2	A26838	prestalk receptor p	340	56	9.5	1136	1	S57845	RNA polymerase (EC
268	57.5	9.8	1356	2	JCL1402	protein-tyrosine k	341	56	9.5	1661	2	T43260	laminin beta-1 cha
269	57.5	9.8	1801	1	MMRTS	laminin beta-2 cha	342	56	9.5	1786	1	MMMSB1	laminin beta-2 cha
270	57.5	9.8	1959	1	AGRT	agrin - rat	343	56	9.5	1797	2	A55677	hypothetical prote
271	57.5	9.8	2265	1	FNBO	fibronectin - bovi	344	56	9.5	2531	2	T16743	hypothetical prote
272	57.5	9.8	2386	1	FNHU	fibronectin precur	345	56	9.5	3191	2	T22945	hypothetical prote
273	57.5	9.8	2481	2	A43908	fibronectin - Afri	346	55.5	9.4	99	2	S40012	fill protein - gar
274	57.5	9.8	2767	1	U1HU	alpha-2-macroglobu	347	55.5	9.4	106	2	A72581	hypothetical prote
275	57.5	9.8	4543	1	A53102	conserved hypothet	348	55.5	9.4	151	2	T20071	hypothetical prote
276	57	9.7	98	2	A75393	thyroglobulin - sl	349	55.5	9.4	264	2	A84868	probable endochiti
277	57	9.7	153	2	A60595	lactoylglutathione	350	55.5	9.4	290	2	T21185	hypothetical prote
278	57	9.7	175	2	C82686	agglutinin isolect	351	55.5	9.4	291	1	U00064	insulin-like growt
279	57	9.7	212	2	T05936	CD27 antigen precu	352	55.5	9.4	292	2	C88072	hypothetical prote
280	57	9.7	250	1	A49053	probable ABC trans	353	55.5	9.4	309	2	T28708	nerve growth facto
281	57	9.7	268	1	G71271	chitinase (EC 3.2.	354	55.5	9.4	416	1	UN0006	oryzain (EC 3.4.22
282	57	9.7	334	2	S20982	hypothetical prote	355	55.5	9.4	471	1	KHRZOB	hypothetical prote
283	57	9.7	334	2	D70918	thrombomodulin - b	356	55.5	9.4	503	2	D70926	cell division cont
284	57	9.7	356	2	A25918	hypothetical prote	357	55.5	9.4	513	1	RGBYC6	urease (EC 3.5.1.5
285	57	9.7	414	2	T24563	hypothetical prote	358	55.5	9.4	569	2	T50711	IG heavy chain, se
286	57	9.7	468	2	T48686	protein apx-1 (imp	359	55.5	9.4	580	2	A46538	hypothetical prote
287	57	9.7	513	2	D88991	hypothetical prote	360	55.5	9.4	674	2	T15524	hypothetical prote
288	57	9.7	514	2	T10559	hypothetical prote	361	55.5	9.4	680	2	T39858	hypothetical prote
289	57	9.7	571	2	S24789	jararagin C precu	362	55.5	9.4	685	2	JC7570	Delta-4 protein -
290	57	9.7	609	2	S55270	catrocollastatin p	363	55.5	9.4	775	2	A61228	collagen alpha 2(I
291	57	9.7	773	2	JQ2187	P87 protein - Card	364	55.5	9.4	788	2	A26547	platelet glycoprot
292	57	9.7	779	2	H71301	probable membrane-	365	55.5	9.4	1039	2	T14802	phytochrome B - so
293	57	9.7	917	2	JC7799	PARIS-1 protein -	366	55.5	9.4	1296	2	T16859	hypothetical prote
294	57	9.7	964	2	JC5545	integrin beta-4 pr	367	55.5	9.4	1746	1	S19694	tenascin precursor
295	57	9.7	1107	2	T15884	hypothetical prote	368	55.5	9.4	1786	1	MMHUB1	laminin beta-1 cha
296	57	9.7	1548	2	S34583	serine proteinase	369	55.5	9.4	2477	2	S14428	fibronectin precur
297	57	9.7	1820	2	A55494	latent transformin	370	55.5	9.4	3570	2	T45025	mucin MUC5B, trach
298	57	9.7	1875	2	A36429	integrin beta-4 ch	371	55.5	9.4	3623	2	T09456	intrinsic factor-B
299	56.5	9.6	113	2	S11532	colicin E1 immunit	372	55	9.3	163	1	H83499	ferredoxin protein
300	56.5	9.6	258	2	T32542	hypothetical prote	373	55	9.3	171	2	S68858	probable membrane
301	56.5	9.6	318	2	S65019	chitinase (EC 3.2.	374	55	9.3	226	2	A12564	hypothetical prote
302	56.5	9.6	409	2	A86240	protein F20B24.10	375	55	9.3	268	2	S25311	chitinase (EC 3.2.
303	56.5	9.6	443	2	T08905	hypothetical prote	376	55	9.3	269	2	S75243	hypothetical prote
304	56.5	9.6	446	2	T31644	hypothetical prote	377	55	9.3	305	2	A46476	B cell-associated
305	56.5	9.6	682	2	T12968	hypothetical prote	378	55	9.3	318	2	E87929	protein T2H2.6 [i
306	56.5	9.6	753	2	B36268	platelet glycoprot	379	55	9.3	323	2	A99211	hypothetical prote
307	56.5	9.6	778	2	A60798	platelet glycoprot	380	55	9.3	324	2	S56694	chitinase (EC 3.2.
308	56.5	9.6	788	2	T77349	platelet glycoprot	381	55	9.3	341	2	AE2445	hypothetical prote
309	56.5	9.6	938	2	I49071	protein kinase - m	382	55	9.3	343	2	S45321	foliostat-in - mous
310	56.5	9.6	948	2	S51605	receptor-like tyro	383	55	9.3	357	2	T32881	hypothetical prote
311	56.5	9.6	1106	2	T44598	hypothetical prote	384	55	9.3	396	1	KXBOZ	plasma protein 2 -
312	56.5	9.6	1106	2	T13938	gene shuttle craft	385	55	9.3	416	2	T25101	hypothetical prote
313	56.5	9.6	1391	2	T20406	hypothetical prote	386	55	9.3	512	2	T06713	probable cytochrom
314	56.5	9.6	1458	2	A45665	adult-specific bru	387	55	9.3	531	2	B83422	probable serine/thr
315	56.5	9.6	1490	2	JC5145	DNA (cytosine-5-) -	388	55	9.3	599	2	JC8009	choline dehydrogen
316	56.5	9.6	1495	2	S22610	DNA (cytosine-5-) -	389	55	9.3	748	2	S66129	disintegrin (EC 3.
317	56.5	9.6	1537	2	JC4172	DNA (cytosine-5-) -	390	55	9.3	850	2	S56015	gastric mucin MUC5
318	56.5	9.6	1557	2	T28811	hypothetical prote	391	55	9.3	853	2	B85429	beta-galactosidase
319	56.5	9.6	1572	2	T00037	brain-specific ang	392	55	9.3	863	1	S51789	VLDL receptor prec
320	56.5	9.6	1584	2	T22674	hypothetical prote	393	55	9.3	865	2	B69074	probable formate d
321	56.5	9.6	1612	2	JC5210	DNA (cytosine-5-) -	394	55	9.3	961	1	TSHUP4	thrombospondin 4 p

395 55 9.3 1038 2 I38935 bone morphogenetic
396 55 9.3 1038 2 JC5227 bone morphogenetic
397 55 9.3 1064 1 A40136 fibropellin Ia - s
398 55 9.3 1133 2 EGRT epidermal growth f
399 55 9.3 1207 1 EGHU epidermal growth f
400 55 9.3 1394 2 A35626 transforming growt
401 55 9.3 1531 1 T42218 split-1 protein hom
402 55 9.3 1609 1 MMHUB2 laminin gamma-1 ch
403 55 9.3 1808 2 TH5099 hypothetical prote
404 55 9.3 2052 2 I52300 FIVE finger-contai
405 55 9.3 3225 2 S27852 giantin - human
406 55 9.3 3229 2 S27852 probable cell-surf
407 55 9.3 3259 1 A56539 giantin - human
408 55 9.3 4660 2 T42737 gp330 protein prec
409 54.5 9.3 57 2 C46654 growth modulatory
410 54.5 9.3 63 2 S08572 chymotrypsin/elast
411 54.5 9.3 90 2 S69488 bombixin B-7 precu
412 54.5 9.3 92 2 D37057 epithelial cell gl
413 54.5 9.3 103 4 S59331 hypothetical prote
414 54.5 9.3 120 2 T31000 cysteine-rich prot
415 54.5 9.3 131 1 KRGT3M keratin high-sulfu
416 54.5 9.3 221 2 C34768 ORF2 protein - Orf
417 54.5 9.3 226 2 JC4868 ribonuclease S2 (E
418 54.5 9.3 243 2 T31144 hypothetical prote
419 54.5 9.3 248 2 T19913 hypothetical prote
420 54.5 9.3 289 2 A12128 ATP-binding protei
421 54.5 9.3 306 2 S38251 follistatin-relate
422 54.5 9.3 310 2 A60967 insulin-like growt
423 54.5 9.3 317 2 I46916 chitinase (EC 3.2.
424 54.5 9.3 318 2 S43317 probable alcohol d
425 54.5 9.3 386 2 S52035 probable Arfasep -
426 54.5 9.3 419 2 E71519 oxidative stress p
427 54.5 9.3 442 2 JC4978 probable acid phos
428 54.5 9.3 462 2 T40420 hypothetical prote
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430 54.5 9.3 530 2 C95334 interleukin-10 rec
431 54.5 9.3 575 2 A49667 epidermal growth f
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433 54.5 9.3 711 2 S43464 brain-specific ser
434 54.5 9.3 761 2 JC5759 integrin beta-3 su
435 54.5 9.3 788 2 I51530 LDL receptor precu
436 54.5 9.3 862 1 QRMSLD chordin precursor
437 54.5 9.3 941 1 A55195 hypothetical prote
438 54.5 9.3 949 2 T44577 thrombospondin 4 -
439 54.5 9.3 955 2 A54441 protein-tyrosine k
440 54.5 9.3 984 1 A34076 hypothetical prote
441 54.5 9.3 1143 2 T10636 hypothetical prote
442 54.5 9.3 1204 2 A96676 hypothetical prote
443 54.5 9.3 1237 2 A34598 ecdysone-induced p
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452 54 9.2 132 1 THUSP anti-leukoproteinas
453 54 9.2 148 2 G82223 p11b-related prote
454 54 9.2 212 2 S09622 agglutinin isolect
455 54 9.2 213 1 AEW22 platelet aggregati
456 54 9.2 216 2 JX0265 hypothetical prote
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463 54 9.2 425 2 T39524 alpha-amylase (EC
464 54 9.2 436 1 ALRGP alpha-amylase (EC
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467 54 9.2 524 2 A29677

468 54 9.2 537 2 JC7127 frizzled protein 4
469 54 9.2 558 2 T17324 hypothetical prote
470 54 9.2 575 1 THHUB thrombomodulin pre
471 54 9.2 595 2 T39228 beta-transducin -
472 54 9.2 640 1 A30452 uromodulin precurs
473 54 9.2 685 2 C56591 E75 B steroid rece
474 54 9.2 732 2 JC4194 lanosterol synthas
475 54 9.2 737 2 S67558 nitrate reductase
476 54 9.2 756 1 IJHULM tMDC II protein -
477 54 9.2 769 1 A39627 leukocyte adhesio
478 54 9.2 790 2 A39627 protein-tyrosine k
479 54 9.2 793 2 JC5339 smoothened protein
480 54 9.2 794 2 F88508 protein H1412.6 [o
481 54 9.2 809 2 S55344 outer envelope mem
482 54 9.2 838 2 T20125 hypothetical prote
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484 54 9.2 1052 2 B49120 probable xanthine
485 54 9.2 1364 2 T51920 MEGF2 protein - hu
486 54 9.2 1364 2 T00250 Xotch protein - Af
487 54 9.2 2524 2 A35844 genome polyprotein
488 54 9.2 2531 2 S18188 notch protein homo
489 54 9.2 2652 1 VFIHB2 von Willebrand fac
490 54 9.2 2813 1 VWHU genome polyprotein
491 54 9.2 3175 1 RRWVEV MEGF1 protein - ra
492 54 9.2 4351 2 T00252 growth modulatory
493 53.5 9.1 57 2 A46654 gibberellin-regula
494 53.5 9.1 96 2 S43910 probable membrane
495 53.5 9.1 109 2 S67091 hypothetical prote
496 53.5 9.1 125 2 S24831 hypothetical prote
497 53.5 9.1 135 2 AH2100 C4b-binding protei
498 53.5 9.1 202 1 A44247 cytochrome-c3 hydr
499 53.5 9.1 232 2 H69315 hypothetical prote
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501 53.5 9.1 273 2 F69199 hypothetical prote
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504 53.5 9.1 314 2 T32985 hypothetical prote
505 53.5 9.1 328 1 A41927 insulin-like growt
506 53.5 9.1 346 2 JA0159 cysteine proteinas
507 53.5 9.1 354 2 E82850 fibriar adhesin p
508 53.5 9.1 373 2 AH0693 conserved hypotet
509 53.5 9.1 390 2 S46540 methionine adenosy
510 53.5 9.1 395 1 TRYX84 alpha-lytic protei
511 53.5 9.1 424 2 S11676 spore coat protein
512 53.5 9.1 466 2 T06416 cysteine proteinas
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515 53.5 9.1 584 2 I50419 receptor tyrosine
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518 53.5 9.1 624 2 T00044 developmental kina
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523 53.5 9.1 774 1 RRVETC hypothetical prote
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528 53.5 9.1 1124 1 I58388 anillin - fruit fl
529 53.5 9.1 1201 2 A57369 agrin - electric r
530 53.5 9.1 1328 2 T43060 protein ZC84.6 [im
531 53.5 9.1 1474 2 D88550 mucin 2, intestina
532 53.5 9.1 1513 2 A54895 dominant autoantig
533 53.5 9.1 1650 2 S53457 189.6K hypothetical
534 53.5 9.1 1678 2 D86481 collagen alpha 2(I
535 53.5 9.1 1707 2 A33526 collagen type IV a
536 53.5 9.1 1761 2 T29764 hypothetical prote
537 53.5 9.1 2180 2 T29764 gamma-zeathionin A
538 53 9.0 47 2 B58319 metallothionein A
539 540 9.0 64 2 A25775

54 9.2 537 2 JC7127 frizzled protein 4
54 9.2 558 2 T17324 hypothetical prote
54 9.2 575 1 THHUB thrombomodulin pre
54 9.2 595 2 T39228 beta-transducin -
54 9.2 640 1 A30452 uromodulin precurs
54 9.2 685 2 C56591 E75 B steroid rece
54 9.2 732 2 JC4194 lanosterol synthas
54 9.2 737 2 S67558 nitrate reductase
54 9.2 756 1 IJHULM tMDC II protein -
54 9.2 769 1 A39627 leukocyte adhesio
54 9.2 790 2 A39627 protein-tyrosine k
54 9.2 793 2 JC5339 smoothened protein
54 9.2 794 2 F88508 protein H1412.6 [o
54 9.2 809 2 S55344 outer envelope mem
54 9.2 838 2 T20125 hypothetical prote
54 9.2 977 2 T00014 protein-tyrosine k
54 9.2 1052 2 B49120 probable xanthine
54 9.2 1364 2 T51920 MEGF2 protein - hu
54 9.2 1364 2 T00250 Xotch protein - Af
54 9.2 2524 2 A35844 genome polyprotein
54 9.2 2531 2 S18188 notch protein homo
54 9.2 2652 1 VFIHB2 von Willebrand fac
54 9.2 2813 1 VWHU genome polyprotein
54 9.2 3175 1 RRWVEV MEGF1 protein - ra
54 9.2 4351 2 T00252 growth modulatory
53.5 9.1 57 2 A46654 gibberellin-regula
53.5 9.1 96 2 S43910 probable membrane
53.5 9.1 109 2 S67091 hypothetical prote
53.5 9.1 125 2 S24831 hypothetical prote
53.5 9.1 135 2 AH2100 C4b-binding protei
53.5 9.1 202 1 A44247 cytochrome-c3 hydr
53.5 9.1 232 2 H69315 hypothetical prote
53.5 9.1 266 2 B72532 conserved hypotet
53.5 9.1 273 2 F69199 hypothetical prote
53.5 9.1 294 2 T23916 hypothetical prote
53.5 9.1 297 2 S06267 surface antigen H
53.5 9.1 314 2 T32985 hypothetical prote
53.5 9.1 328 1 A41927 insulin-like growt
53.5 9.1 346 2 JA0159 cysteine proteinas
53.5 9.1 354 2 E82850 fibriar adhesin p
53.5 9.1 373 2 AH0693 conserved hypotet
53.5 9.1 390 2 S46540 methionine adenosy
53.5 9.1 395 1 TRYX84 alpha-lytic protei
53.5 9.1 424 2 S11676 spore coat protein
53.5 9.1 466 2 T06416 cysteine proteinas
53.5 9.1 473 2 C81984 probable lipopolys
53.5 9.1 509 2 T02864 s-glicerol precurs
53.5 9.1 584 2 I50419 receptor tyrosine
53.5 9.1 605 2 JC5673 developmental kina
53.5 9.1 610 2 I48612 vacuolar sorting r
53.5 9.1 624 2 T00044 developmental kina
53.5 9.1 626 2 I48614 hypothetical prote
53.5 9.1 704 2 B84685 semaphorin III fam
53.5 9.1 753 2 G02173 integrin beta-8 ch
53.5 9.1 768 2 B41029 RNA-directed RNA p
53.5 9.1 774 1 RRVETC hypothetical prote
53.5 9.1 792 2 T42963 hypothetical prote
53.5 9.1 957 2 T15976 tyrosine kinase Mp
53.5 9.1 977 2 S49004 receptor tyrosine
53.5 9.1 998 2 JC5672 protein-tyrosine k
53.5 9.1 1124 1 I58388 anillin - fruit fl
53.5 9.1 1201 2 A57369 agrin - electric r
53.5 9.1 1328 2 T43060 protein ZC84.6 [im
53.5 9.1 1474 2 D88550 mucin 2, intestina
53.5 9.1 1513 2 A54895 dominant autoantig
53.5 9.1 1650 2 S53457 189.6K hypothetical
53.5 9.1 1678 2 D86481 collagen alpha 2(I
53.5 9.1 1707 2 A33526 collagen type IV a
53.5 9.1 1761 2 T29764 hypothetical prote
53.5 9.1 2180 2 T29764 gamma-zeathionin A
53 9.0 47 2 B58319 metallothionein A
540 9.0 64 2 A25775

541	53	9.0	77	2	S29563	endothelin 2 precu	614	52.5	8.9	397	2	S26731	neuro-D4 protein -
542	53	9.0	141	2	T08790	hypothetical prote	615	52.5	8.9	403	2	T26326	hypothetical prote
543	53	9.0	156	2	T43957	hypothetical prote	616	52.5	8.9	407	1	KFB07	coagulation factor
544	53	9.0	177	2	B1682	probable ubiquinol	617	52.5	8.9	418	2	E90925	probable enzyme EC
545	53	9.0	240	2	A39842	insulin-like growt	618	52.5	8.9	418	2	A85774	probable enzyme 22
546	53	9.0	255	2	I38426	lymphocyte activat	619	52.5	8.9	418	2	B4924	hypothetical prote
547	53	9.0	272	1	G69587	L-arabinose operon	620	52.5	8.9	431	2	T37621	hypothetical prote
548	53	9.0	309	2	T22402	hypothetical prote	621	52.5	8.9	473	2	C81039	lipopolysaccharide
549	53	9.0	343	2	I49067	zinc finger protei	622	52.5	8.9	474	2	T27297	hypothetical prote
550	53	9.0	345	2	T34998	probable transmem	623	52.5	8.9	559	2	C85073	probable transposo
551	53	9.0	393	1	A48357	nonstructural prot	624	52.5	8.9	740	2	A71141	hypothetical prote
552	53	9.0	393	2	S40123	polygalacturonase	625	52.5	8.9	747	2	T39744	conserved hypotet
553	53	9.0	404	2	C96396	hypothetical prote	626	52.5	8.9	788	2	A37057	integrin beta-6 ch
554	53	9.0	413	2	T34133	hypothetical prote	627	52.5	8.9	826	2	A60385	monocyte surface a
555	53	9.0	429	2	T21113	hypothetical prote	628	52.5	8.9	873	1	A49729	VLDL receptor prec
556	53	9.0	460	2	B87455	DNA repair protein	629	52.5	8.9	898	2	S47489	receptor tyrosine
557	53	9.0	469	1	NNIV27	exo-alpha-sialidas	630	52.5	8.9	909	1	ORXLL2	LDL receptor 2 pre
558	53	9.0	493	2	JC5486	membrane glycoprot	631	52.5	8.9	1106	2	T04015	hypothetical prote
559	53	9.0	524	2	S38539	disintegrin-like m	632	52.5	8.9	2027	2	S60123	hypothetical prote
560	53	9.0	527	2	S03974	amine oxidase (fla	633	52.5	8.9	2056	2	G88564	protein R10811.1 l
561	53	9.0	551	2	S51941	prunin 1 precursor	634	52	8.8	75	1	GSFF8	salivary glue prot
562	53	9.0	578	2	S50446	VAC8 protein - yea	635	52	8.8	90	2	B86560	9 kDa-Cysteine-ric
563	53	9.0	613	2	A88448	DNA-directed RNA p	636	52	8.8	90	2	A72064	cysteine rich oute
564	53	9.0	636	2	H64429	succinate dehydrog	637	52	8.8	107	2	T49527	hypothetical prote
565	53	9.0	664	1	JX0336	disintegrin-like m	638	52	8.8	127	2	G84999	hypothetical prote
566	53	9.0	670	2	I65967	phospholipase C -	639	52	8.8	181	1	MXRRD	nonstructural prot
567	53	9.0	684	2	I39595	macrophage-stimula	640	52	8.8	189	2	JC6064	RNA-binding protei
568	53	9.0	711	1	A47136	probable kinase/ph	641	52	8.8	191	2	T50306	hypothetical prote
569	53	9.0	725	2	T35114	Notch homolog Mcc	642	52	8.8	197	2	S56662	protease inhibit
570	53	9.0	861	2	A48825	hypothetical prote	643	52	8.8	213	1	D70416	phosphoglycolate p
571	53	9.0	874	2	B70914	hypothetical prote	644	52	8.8	221	2	G69420	hydrogenase expres
572	53	9.0	922	2	T23573	hypothetical prote	645	52	8.8	227	1	LNRZ	lectin precursor -
573	53	9.0	1069	2	T42681	kalinin B1 - mouse	646	52	8.8	281	2	I39199	C2H2-150 - human
574	53	9.0	1168	2	I56985	phosphoribosylform	647	52	8.8	317	2	A2129	hypothetical prote
575	53	9.0	1354	2	T13363	hypothetical prote	648	52	8.8	325	2	A13096	proteinase [import
576	53	9.0	1360	2	T33922	protein ZC84.1 (im	649	52	8.8	325	2	H98189	probable proteinas
577	53	9.0	1416	2	E88550	MEGF8 protein - hu	650	52	8.8	327	2	T09687	chitinase (EC 3.2.
578	53	9.0	1737	2	T00209	integrin beta-4 ch	651	52	8.8	347	2	T32768	hypothetical prote
579	53	9.0	1748	1	JN0786	laminin beta-2 cha	652	52	8.8	348	1	S32484	L-iditol 2-dehydro
580	53	9.0	1798	2	S53869	integrin beta-4 ch	653	52	8.8	348	2	A40578	beta 1G-M2 protein
581	53	9.0	1807	2	JC6319	myosin heavy chain	654	52	8.8	384	2	AF0295	conserved hypotet
582	53	9.0	2017	1	A36014	myosin II heavy ch	655	52	8.8	393	2	D86168	hypothetical prote
583	53	9.0	2062	2	S61477	calcium channel al	656	52	8.8	435	2	I54182	tumor necrosis fac
584	53	9.0	2267	2	T30890	hypothetical prote	657	52	8.8	435	2	S40993	hypothetical prote
585	53	9.0	2844	1	S52891	laminin alpha-2 ch	658	52	8.8	456	1	KX80	protein C (activat
586	53	9.0	3106	1	S53868	hypothetical prote	659	52	8.8	467	2	D86485	reverse transcript
587	53	9.0	4307	2	T20721	hypothetical prote	660	52	8.8	475	2	S4996	type I serine-thre
588	52.5	8.9	70	2	A55824	drosomycin precurs	661	52	8.8	505	2	I53417	hypothetical prote
589	52.5	8.9	77	2	S47158	metallothionein II	662	52	8.8	541	2	T48811	fertilin alpha pre
590	52.5	8.9	99	2	S60230	gibberellin-regula	663	52	8.8	600	2	I49281	hypothetical prote
591	52.5	8.9	101	2	C35834	isocitrate dehydro	664	52	8.8	610	2	T16761	hypothetical prote
592	52.5	8.9	154	2	A86086	hypothetical prote	665	52	8.8	635	2	C81861	probable membrane
593	52.5	8.9	163	2	E91238	hypothetical prote	666	52	8.8	716	1	JC5061	macrophage-stimula
594	52.5	8.9	203	2	T02696	probable disease r	667	52	8.8	736	2	S47645	tMDC I protein - c
595	52.5	8.9	236	2	B98315	exsB protein [impo	668	52	8.8	786	2	T31793	hypothetical prote
596	52.5	8.9	236	2	A12967	succinoglycan bios	669	52	8.8	873	1	I48952	VLDL receptor prec
597	52.5	8.9	250	2	T01779	trypsin (EC 3.4.21	670	52	8.8	873	1	QRRBVD	VLDL receptor prec
598	52.5	8.9	250	2	S31384	trypsin (EC 3.4.21	671	52	8.8	893	2	H95953	probable bifunctio
599	52.5	8.9	252	2	A81030	probable membrane	672	52	8.8	909	1	ORXLL1	LDL receptor 1 pre
600	52.5	8.9	253	2	T49971	hypothetical prote	673	52	8.8	961	2	A55380	faciogenital dyspl
601	52.5	8.9	255	2	T44991	oxidoreductase (im	674	52	8.8	1162	2	T21557	hypothetical prote
602	52.5	8.9	261	2	S17889	class II histocomp	675	52	8.8	1172	2	C70619	probable lysX prot
603	52.5	8.9	278	2	H96611	hypothetical prote	676	52	8.8	1188	2	D86236	protein F14N23.5 [
604	52.5	8.9	280	2	D82017	hypothetical prote	677	52	8.8	1197	1	VGUVUF	M polyprotein - Ri
605	52.5	8.9	282	2	S50031	prostacyclin-stimu	678	52	8.8	1299	2	T43251	furin (EC 3.4.21.7
606	52.5	8.9	287	2	T09035	hypothetical prote	679	52	8.8	1300	2	A36502	insulin receptor-r
607	52.5	8.9	288	2	D81002	conserved hypotet	680	52	8.8	1321	2	JR0352	mucin MUC5B, trach
608	52.5	8.9	349	2	S47093	hypothetical prote	681	52	8.8	1358	1	XOCHDH	xanthine dehydroge
609	52.5	8.9	362	2	G56755	probable proline-r	682	52	8.8	1435	2	T01075	polyprotein - hepa
610	52.5	8.9	370	2	A83479	alcohol dehydrogen	683	52	8.8	2491	1	A28372	insulin-like growt
611	52.5	8.9	372	2	A42778	agglutinin precurs	684	52	8.8	3672	2	T23433	hypothetical prote
612	52.5	8.9	375	1	S62640	alcohol dehydrogen	685	52	8.8	3704	2	T37316	probable laminin a
613	52.5	8.9	387	2	I38449	extracellular prot	686	52	8.8				

687	51.5	8.7	46	2	I48947	cellular disintegr	760	51	8.7	257	2	I38025	keratin-like prote
688	51.5	8.7	77	2	AF2564	hypothetical prote	761	51	8.7	259	1	IOHUL	insulin-like growt
689	51.5	8.7	87	2	JN0670	Na+-channel-blocki	762	51	8.7	260	2	S11562	probable MASH-1 pr
690	51.5	8.7	144	2	S54244	Ig mu heavy chain	763	51	8.7	261	2	S51678	chitinase (BC 3.2.
691	51.5	8.7	214	2	T51027	hypothetical prote	764	51	8.7	269	2	T36639	probable substrate
692	51.5	8.7	221	2	S59832	hypothetical prote	765	51	8.7	274	2	T18768	hypothetical prote
693	51.5	8.7	238	2	R85597	arginine 3rd trans	766	51	8.7	284	2	A28008	troponin T, cardia
694	51.5	8.7	238	2	A90747	arginine 3rd trans	767	51	8.7	297	2	T45705	hypothetical prote
695	51.5	8.7	245	2	T49889	zinc finger transc	768	51	8.7	313	2	S44208	extracellular matr
696	51.5	8.7	251	2	G96006	probable SUP1-like	769	51	8.7	319	2	D97081	ketopantoate reduc
697	51.5	8.7	261	2	A55242	MHC class II histo	770	51	8.7	330	2	D87068	hypothetical prote
698	51.5	8.7	281	2	AE0671	N-hydroxyarylamine	771	51	8.7	332	2	T21458	hypothetical prote
699	51.5	8.7	281	2	A38090	N-hydroxyarylamine	772	51	8.7	342	2	A83263	hypothetical prote
700	51.5	8.7	282	2	A48516	surfactant protein	773	51	8.7	353	2	T27800	dihydroorotate deh
701	51.5	8.7	284	2	JC7686	activator of cAMP-	774	51	8.7	374	1	A53142	hypothetical prote
702	51.5	8.7	323	2	T27450	hypothetical prote	775	51	8.7	374	1	S35669	alcohol dehydrogen
703	51.5	8.7	326	2	A14266	uracil-DNA glycosy	776	51	8.7	375	1	DEHOAL	alcohol dehydrogen
704	51.5	8.7	335	2	S39579	c-myc promoter-bin	777	51	8.7	381	2	H95288	probable FMN-depen
705	51.5	8.7	335	2	A39579	hypothetical prote	778	51	8.7	388	2	A82045	Cystathionine gamm
706	51.5	8.7	394	2	T24860	hypothetical prote	779	51	8.7	394	2	AE2211	S-adenosylmethioni
707	51.5	8.7	410	2	T47926	hypothetical prote	780	51	8.7	394	2	AH1858	3-dehydroquinat s
708	51.5	8.7	414	2	H95843	hypothetical prote	781	51	8.7	406	2	D64934	succinylornithine
709	51.5	8.7	451	2	T20798	hypothetical prote	782	51	8.7	406	2	B85784	acetylornithine de
710	51.5	8.7	480	1	A30065	trigraamin precursor	783	51	8.7	406	2	F90935	acetylornithine de
711	51.5	8.7	485	2	S36772	E-selectin - bovin	784	51	8.7	417	2	A53010	copper transport p
712	51.5	8.7	488	2	T47697	Regulator of chrom	785	51	8.7	417	2	T45857	hypothetical prote
713	51.5	8.7	497	2	T27012	hypothetical prote	786	51	8.7	452	1	A30351	coagulation factor
714	51.5	8.7	518	2	T23120	hypothetical prote	787	51	8.7	460	2	T17011	polygalacturonase
715	51.5	8.7	523	2	F71302	asparagine-tRNA li	788	51	8.7	505	2	T38859	activin A receptor
716	51.5	8.7	562	2	T49386	hypothetical prote	789	51	8.7	525	2	T35084	hypothetical prote
717	51.5	8.7	585	2	S43572	COSB5.5 protein (C	790	51	8.7	560	2	JC4795	plasma hyaluronan-
718	51.5	8.7	585	2	R88571	protein COSB5.5 [i	791	51	8.7	560	2	D69587	L-ribulokinase ara
719	51.5	8.7	591	2	T48596	ankyrin-like prote	792	51	8.7	573	2	JC4335	anti-mullerian hor
720	51.5	8.7	592	2	T21536	hypothetical prote	793	51	8.7	604	2	D71377	phenylalanine-tRNA
721	51.5	8.7	675	1	KXMS8	plasma protein S p	794	51	8.7	651	2	JC7705	death receptor-6 -
722	51.5	8.7	686	2	JC7569	Delta-4 protein -	795	51	8.7	714	2	JC7735	nitratre reductase
723	51.5	8.7	719	2	T00266	hypothetical prote	796	51	8.7	735	2	A59434	KiAA1501 protein [
724	51.5	8.7	730	2	B87251	isoquinoline 1-oxi	797	51	8.7	736	2	S57961	dimethylamine dehy
725	51.5	8.7	740	2	A75011	hypothetical prote	798	51	8.7	751	2	F87789	protein C34G6.2 [i
726	51.5	8.7	765	2	T15447	hypothetical prote	799	51	8.7	780	2	A34102	von Willebrand fac
727	51.5	8.7	877	2	T48967	brain-specific kin	800	51	8.7	854	1	QRHLD	LDL receptor precu
728	51.5	8.7	899	2	G02428	subtilisin-like pr	801	51	8.7	915	2	T21773	hypothetical prote
729	51.5	8.7	915	2	JC6148	subtilisin-like pr	802	51	8.7	927	2	B21772	hypothetical prote
730	51.5	8.7	962	2	JC5571	subtilisin-like pr	803	51	8.7	1345	2	B71608	DNA-directed RNA p
731	51.5	8.7	972	2	A30363	glycoprotein GP330	804	51	8.7	1356	2	A45445	janusin precursor,
732	51.5	8.7	975	2	JC5570	subtilisin-like pr	805	51	8.7	1379	2	T37752	hypothetical serin
733	51.5	8.7	981	2	A41401	mineralocorticoid	806	51	8.7	1700	2	S08167	Barbani ring 3 pr
734	51.5	8.7	984	2	A29513	mineralocorticoid	807	51	8.7	2233	2	T28669	surface protein 51
735	51.5	8.7	1001	2	S30385	G9a protein - huma	808	51	8.7	2254	2	T09053	low voltage-activa
736	51.5	8.7	1038	2	T13177	sog protein - frui	809	51	8.7	2415	1	A39086	aggreacan precursor
737	51.5	8.7	1057	2	S09112	hypothetical prote	810	51	8.7	2766	2	T39165	hypothetical prote
738	51.5	8.7	1165	2	S27809	Grpase-activating	811	51	8.7	3288	2	T03099	mucin, submaxillar
739	51.5	8.7	2023	2	T13154	polycomb protein e	812	50.5	8.6	47	2	S69145	gamma-chionin SI-a
740	51.5	8.7	2809	2	T30213	G-cadherin - sea u	813	50.5	8.6	62	2	I51538	metallothionein -
741	51.5	8.7	2895	2	H85362	hypothetical prote	814	50.5	8.6	90	2	PC2137	hypothetical 90 pr
742	51.5	8.7	3512	2	T17121	CPY protein - midg	815	50.5	8.6	90	2	PC2136	LIM1 protein - tru
743	51	8.7	84	2	JN0469	85K MKK-20 recogni	816	50.5	8.6	118	2	S38491	Ig heavy chain - h
744	51	8.7	87	2	A39439	small cysteine-ric	817	50.5	8.6	122	2	T28977	hypothetical prote
745	51	8.7	114	1	S22168	lipid transfer pro	818	50.5	8.6	124	2	A21761	high-cysteine chor
746	51	8.7	120	2	J01740	hypothetical 12.7K	819	50.5	8.6	144	2	A42585	trypsin inhibitor
747	51	8.7	137	2	T15609	hypothetical prote	820	50.5	8.6	151	2	T34245	hypothetical prote
748	51	8.7	142	2	A71097	hypothetical prote	821	50.5	8.6	153	1	XKPOC1	proteinase inhibit
749	51	8.7	146	2	D86419	hypothetical prote	822	50.5	8.6	154	2	EX7530	isoquinoline 1-oxi
750	51	8.7	150	2	D87652	hypothetical prote	823	50.5	8.6	185	2	T34807	probable transcrip
751	51	8.7	168	2	T49250	zinc finger protei	824	50.5	8.6	201	2	T07011	proteinase inhibit
752	51	8.7	169	2	H69956	5-formyltetrahydro	825	50.5	8.6	214	2	T19930	hypothetical prote
753	51	8.7	187	2	T27278	hypothetical prote	826	50.5	8.6	230	2	T34854	hypothetical prote
754	51	8.7	205	2	T18250	collagen alpha 1(I	827	50.5	8.6	247	2	D75027	dihydroorotate deh
755	51	8.7	216	2	S05575	sporozoite antigen	828	50.5	8.6	256	2	B32393	T-call antigen 4-1
756	51	8.7	226	2	E71478	probable phosphogl	829	50.5	8.6	260	1	A46517	CD27 antigen precu
757	51	8.7	233	2	B69202	endonuclease III -	830	50.5	8.6	266	1	A35037	insulin-like growt
758	51	8.7	240	2	T47864	GATA transcription	831	50.5	8.6	267	2	F87665	hypothetical prote
759	51	8.7	253	2	T25768	hypothetical prote	832	50.5	8.6	272	2	H95314	probable transposa

979	49.5	8.4	142	2	S54243	Ig mu heavy chain	1052	49.5	8.4	1745	2	A46431	tight junction-ass
980	49.5	8.4	142	2	H72600	hypothetical prote	1053	49.5	8.4	2025	2	T03884	hypothetical prote
981	49.5	8.4	147	2	G83586	hypothetical prote	1054	49.5	8.4	2149	2	T47655	genome polyprotein
982	49.5	8.4	163	2	B83445	probable oxidoredu	1055	49.5	8.4	2156	1	RVUNE	odx protein - frui
983	49.5	8.4	165	2	E95890	probable oxidoredu	1056	49.5	8.4	2406	2	A54148	tenascin-like prot
984	49.5	8.4	170	2	T51042	hypothetical prote	1057	49.5	8.4	2515	2	S47008	chondroitin sulfat
985	49.5	8.4	176	2	T48699	hypothetical prote	1058	49.5	8.4	3562	2	A47171	metallothionein I
986	49.5	8.4	202	2	T24524	deoxyphosphoglucon	1059	49.5	8.3	63	2	A34905	carboxypeptidase A
987	49.5	8.4	208	2	C96948	hypothetical prote	1060	49.5	8.3	65	2	S03858	hypothetical prote
988	49.5	8.4	212	2	E71212	probable respirato	1061	49.5	8.3	67	2	PC4008	orf 5' to pheC - p
989	49.5	8.4	246	2	E70556	fibroblast growth	1062	49.5	8.3	72	2	A42325	salivary glue prot
990	49.5	8.4	256	2	T50658	expansin 9 [import	1063	49.5	8.3	74	1	GSFF7	hypothetical prote
991	49.5	8.4	257	2	G84353	plasma membrane in	1064	49.5	8.3	74	2	T24715	pancreatic ribonuc
992	49.5	8.4	274	2	T06434	insulin-like growt	1065	49.5	8.3	93	2	S72363	protein P12A21.1
993	49.5	8.4	285	2	I48601	anaerobic sulfite	1066	49.5	8.3	96	2	B96701	hypothetical prote
994	49.5	8.4	305	2	G97086	UDP-N-acetylglucos	1067	49.5	8.3	116	2	H69338	When acidic protei
995	49.5	8.4	320	2	C72022	peptidoglycan tran	1068	49.5	8.3	117	2	A24178	pancreatic-type ri
996	49.5	8.4	357	2	F86603	DNA-binding protei	1069	49.5	8.3	127	1	NRBOK2	iron-sulfur cofact
997	49.5	8.4	357	2	F86603	conglutinin precu	1070	49.5	8.3	131	2	H71651	hypothetical prote
998	49.5	8.4	369	2	S72734	conglutinin - bovi	1071	49.5	8.3	132	2	T20463	Ig heavy chain V r
999	49.5	8.4	371	1	JN0450	alcohol dehydrogen	1072	49.5	8.3	134	2	S54906	phospholipase A2
1000	49.5	8.4	371	2	I45878	site-specific DNA-	1073	49.5	8.3	145	1	PSK220	NADH2 dehydrogenas
1001	49.5	8.4	375	1	DEM8AA	type II DNA modifi	1074	49.5	8.3	155	2	S59155	paba protein Ser
1002	49.5	8.4	379	1	F64633	hypothetical prote	1075	49.5	8.3	191	2	S09635	surface protein -
1003	49.5	8.4	381	2	A71882	probable FAD-link	1076	49.5	8.3	193	2	PQ0504	omega-conotoxin re
1004	49.5	8.4	397	2	T22932	transporter, proba	1077	49.5	8.3	195	2	JH0719	hypothetical prote
1005	49.5	8.4	408	2	H87193	hypothetical prote	1078	49.5	8.3	203	2	H75434	ZNF80 homolog - gr
1006	49.5	8.4	411	2	T32458	hypothetical acyl ca	1079	49.5	8.3	213	2	I36929	hypothetical prote
1007	49.5	8.4	416	2	S56163	probable solute-bi	1080	49.5	8.3	219	2	B82825	probable oxalate o
1008	49.5	8.4	420	2	AF0302	3-oxoacyl-acyl car	1081	49.5	8.3	221	2	T02923	conserved hypoteth
1009	49.5	8.4	428	2	F97493	probable cytochrom	1082	49.5	8.3	221	2	F83366	trypsin (SC 3.4.21
1010	49.5	8.4	442	2	T06712	probable cytochrom	1083	49.5	8.3	247	2	S13813	probable ring fing
1011	49.5	8.4	483	2	T06711	probable cytochrom	1084	49.5	8.3	295	2	T04483	hypothetical prote
1012	49.5	8.4	490	2	T06711	tumor necrosis fac	1085	49.5	8.3	300	2	T49748	hypothetical prote
1013	49.5	8.4	501	2	S56163	amine oxidase (fla	1086	49.5	8.3	302	2	T26513	oligogalacturonide
1014	49.5	8.4	526	2	JT0528	low density lipopr	1087	49.5	8.3	325	2	E95349	Runt domain contai
1015	49.5	8.4	527	2	JB0373	glucuronosyltransf	1088	49.5	8.3	358	2	T33484	hypothetical prote
1016	49.5	8.4	530	2	C47113	hypothetical prote	1089	49.5	8.3	375	1	A60004	hypothetical prote
1017	49.5	8.4	554	2	B85072	probable cytosolic	1090	49.5	8.3	375	1	MFNZMS	matrix protein - m
1018	49.5	8.4	573	2	H96744	MBV-related transc	1091	49.5	8.3	375	2	S05390	fibromodulin precu
1019	49.5	8.4	608	2	T02684	uromodulin precu	1092	49.5	8.3	386	2	JC0189	45K WW domain-cont
1020	49.5	8.4	642	1	S52111	P-selectin precurs	1093	49.5	8.3	386	2	TQ0189	oligogalacturonide
1021	49.5	8.4	646	2	JN0473	probable CHP-rich	1094	49.5	8.3	415	2	S60078	hexokinase (EC 2.7
1022	49.5	8.4	651	2	B85024	hypothetical prote	1095	49.5	8.3	430	2	T46317	neurexin I-beta pr
1023	49.5	8.4	661	2	T42754	adhesion-type prot	1096	49.5	8.3	439	2	A36385	cationic amino aci
1024	49.5	8.4	679	2	A40351	Kallmann syndrome	1097	49.5	8.3	453	2	T01114	membrane-bound rib
1025	49.5	8.4	680	2	S17982	protein MEDEA [imp	1098	49.5	8.3	465	2	I49693	probable cytochrom
1026	49.5	8.4	689	2	T52060	NADH2 dehydrogenas	1099	49.5	8.3	468	2	B40228	hexokinase (EC 2.7
1027	49.5	8.4	741	2	T13042	NADH2 dehydrogenas	1100	49.5	8.3	476	2	A44170	neurexin I-beta pr
1028	49.5	8.4	741	2	T13658	NADH2 dehydrogenas	1101	49.5	8.3	490	2	T06714	cationic amino aci
1029	49.5	8.4	744	2	T13757	probable protein k	1102	49.5	8.3	498	2	H96570	membrane-bound rib
1030	49.5	8.4	756	2	S60966	fertilin alpha-II	1103	49.5	8.3	500	2	S12061	probable cytochrom
1031	49.5	8.4	825	2	S55060	ribonucleoside-dip	1104	49.5	8.3	500	2	H96570	hexokinase (EC 2.7
1032	49.5	8.4	826	1	QB0E11	probable beta-gala	1105	49.5	8.3	524	2	JH0174	hypothetical prote
1033	49.5	8.4	853	2	T04600	late expression fa	1106	49.5	8.3	524	2	T44889	probable aminopept
1034	49.5	8.4	874	2	T30398	receptor-like tyro	1107	49.5	8.3	525	2	T41663	probable transcrip
1035	49.5	8.4	893	2	S51603	fertilin alpha-I -	1108	49.5	8.3	527	2	T04329	importin alpha - t
1036	49.5	8.4	905	2	S55059	subtilisin-like pr	1109	49.5	8.3	556	1	S12602	60K cysteine-rich
1037	49.5	8.4	915	1	A48225	telencephalin prec	1110	49.5	8.3	556	2	A86560	conserved hypoteth
1038	49.5	8.4	917	2	I48950	endopeptidase Clp	1111	49.5	8.3	556	2	E95289	mullerian-inhibiti
1039	49.5	8.4	926	1	A35905	protein-tyrosine k	1112	49.5	8.3	568	2	JC5629	RNase L inhibitor
1040	49.5	8.4	988	2	I58351	receptor protein-t	1113	49.5	8.3	586	2	D69250	probable short-cha
1041	49.5	8.4	1005	2	S49015	receptor tyrosine	1114	49.5	8.3	592	2	B83231	coagulation factor
1042	49.5	8.4	1188	2	T05846	DNA-directed RNA p	1115	49.5	8.3	593	2	A54281	prostaglandin-endo
1043	49.5	8.4	1191	2	S65068	DNA-directed RNA p	1116	49.5	8.3	603	2	S38630	netrin-1 precursor
1044	49.5	8.4	1221	2	T23472	hypothetical prote	1117	49.5	8.3	606	2	A54665	ecarin precursor -
1045	49.5	8.4	1255	1	B44213	structural polypro	1118	49.5	8.3	616	2	A55796	plasma protein S p
1046	49.5	8.4	1367	2	A41228	protein-tyrosine k	1119	49.5	8.3	642	2	S53433	hypothetical prote
1047	49.5	8.4	1372	2	T25933	hypothetical prote	1120	49.5	8.3	658	2	A86231	arachidonate 12-li
1048	49.5	8.4	1607	1	MMMSB2	hypothetical prote	1121	49.5	8.3	663	1	A38283	hypothetical prote
1049	49.5	8.4	1614	2	T29861	laminin gamma-1 ch	1122	49.5	8.3	682	2	B86336	hypothetical prote
1050	49.5	8.4	1614	2	T29861	hypothetical prote	1123	49.5	8.3	686	2	G87446	potassium-transpor
1051	49.5	8.4	1711	2	AD1842	WD-40 repeat prote	1124	49.5	8.3	686	2	G87446	potassium-transpor

1125	49	8.3	687	2	T49226	hypothetical prote	1198	48.5	8.2	232	2	A41551	vascular endotheli
1126	49	8.3	699	2	T12170	NADH2 dehydrogenas	1199	48.5	8.2	237	2	S08073	cyclic nucleotide
1127	49	8.3	700	2	T06088	hypothetical prote	1200	48.5	8.2	250	2	C87489	biotin protein lig
1128	49	8.3	712	2	T02222	major surface glyc	1201	48.5	8.2	250	2	T30124	hypothetical prote
1129	49	8.3	727	2	E84847	probable CCH-type	1202	48.5	8.2	257	2	D71544	hypothetical prote
1130	49	8.3	736	2	A99279	hypothetical prote	1203	48.5	8.2	281	2	T09124	probable aquaporin
1131	49	8.3	739	2	H85245	Vpi like protein [1204	48.5	8.2	289	2	JC7279	Down syndrome crit
1132	49	8.3	739	2	T05163	hypothetical prote	1205	48.5	8.2	291	2	AF0740	probable cation tr
1133	49	8.3	754	2	AH3004	vgrg protein [lmpo	1206	48.5	8.2	298	2	T27644	hypothetical prote
1134	49	8.3	786	2	T02729	serine/threonine-s	1207	48.5	8.2	304	2	A33274	insulin-like growt
1135	49	8.3	790	2	H71509	phenylalanine-tRNA	1208	48.5	8.2	305	2	JN0508	insulin-like growt
1136	49	8.3	798	2	B27079	fibronectin recept	1209	48.5	8.2	306	2	E97471	hypothetical prote
1137	49	8.3	814	2	T49207	receptor kinase-li	1210	48.5	8.2	307	2	F71294	hypothetical prote
1138	49	8.3	816	2	B98196	hypothetical prote	1211	48.5	8.2	317	2	A36066	trans-activator of
1139	49	8.3	816	2	AH3090	Vgrg protein [lmpo	1212	48.5	8.2	317	2	D86070	regulator for metE
1140	49	8.3	875	2	F96027	probable maltoolig	1213	48.5	8.2	317	2	F91223	regulator for metE
1141	49	8.3	879	1	QRRTLD	LDL receptor precu	1214	48.5	8.2	320	2	S22450	3-o-oxoacyl-(acyl-ca
1142	49	8.3	910	2	A34721	androgen receptor	1215	48.5	8.2	320	2	A53119	cell adhesion glyc
1143	49	8.3	911	2	B34721	androgen receptor	1216	48.5	8.2	343	2	S03415	hypothetical prote
1144	49	8.3	925	2	JC2033	G protein-coupled	1217	48.5	8.2	346	2	T34129	hypothetical prote
1145	49	8.3	973	2	T01862	hypothetical prote	1218	48.5	8.2	350	2	S06758	glycerol-3-phospha
1146	49	8.3	976	2	A36355	protein-tyrosine k	1219	48.5	8.2	351	2	S72817	probable glycoprot
1147	49	8.3	1019	2	T13039	tyrosine kinase re	1220	48.5	8.2	352	2	J50023	glycerol-3-phospha
1148	49	8.3	1042	2	T26644	hypothetical prote	1221	48.5	8.2	353	2	S06760	glycerol-3-phospha
1149	49	8.3	1081	2	T15692	hypothetical prote	1222	48.5	8.2	353	2	S31790	glycerol-3-phospha
1150	49	8.3	1115	2	S40241	G protein-coupled	1223	48.5	8.2	354	1	LC4243	proteoglycan link
1151	49	8.3	1176	2	C26427	period clock prote	1224	48.5	8.2	355	1	LXCH	proteoglycan link
1152	49	8.3	1176	2	S40899	Vrs8 protein - yea	1225	48.5	8.2	357	2	S09267	Ig alpha chain C r
1153	49	8.3	1260	1	TVRTNU	protein-tyrosine k	1226	48.5	8.2	360	1	S06759	glycerol-3-phospha
1154	49	8.3	1343	2	T20718	hypothetical prote	1227	48.5	8.2	362	2	S21963	glycerol-3-phospha
1155	49	8.3	1353	1	JQ2168	E2 glycoprotein pr	1228	48.5	8.2	362	2	C71281	conserved hypotet
1156	49	8.3	1361	2	S29998	surface protein -	1229	48.5	8.2	363	2	S23137	glycerol-3-phospha
1157	49	8.3	1362	2	A37474	surface glycoprote	1230	48.5	8.2	369	2	T48612	hypothetical prote
1158	49	8.3	1363	1	VGIHOU	E2 glycoprotein pr	1231	48.5	8.2	372	2	S01028	lignin peroxidase
1159	49	8.3	1363	1	VGIHVA	E2 glycoprotein pr	1232	48.5	8.2	372	2	JT0402	lignin peroxidase
1160	49	8.3	1363	1	VGIHFL	E2 glycoprotein pr	1233	48.5	8.2	372	2	A32322	lignin peroxidase
1161	49	8.3	1363	1	VGIHFL	E2 glycoprotein pr	1234	48.5	8.2	375	1	S62638	alcohol dehydrogen
1162	49	8.3	1363	1	VGIHNM	E2 glycoprotein pr	1235	48.5	8.2	396	1	WZBE8	durp diphosphatase
1163	49	8.3	1363	2	S44241	surface protein -	1236	48.5	8.2	397	2	D83311	conserved hypotet
1164	49	8.3	1363	2	S44240	surface protein -	1237	48.5	8.2	400	2	T46383	hypothetical prote
1165	49	8.3	1425	2	T30811	hepatocyte growth	1238	48.5	8.2	404	2	S75529	beta ketoacyl-acyl
1166	49	8.3	1516	2	T01055	hypothetical prote	1239	48.5	8.2	433	1	JN0560	u-plasminogen acti
1167	49	8.3	1526	2	T19473	hypothetical prote	1240	48.5	8.2	433	2	B82965	hypothetical prote
1168	49	8.3	1645	2	T31339	carbamoyl-phosphat	1241	48.5	8.2	448	2	S41725	integrase - Saccha
1169	49	8.3	1770	2	S56221	hypothetical prote	1242	48.5	8.2	455	2	S33033	hypothetical prote
1170	49	8.3	2019	1	JQ1322	tenascin precursor	1243	48.5	8.2	464	2	G83370	hydrogen cyanide s
1171	49	8.3	2155	2	T30197	alpha tectorin - m	1244	48.5	8.2	470	2	A12188	hypothetical prote
1172	49	8.3	2588	2	T14342	NSDI protein - mou	1245	48.5	8.2	476	2	S57963	methyl CpG binding
1173	49	8.3	3938	2	T42761	Bassoon protein -	1246	48.5	8.2	489	2	T06715	probable cytochrom
1174	49	8.3	4302	2	A38971	polycystic kidney	1247	48.5	8.2	498	2	H82679	two-component syst
1175	48.5	8.2	54	1	S23075	protein PMP-D1 - m	1248	48.5	8.2	504	2	T27914	hypothetical prote
1176	48.5	8.2	79	2	T06381	proteinase inhibit	1249	48.5	8.2	506	2	S37583	RING finger protei
1177	48.5	8.2	112	2	S54832	gpi protein - gar	1250	48.5	8.2	513	1	TVHURF	ret finger protein
1178	48.5	8.2	118	1	PSKFT2	phospholipase A2 (1251	48.5	8.2	521	2	I51693	XPolycomb - Africa
1179	48.5	8.2	119	2	T14396	lipid transfer pro	1252	48.5	8.2	524	2	T23907	hypothetical prote
1180	48.5	8.2	120	2	PH1650	Ig heavy chain V r	1253	48.5	8.2	543	2	G87635	phytoene dehydroge
1181	48.5	8.2	127	2	S24689	Ig heavy chain V6	1254	48.5	8.2	577	2	T33227	hypothetical prote
1182	48.5	8.2	134	2	AH1877	hypothetical prote	1255	48.5	8.2	586	2	F85857	probable ATP-depen
1183	48.5	8.2	135	2	G83671	hypothetical prote	1256	48.5	8.2	586	2	D91013	probable ATP-depen
1184	48.5	8.2	144	2	T12152	hypothetical prote	1257	48.5	8.2	586	2	G49897	yejH protein - Esc
1185	48.5	8.2	150	2	T46301	hypothetical prote	1258	48.5	8.2	605	2	H69581	transcription acti
1186	48.5	8.2	151	2	T25047	hypothetical prote	1259	48.5	8.2	614	2	S42526	finger protein unk
1187	48.5	8.2	165	2	T39626	nicotine dehydroge	1260	48.5	8.2	634	1	S35574	transcription fact
1188	48.5	8.2	169	1	I38946	ultra high-sulfur	1261	48.5	8.2	640	2	T19346	hypothetical prote
1189	48.5	8.2	172	2	AD0570	fimbria-like prote	1262	48.5	8.2	642	2	S53434	plasma protein S p
1190	48.5	8.2	174	2	T15176	hypothetical prote	1263	48.5	8.2	668	1	Q0BEW1	ULS2 protein - hum
1191	48.5	8.2	177	1	CYDFAA	alpha-crystallin c	1264	48.5	8.2	675	1	KXBOS	plasma protein S p
1192	48.5	8.2	188	2	E97428	hypothetical prote	1265	48.5	8.2	702	2	E72775	probable helicase
1193	48.5	8.2	190	2	S52130	vascular endotheli	1266	48.5	8.2	726	2	H82774	phage-related DNA
1194	48.5	8.2	203	2	S54800	nitrite hydratase	1267	48.5	8.2	772	2	T02805	chloride channel p
1195	48.5	8.2	203	2	S19714	nitrite hydratase	1268	48.5	8.2	786	2	AG2375	WD-40 repeat-prote
1196	48.5	8.2	207	2	C70856	hypothetical prote	1269	48.5	8.2	810	2	B30848	plasma (EC 3.4.21
1197	48.5	8.2	207	2	B83523	hypothetical prote	1270	48.5	8.2	860	2	T39502	hypothetical prote

1271	48.5	8.2	932	2	T45894	hypothetical prote	1344	48	8.1	431	2	S56228	alpha-factor recep
1272	48.5	8.2	958	2	H84783	probable PHD-type	1345	48	8.1	442	2	S50062	cell wall glycopro
1273	48.5	8.2	982	2	B83021	glutamate-amonia-	1346	48	8.1	455	2	T32189	zinc finger protei
1274	48.5	8.2	1019	2	A38738	coagulation factor	1347	48	8.1	457	2	S20662	glycine receptor a
1275	48.5	8.2	1021	2	T05108	hypothetical prote	1348	48	8.1	482	2	G83490	probable outer mem
1276	48.5	8.2	1074	2	J05928	semaphorin F precu	1349	48	8.1	487	1	LQBP34	DNA ligase (ATP) (
1277	48.5	8.2	1163	1	RWHU1C	cell surface glyco	1350	48	8.1	487	2	S06464	DNA ligase (ATP) (
1278	48.5	8.2	1222	2	S40977	hypothetical prote	1351	48	8.1	487	2	C47080	copper resistance
1279	48.5	8.2	1490	2	S72351	nonstructural poly	1352	48	8.1	495	2	S32179	tniQ protein homol
1280	48.5	8.2	1506	2	T30886	integumentary muc	1353	48	8.1	506	2	S13720	coat protein - ara
1281	48.5	8.2	1508	2	B87696	glutamate synthase	1354	48	8.1	513	2	S28358	probable pitB prot
1282	48.5	8.2	1895	2	T15881	hypothetical prote	1355	48	8.1	523	2	S28358	probable pitB prot
1283	48.5	8.2	1965	2	T33216	hypothetical prote	1356	48	8.1	537	2	A54424	carboxypeptidase C
1284	48.5	8.2	2182	2	T14320	calcineurin inhibi	1357	48	8.1	552	2	E70731	acrosomal protein
1285	48.5	8.2	2643	2	T29149	hypothetical prote	1358	48	8.1	561	2	E70610	hypothetical prote
1286	48.5	8.2	3005	1	GNVSIV	genome polypotein	1359	48	8.1	575	2	S58647	vacuolar transport
1287	48	8.1	61	2	B23889	metallothionein 2	1360	48	8.1	580	2	D84772	probable sugar tra
1288	48	8.1	61	2	S00811	metallothionein II	1361	48	8.1	580	2	A46758	glutamate decarbox
1289	48	8.1	66	2	S59621	metallothionein is	1362	48	8.1	594	2	JC4085	glutamate decarbox
1290	48	8.1	67	2	B69830	hypothetical prote	1363	48	8.1	596	2	T04506	hypothetical prote
1291	48	8.1	68	2	S25775	testis-specific pr	1364	48	8.1	606	2	D86443	probable PPR-repea
1292	48	8.1	74	2	AF3436	hypothetical prote	1365	48	8.1	615	2	KFHU12	coagulation factor
1293	48	8.1	107	1	WNBEL2	latency-related pr	1366	48	8.1	616	2	T32131	hypothetical prote
1294	48	8.1	108	2	T51146	ring-box protein 1	1367	48	8.1	621	2	T32131	low density lipopr
1295	48	8.1	117	2	T07645	pEARL1 1 protein h	1368	48	8.1	634	2	T02594	hypothetical prote
1296	48	8.1	131	1	ZYSWN	metalloproteinase	1369	48	8.1	648	2	T21467	hypothetical prote
1297	48	8.1	133	2	T20467	hypothetical prote	1370	48	8.1	651	2	A39372	potassium channel
1298	48	8.1	134	1	WTBO	seminal fluid prot	1371	48	8.1	652	2	T02001	hypothetical prote
1299	48	8.1	142	2	JC4272	pleiotrophic facto	1372	48	8.1	661	2	B96596	hypothetical prote
1300	48	8.1	147	2	T30616	hypothetical prote	1373	48	8.1	662	2	T23271	hypothetical prote
1301	48	8.1	147	2	JC7263	receptor activitiy	1374	48	8.1	690	2	G84638	hypothetical prote
1302	48	8.1	161	2	S12246	anther-specific pr	1375	48	8.1	698	2	T23469	hypothetical prote
1303	48	8.1	170	2	A64347	conserved hypothet	1376	48	8.1	706	2	T49899	zinc finger transc
1304	48	8.1	191	2	T46412	keratin KAPS.4 - s	1377	48	8.1	713	2	A35502	major surface-labe
1305	48	8.1	192	2	AF2851	hypothetical prote	1378	48	8.1	724	2	B71404	hypothetical prote
1306	48	8.1	192	2	T15218	hypothetical prote	1379	48	8.1	729	2	AH2857	anthranilate synth
1307	48	8.1	201	2	T31492	hypothetical prote	1380	48	8.1	739	2	T21431	hypothetical prote
1308	48	8.1	204	2	S63145	probable membrane	1381	48	8.1	739	2	T21431	fibroblast growth
1309	48	8.1	207	2	F95966	probable aldehyde	1382	48	8.1	750	2	S41051	chloride channel p
1310	48	8.1	219	2	H85358	hypothetical prote	1383	48	8.1	764	2	T87608	HF-1 regulatory el
1311	48	8.1	229	2	D97628	ubiquinol-cytochro	1384	48	8.1	780	2	A48143	progesterone recep
1312	48	8.1	237	2	I47031	insulin-like growt	1385	48	8.1	786	2	A35466	phenylalanine-tRNA
1313	48	8.1	250	2	S30157	osmotin precursor	1386	48	8.1	786	2	A35466	hypothetical prote
1314	48	8.1	251	2	B71298	hypothetical prote	1387	48	8.1	818	2	T32154	hypothetical prote
1315	48	8.1	260	2	T47391	hypothetical prote	1388	48	8.1	822	2	T25866	hypothetical prote
1316	48	8.1	268	2	B42424	chitinase (EC 3.2.	1389	48	8.1	824	2	T23923	hypothetical prote
1317	48	8.1	271	2	S12783	OX40 antigen precu	1390	48	8.1	834	2	S13442	hemocyanin type A
1318	48	8.1	301	2	A81066	transcription regu	1391	48	8.1	840	2	AG0526	penicillin-binding
1319	48	8.1	302	2	T39146	hypothetical prote	1392	48	8.1	860	1	QRHULD	LDL receptor precu
1320	48	8.1	303	2	T46715	hypothetical prote	1393	48	8.1	892	2	F87325	hypothetical prote
1321	48	8.1	321	1	LNHUR	IGE Fc receptor II	1394	48	8.1	907	2	B75182	DNA-directed RNA p
1322	48	8.1	332	2	T19150	hypothetical prote	1395	48	8.1	923	2	A39596	progesterone recep
1323	48	8.1	335	2	H75518	probable cytochrome	1396	48	8.1	923	2	I53280	progesterone recep
1324	48	8.1	336	2	B71366	probable phosphate	1397	48	8.1	930	2	A25923	progesterone recep
1325	48	8.1	338	2	T46981	hypothetical prote	1398	48	8.1	933	1	QRHUP	sensor protein Rcs
1326	48	8.1	338	2	AD0241	probable dehydroge	1399	48	8.1	948	2	AD0790	potassium channel
1327	48	8.1	338	2	AB1816	hypothetical prote	1400	48	8.1	962	2	I53197	hypothetical prote
1328	48	8.1	342	2	T09355	hypothetical prote	1401	48	8.1	965	2	S62935	potassium channel
1329	48	8.1	344	2	I57698	folliostatin - rat	1402	48	8.1	989	2	I48912	receptor-type prot
1330	48	8.1	348	2	T28467	major envelope ant	1403	48	8.1	1013	2	I50615	hypothetical prote
1331	48	8.1	348	2	C72154	E5L protein - vari	1404	48	8.1	1014	2	T24412	pol protein homolo
1332	48	8.1	348	2	A34705	collagen - Caenorh	1405	48	8.1	1068	2	T04112	hypothetical prote
1333	48	8.1	356	2	C70398	hypothetical prote	1406	48	8.1	1076	2	F96831	hypothetical prote
1334	48	8.1	363	2	G82070	3-isopropylmalate	1407	48	8.1	1100	2	G83376	probable trehalose
1335	48	8.1	365	2	T33499	hypothetical prote	1408	48	8.1	1146	2	A38587	collagen, cornea-s
1336	48	8.1	367	2	T39752	hypothetical prote	1409	48	8.1	1173	1	VGIHHC	E2 glycoprotein pr
1337	48	8.1	368	1	S74797	GTP-binding protei	1410	48	8.1	1173	2	S48877	Ca2+-transporting
1338	48	8.1	369	2	S41971	3beta-hydroxy-Delt	1411	48	8.1	1173	2	S48877	hypothetical prote
1339	48	8.1	373	2	D71094	probable cofactor	1412	48	8.1	1352	2	G84473	serum albumin - se
1340	48	8.1	374	2	A95960	probable cytochrom	1413	48	8.1	1423	1	S27941	bullous pemphigoid
1341	48	8.1	390	2	S52036	probable alcohol d	1414	48	8.1	1433	2	A46053	collagen alpha 1(X
1342	48	8.1	414	2	AE0239	succinylornithine	1415	48	8.1	1532	2	A61262	hypothetical prote
1343	48	8.1	414	2	T46998	hypothetical prote	1416	48	8.1	1571	2	T00062	hypothetical prote

1417 48 8.1 1611 2 G84493
1418 48 8.1 1767 2 T00458
1419 48 8.1 1959 1 A33977
1420 48 8.1 1967 2 S64604
1421 48 8.1 2214 2 T16305
1422 48 8.1 2339 2 A45597
1423 48 8.1 2440 2 S39162
1424 48 8.1 2610 2 I50726
1425 48 8.1 2610 2 T20968
1426 48 8.1 2896 2 T30939
1427 48 8.1 3011 1 GNWVC3
1428 48 8.1 3391 2 JS0219
1429 48 8.1 3430 1 GNWVWV
1430 48 8.1 3712 1 YGCEVC
1431 47.5 8.1 48 2 S13963
1432 47.5 8.1 58 2 S59072
1433 47.5 8.1 65 1 NTSR3C
1434 47.5 8.1 72 2 A37417
1435 47.5 8.1 86 2 S37381
1436 47.5 8.1 88 2 J55203
1437 47.5 8.1 88 2 J00514
1438 47.5 8.1 88 2 S12125
1439 47.5 8.1 92 2 T30632
1440 47.5 8.1 97 2 S26890
1441 47.5 8.1 97 2 S71371
1442 47.5 8.1 98 2 I47086
1443 47.5 8.1 107 2 E82465
1444 47.5 8.1 108 2 PH1651
1445 47.5 8.1 113 2 D75583
1446 47.5 8.1 115 2 S45370
1447 47.5 8.1 118 2 T14464
1448 47.5 8.1 121 2 C97805
1449 47.5 8.1 130 2 T08584
1450 47.5 8.1 135 2 T15610
1451 47.5 8.1 140 2 S54240
1452 47.5 8.1 143 2 B84128
1453 47.5 8.1 152 2 A56939
1454 47.5 8.1 155 2 A45293
1455 47.5 8.1 159 2 I51077
1456 47.5 8.1 172 1 K8SHHA
1457 47.5 8.1 182 1 K8SHHD
1458 47.5 8.1 186 2 A45910
1459 47.5 8.1 189 2 T02423
1460 47.5 8.1 197 2 I46413
1461 47.5 8.1 201 2 T10190
1462 47.5 8.1 205 2 T10384
1463 47.5 8.1 209 2 T02394
1464 47.5 8.1 217 2 A33282
1465 47.5 8.1 225 2 G84180
1466 47.5 8.1 228 2 B65133
1467 47.5 8.1 230 2 A38346
1468 47.5 8.1 232 2 J07972
1469 47.5 8.1 231 2 B06691
1470 47.5 8.1 231 2 D84774
1471 47.5 8.1 231 2 F85541
1472 47.5 8.1 236 2 H71287
1473 47.5 8.1 238 1 TRWVSY
1474 47.5 8.1 253 2 T00838
1475 47.5 8.1 264 2 T16271
1476 47.5 8.1 266 2 T46533
1477 47.5 8.1 281 2 C98638
1478 47.5 8.1 308 2 T05297
1479 47.5 8.1 312 2 T25048
1480 47.5 8.1 317 2 A00461
1481 47.5 8.1 321 2 D81388
1482 47.5 8.1 323 1 SYEBAC
1483 47.5 8.1 323 2 A00810
1484 47.5 8.1 324 2 T10802
1485 47.5 8.1 324 2 JC2395
1486 47.5 8.1 325 2 T02455
1487 47.5 8.1 327 2 D71491
1488 47.5 8.1 328 2 D81650
1489 47.5 8.1 329 2 T32783

probable retroelasm
hypothetical prote
myosin heavy chain
hypothetical prote
hypothetical prote
DNA-directed RNA p
transcription coac
cation-independent
hypothetical prote
hemocyanin G-type
genome polyprotein
genome polyprotein
alpha-aminoadipyl-
metallothionein is
neurotoxin 3 - bar
thrombin inhibitor
chitin-binding ant
outer membrane pro
cysteine-rich 9K p
cysteine-rich oute
probable virion co
Ig heavy chain V r
gibberellin-regula
BiliB4 high-sulfur
hypothetical prote
Ig heavy chain V r
hypothetical prote
lipid transfer pro
competence protein
hypothetical prote
hypothetical prote
Ig mu heavy chain
cell wall hydrolas
isoquinoline 1-oxi
conopressin precu
isotocin-I precu
keratin high-sulfu
keratin high-sulfu
ultra-high-sulfur
probable low tempe
keratin KAP5.5 - s
hypothetical prote
hypothetical prote
hypothetical prote
transaldolase (EC
hypothetical prote
ultra-high-sulfur
spermatogenesis-re
hypothetical prote
ybaX protein - Esc
hypothetical prote
conserved hypotet
trypsin-like prote
hypothetical prote
hypothetical prote
hypothetical prote
protein F58F6.1 [i
hypothetical prote
hypothetical prote
lysR-family transc
probable succinate
cysteine synthase
cysteine synthase
chitinase (EC 3.2.
Fas antigen precu
hypothetical prote
hypothetical prote
conserved hypotet
hypothetical prote

1490 47.5 8.1 333 2 T20436
1491 47.5 8.1 337 2 A12144
1492 47.5 8.1 338 2 JC4776
1493 47.5 8.1 340 2 A12922
1494 47.5 8.1 342 2 T18993
1495 47.5 8.1 344 2 B97697
1496 47.5 8.1 347 2 T48323
1497 47.5 8.1 347 2 T34131
1498 47.5 8.1 354 2 T19856
1499 47.5 8.1 357 2 S23403
1500 47.5 8.1 365 2 JC4726

hypothetical prote
hypothetical prote
limbic-system-asso
hypothetical prote
hypothetical prote
sugar ABC transpor
hypothetical prote
hypothetical prote
sperm surface prot
manganese peroxida

ALIGNMENTS

RESULT 1

JC7188

REIC protein - human

C:Species: Homo sapiens (man)

C:Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 11-May-2000

C:Accession: JC7188

R:Tsuji, T.; Miyazaki, M.; Sakaguchi, M.; Inoue, Y.; Namba, M.

Biochem. Biophys. Res. Commun. 268, 20-24, 2000.

A:Title: A REIC gene shows down-regulation in human immortalized cells and human tumor

A:Reference number: JC7188; MUID:20119095; PMID:10652205

A:Accession: JC7188

A:Molecule type: mRNA

A:Residues: 1-350 <TSU>

A:Cross-references: UNIPARC:UPI0000179471; DDBJ:AB034203

A:Experimental source: heart

C:Comment: This protein is a secreted glycoprotein for head induction in amphibian embri

C:Genetics:

A:Gene: reic

C:Superfamily: human REIC protein

C:Keywords: cardiac muscle; coiled coil; glycoprotein; heart; tumor

Query Match

Best Local Similarity 17.1%; Score 100.5; DB 2; Length 350;

Matches 26; Conservative 3; Mismatches 29; Indels 11; Gaps 4;

QY 26 CERDVQCGAGTCCALSILWLRL--RMCTPLRGEGECH-PGSHKVPFFFRKRKH-----HT 77

DB 208 CDNRDCCPGLCCAFQ---RGLLPVCTPLPVEGLCHDPASRLLDLTWELEPDGALDR 264

QY 78 CPELPNLC 86

DB 265 CPCASGLLC 273

RESULT 2

T08179

LRG5 protein - Chlamydomonas reinhardtii

C:Species: Chlamydomonas reinhardtii

C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C:Accession: T08179

R:Gloeckner, G.; Beck, C.F.

submitted to the EMBL Data Library, October 1996

A:Description: Molecular characterization of a gene (LRG5) involved in blue light sign

A:Reference number: Z16399

A:Accession: T08179

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-640 <GLO>

A:Cross-references: UNIPROT:Q96397; UNIPARC:UPI000009E362; EMBL:U73817; NID:G1644369;

C:Genetics:

A:Gene: LRG5

Query Match

Best Local Similarity 15.0%; Score 88.5; DB 2; Length 640;

Matches 24; Conservative 5; Mismatches 24; Indels 23; Gaps 4;

QY 32 CGAGTCCAISLWLRLGRLMCTPLRGEGECHPGSHKVPFFFRKRKHHTCPCPLNLCSRF-- 89

Db 488 CTAGRC---WM---TCLPMWGGGTWPRPLMTF-----SRTACCLPTCCSRWLR 533
 QY 90 -----PDGRYRCSM 98
 Db 534 RWRGWAAPGGRWRCSL 549

RESULT 3
 T16840
 hypothetical protein T10E10.4 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C;Accession: T16840
 R;Geisel, C.
 submitted to the EMBL Data Library, October 1995
 A;Description: The sequence of C. elegans cosmid T10E10.
 A;Reference number: Z18588
 A;Accession: T16840
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-1101 <GEI>
 A;Cross-references: UNIPROT:Q22378; UNIPARC:UPI000017BB8F; EMBL:U39644; NID:g1049339; PI
 A;Experimental source: strain Bristol N2
 C;Genetics:
 A;Gene: CESP:T10E10.4
 A;Introns: 93/2; 152/2; 191/3; 209/2; 283/3; 303/1; 399/3; 421/1; 440/1; 465/1; 547/3; 7
 Query Match 14.1%; Score 83; DB 2; Length 1101;
 Best Local Similarity 24.4%; Pred. No. 1.3;
 Matches 32; Conservative 9; Mismatches 40; Indels 50; Gaps 6;
 QY 13 LTVVSDCAVITGACERDVQAGTCCALISLWLRG----- 46
 Db 749 LMSVORCAMGIG-CPPGNQCENGVCPPMPCSSGSIASVCGMANSCPIGYICEGRCCL 807
 QY 47 --LRMCTPLGR-----EGECHPG-----SHKVPFFRKRKHHTCPCLPPLLCS 87
 Db 808 EPLPLCPNGGRASMRVCGAECPPGYCTPLGGCCLLSMEVCPTRSNVAVQCSPNNVC- 866
 QY 88 RFPDGRYRCSM 98
 Db 867 --PFGA-SCIM 874

RESULT 4
 T09059
 notch4 - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
 C;Accession: T09059
 R;Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; S
 submitted to the EMBL Data Library, October 1997
 A;Description: Sequence of the mouse major histocompatibility locus class III region.
 A;Reference number: Z16543
 A;Accession: T09059
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-1964 <ROM>
 A;Cross-references: UNIPROT:P31695; UNIPARC:UPI000016C7F1; EMBL:AF030001; NID:g2564945;
 C;Genetics:
 A;Gene: notch4
 A;Map position: 17
 A;Introns: 22/1; 49/2; 148/1; 264/1; 305/1; 384/1; 436/1; 501/1; 539/1; 577/1; 618/1; 67
 1679/3; 1729/1; 1761/3
 C;Superfamily: notch protein; ankyrin repeat homology; EGF homology
 C;Keywords: receptor; signal transduction
 F;514-545/Domain: EGF homology <EGF>

Query Match 13.8%; Score 81; DB 2; Length 1964;
 Best Local Similarity 30.4%; Pred. No. 3.4;
 Matches 24; Conservative 7; Mismatches 22; Indels 26; Gaps 5;

QY 26 CERDVQ-----CGAGTCCALISLWLRGMC-TPLRGREGECCHPGSHKVPFFRKRKH 76
 Db 188 CERDINECFLEPGCPQGTSCNTL---GSYCLCPVGGQPQC-----KLRKG 233
 QY 77 TCP---CLPNLLGSRFPDG 92
 Db 234 ACPPGSCINGTCLVPEG 252

RESULT 5
 XLHU
 colipase precursor [validated] - human
 N;Alternate names: procolipase
 C;Species: Homo sapiens (man)
 C;Date: 04-Dec-1986 #sequence_revision 19-May-1995 #text_change 09-Jul-2004
 C;Accession: A42568; A33949; A03163
 R;Sims, H.F.; Lowe, M.E.
 Biochemistry 31, 7120-7125, 1992
 A;Title: The human colipase gene: isolation, chromosomal location, and tissue-specific
 A;Reference number: A42568; MUID:92353041; PMID:1643046
 A;Accession: A42568
 A;Molecule type: DNA
 A;Residues: 1-112 <STM>
 A;Cross-references: UNIPROT:P04118; UNIPARC:UPI0000127E78; GB:M95529; NID:g180842; PIDN
 A;Note: sequence extracted from NCBI backbone (NCBIN:110576, NCBIN:110578, NCBIN:110580
 R;Lowe, M.E.; Rosenbium, J.L.; McEwen, P.; Strauss, A.W.
 Biochemistry 29, 823-828, 1990
 A;Title: Cloning and characterization of the human colipase cDNA.
 A;Reference number: A33949; MUID:90248429; PMID:2337598
 A;Accession: A33949
 A;Molecule type: mRNA
 A;Residues: 1-112 <LOW>
 A;Cross-references: UNIPARC:UPI0000127E78; GB:J02883; NID:g180885; PIDN:AA52054.1; PID
 A;Note: evidence of partial N-glycosylation, possibly at Asn-43
 R;Sternby, B.; Engstrom, A.; Hellman, U.; Vihert, A.M.; Sternby, N.H.; Borgstrom, B.
 Biochim. Biophys. Acta 784, 75-80, 1984
 A;Title: The primary sequence of human pancreatic colipase.
 A;Reference number: A90652; MUID:84104937; PMID:6691986
 A;Accession: A03163
 A;Molecule type: protein
 A;Residues: 23-108 <STE>
 A;Cross-references: UNIPARC:UPI0000174141
 C;Comment: Colipase, a cofactor of triacylglycerol lipase (EC 3.1.1.3), forms a 1:1 sto
 se the enzyme is washed off by bile salts, which are known to have an inhibitory effect
 C;Genetics:
 A;Gene: GDB:CLPS
 A;Cross-references: GDB:127277; OMIM:120105
 A;Map position: 6pter-6p21.1
 A;Introns: 28/3; 69/3
 C;Superfamily: colipase
 C;Keywords: lipid digestion; lipid hydrolysis; pancreas
 F;1-17/Domain: signal sequence #status predicted <SIG>
 F;18-22/Domain: amino-terminal propeptide #status predicted <APP>
 F;23-108/Product: colipase #status experimental <MAT>
 F;109-112/Domain: carboxyl-terminal propeptide #status predicted <CPP>
 F;34-104, 40-56, 44-80, 45-78, 66-86/Disulfide bonds: #status predicted
 F;69, 72, 75, 76/Binding site: micellar substrate (Lys, Tyr, Tyr, Tyr) #status predicted

Query Match 13.4%; Score 79; DB 1; Length 112;
 Best Local Similarity 28.4%; Pred. No. 0.48;
 Matches 31; Conservative 9; Mismatches 45; Indels 24; Gaps 6;

QY 9 IMLLVTVSDCAVITG-----ACERDVQAGTCCALISLWLRGRLMCTPLGRE 56
 Db 5 LITLLVALSVAVAPGPGIINLNGELCMNSAQCKSNCCQHSALGLARCTSWASE 62
 QY 57 GECCHPGSHKVPFFRKRKHHTCPCLPPLLCSRFPDGRYRCMDLKNIN 105
 Db 63 NSEC---SVKTLV---GIYKPCERGLTC---EGDKTIVGSIITN 101

RESULT 6
 A56175

adhesive plaque protein Mgfp2 precursor - Mediterranean mussel
C:Species: Mytilus galloprovincialis (Mediterranean mussel)
C>Date: 27-Apr-1995 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004
C:Accession: A56175
R;Inoue, K.; Takeuchi, Y.; Miki, D.; Odo, S.
J. Biol. Chem. 270, 6698-6701, 1995
A;Title: Mussel adhesive plaque protein gene is a novel member of epidermal growth factor family
A;Reference number: A56175; MUID:95204464; PMID:7896812
A;Accession: A56175
A;Molecule type: mRNA
A;Residues: 1-473 <INO>
A;Cross-references: UNIPROT:Q25464; UNIPARC:UPI000012AB7B; GB:D43794; NID:g602767; PIDN:
C;Keywords: duplication
F;1-17/Domain: signal sequence #status predicted <SIG>
F;387-419/Domain: EGF homology <EGF>
F;429-460/Domain: EGF homology <EGF>
F;23,36,43,56,75,382,424,455,468,473/Modified site: 3',4'-dihydroxyphenylalanine (Tyr) #

Query Match 13.2%; Score 77.5; DB 2; Length 473;
Best Local Similarity 31.2%; Pred. No. 2.3;
Matches 24; Conservative 11; Mismatches 23; Indels 19; Gaps 7;
QY 26 CERDVQCGAGTCCALISLWLRGLRMCTPLGREGECH-PGSHKVPFFRKHKHTC---PCL 81
Db 117 CEKNV-CSPNPC-----KNGKCSPLGKGYKTCGSGYTGP---RCEVHACKPNPCK 165

QY 82 PNLLCSRPDGR--YRC 96
Db 166 NKGRC--FPDGKTYKC 180

RESULT 7
A55035
cysteine-rich protein CRP1 - earthworm (Enchytraeus buchholzi)
C:Species: Enchytraeus buchholzi
C>Date: 14-Nov-1994 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C:Accession: A55035; S45034
R;Willuhn, J.; Schmitt-Wrede, H.P.; Greven, H.; Wunderlich, F.
J. Biol. Chem. 269, 24688-24691, 1994
A;Title: cDNA cloning of a cadmium-inducible mRNA encoding a novel cysteine-rich, non-me
A;Reference number: A55035; MUID:95014230; PMID:7929141
A;Accession: A55035
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-251 <WIL>
A;Cross-references: UNIPROT:Q24774; UNIPARC:UPI000007D243; EMBL:X79344; NID:g488802; PID
C;Superfamily: ultra-high-sulfur keratin

Query Match 13.1%; Score 77; DB 2; Length 251;
Best Local Similarity 30.9%; Pred. No. 1.5;
Matches 25; Conservative 7; Mismatches 45; Indels 4; Gaps 3;
QY 17 SDCAVITGACERDVQCGAGTCCALISLWLRGLRMCTPLGREGECHPGSHKVPFFRKHKH 76
Db 77 SQCKCEKGECKG--CKEG--CCAPKGVAGSCGSGCKEKGCKPGCTKRCCTGCGTGC 133

QY 77 TCPCPLNLLCSRPDPGRYRCS 97
Db 134 DCPGSPCKEK-GDCKVNGS 153

RESULT 8
MEGF6 protein - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T13954
R;Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
A;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A;Reference number: T14126; MUID:98360089; PMID:9693030
A;Accession: T13954
A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA
A;Residues: 1-1574 <NAK>
A;Cross-references: UNIPROT:O88281; UNIPARC:UPI0000043BEE; EMBL:AB011532; NID:g3449293
A;Experimental source: strain Sprague-Dawley; brain
C;Genetics:
A;Gene: MEGF6

Query Match 12.8%; Score 75.5; DB 2; Length 1574;
Best Local Similarity 28.6%; Pred. No. 10;
Matches 24; Conservative 6; Mismatches 33; Indels 21; Gaps 4;
QY 19 CAVITGAC-----ERDVQCGAGTCCALISLWLRGLRMCTPLGREGECHPGSHKVPFFRKR 73
Db 755 CHRVTGECLCPGKGTGDCGAD--CPEGRWGLGQCEICPACEHGASCNP----- 801

QY 74 KHHTCPCLPNLLCSRPDPGRYRCS 97
Db 802 ETGTCCLCPGFVGSRCQD---TCS 822

RESULT 9
JC4861
fertilin beta chain - human
C:Species: Homo sapiens (man)
C>Date: 15-Aug-1996 #sequence_revision 18-Oct-1996 #text_change 09-Jul-2004
C:Accession: JC4861
R;Gupta, S.K.; Alves, K.; O'Neil Palladino, L.; Mark, G.E.; Hollis, G.F.
Biochem. Biophys. Res. Commun. 224, 318-326, 1996
A;Title: Molecular cloning of the human fertilin beta subunit.
A;Reference number: JC4861; MUID:96295488; PMID:8702389
A;Accession: JC4861
A;Molecule type: mRNA
A;Residues: 1-734 <GUP>
A;Cross-references: UNIPROT:Q99965; UNIPARC:UPI0000161BD9; GB:U38805; NID:g4151118; PID
C;Comment: This protein is an integral sperm membrane glycoprotein, and plays a role in
C;Superfamily: mouse meltrin alpha; disintegrin homology
C;Keywords: glycoprotein; integrin binding; transmembrane protein
F;382-734/Product: fertilin beta chain #status predicted <NAT>
F;382-467/Domain: disintegrin homology <DIS>
F;448-450/Region: integrin binding #status predicted
F;686-708/Domain: transmembrane #status predicted <TM>
F;121,219,352,458,565/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 12.7%; Score 75; DB 2; Length 734;
Best Local Similarity 28.8%; Pred. No. 6;
Matches 21; Conservative 7; Mismatches 29; Indels 16; Gaps 3;
QY 15 TVSDCAVITGAC-----ERDVQCGAGTCCALISLWLRGLRMCTPLGREGECHPGSHK 66
Db 401 TEQDCALIGETCCDIATCRFKAGSNCAEGPCCNCLFMSKERMCRP---SPSEC-----D 452

QY 67 VPFFRKHKHTCP 79
Db 453 LPEYNGSSASCP 465

RESULT 10
S45306
notch 3 protein - mouse
C:Species: Mus musculus (house mouse)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S45306
R;Lardelli, M.; Dahlstrand, J.; Lendahl, U.
Mech. Dev. 46, 123-136, 1994
A;Title: The novel Notch homologue mouse Notch 3 lacks specific epidermal growth factor
A;Reference number: S45306; MUID:95001556; PMID:7918097
A;Accession: S45306
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-2318 <LAR>
A;Cross-references: UNIPROT:Q61982; UNIPARC:UPI000002930C; EMBL:X74760; NID:g483580; P
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology
F;163-195/Domain: EGF homology <EGF1>

F;474-505/Domain: EGF homology <EGF>
F;854-885/Domain: EGF homology <EGF2>
F;1839-1871/Domain: ankyrin repeat homology <AN1>
F;1872-1904/Domain: ankyrin repeat homology <AN2>
F;1906-1938/Domain: ankyrin repeat homology <AN3>
F;1939-1971/Domain: ankyrin repeat homology <AN4>
F;1972-2004/Domain: ankyrin repeat homology <AN5>

Query Match 12.78; Score 75; DB 2; Length 2318;
Best Local Similarity 28.18; Pred. No. 16; Indels 25; Gaps 5;
Matches 25; Conservative 5; Mismatches 34;

QY 19 CAVITGACERDVQCGAGTCCATSLWLRGLRMCTPLGRGEGEC-----60
DB 1287 CERVASC-RELQCPVGIPCOQT--ARGPRCAPPGLSGSCRSVRASPSGATNASCASA 1343
QY 61 ---HPGS-----HKVPFPRKRKHHKTCPLP 82
DB 1344 PCLHGSSCLPVSQSVPPFR-----CVCAP 1366

RESULT 11
T31070
notch homolog - sea urchin (Lytechinus variegatus)
C;Species: Lytechinus variegatus (variegated urchin)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 31-Jan-2000
C;Accession: T31070
R;Sherwood, D.R.; McClay, D.R.
Development 124, 3363-3374, 1997
A;Title: Identification and localization of a sea urchin Notch homologue: insights into
A;Reference number: 220966; MUID:97454256; PMID:9310331
A;Accession: T31070
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-2531 <SHE>
A;Cross-references: UNIPARC:UPI000007E31C; EMBL:AF000634; NID:G2570350; PID:G2570351; PI
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology

Query Match 12.78; Score 75; DB 2; Length 2531;
Best Local Similarity 29.98; Pred. No. 17; Indels 14; Gaps 5;
Matches 23; Conservative 8; Mismatches 32;

QY 22 ITGACERDVQCGAGTCCAI--SLWLRGLRMCTPLGRGEECHPGSHKVPFPRKRKHHKTC 79
DB 120 VDNVCKLEEPQNGGTCLRTLSLDYEC-FCTP-ANTGENCTDDNHCV-----SNP 168
QY 80 CLPNLLCSRPDPGRYRC 96
DB 169 CLNGAVCTSSSDG-YSC 184

RESULT 12
I51909
collipase precursor - rat
N;Alternate names: procollipase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: A34623
R;Payne, R.M.; Sims, H.F.; Jennens, M.L.; Lowe, M.E.
Am. J. Physiol. 286, G914-G921, 1994
A;Title: Rat pancreatic lipase and two related proteins: enzymatic properties and mRNA
A;Reference number: 151909; MUID:94262798; PMID:8203536
A;Accession: I51909
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-112 <PAY>
A;Cross-references: UNIPROT:P17084; UNIPARC:UPI0000127E7C; GB:M58370; NID:G203504; PIDN:
R;Wickner, C.; Puigserver, A.
Biochem. Biophys. Res. Commun. 167, 130-136, 1990
A;Title: Rat pancreatic collipase mRNA: nucleotide sequence of a cDNA clone and nutrition
A;Reference number: A34623; MUID:90179738; PMID:2129524
A;Accession: A34623
A;Status: preliminary

A;Molecule type: mRNA
A;Residues: 1-17, 'V', 19-112 <WTC>
A;Cross-references: UNIPARC:UPI00001708E5; GB:M33333; NID:G203502; PIDN:AAA40943.1; PID:
C;Superfamily: collipase
C;Keywords: lipid digestion; lipid hydrolysis; pancreas
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-112/Product: collipase #status predicted <MAT>

Query Match 12.68; Score 74; DB 2; Length 112;
Best Local Similarity 25.88; Pred. No. 1.5; Indels 20; Gaps 4;
Matches 24; Conservative 10; Mismatches 39;

QY 6 RVSIMLLLVTVSDCAVITG-----ACERDVQCGAGTCCATSLWLRGLRMCTPL 53
DB 2 KVLVLLVTLVAVAYAAPGRGLFINLEDGIEICVNSMQC-KSRCCQHDITIL-GIARCTHK 59
QY 54 GREGECHPGSHKVPFPRKRKHHKTCPLP 86
DB 60 AMENSECSPKTYGIYYR-----CPCERGLTC 86

RESULT 13
T27283
hypothetical protein Y64G10A.f - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T27283
R;Ainscough, R.
submitted to the EMBL Data Library, September 1999
A;Reference number: 220336
A;Accession: T27283
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1620 <WIL>
A;Cross-references: UNIPARC:UPI000017BCB4; EMBL:AL110498; NID:el542303; PIDN:CAB54471.1
A;Experimental source: clone Y64G10A
C;Genetics:
A;Gene: CESP:Y64G10A.f
A;Introns: 77/1; 116/1; 198/1; 282/1; 365/1; 425/1; 466/1; 548/1; 559/1; 601/1; 625/1;
Query Match 12.68; Score 74; DB 2; Length 1620;
Best Local Similarity 27.58; Pred. No. 15; Indels 16; Gaps 4;
Matches 22; Conservative 4; Mismatches 16;

QY 16 VSDCAVITGACERDVQCGAG-----TCCATSLWLRGLRMCTPLGRGEECHPGSHKVP 68
DB 1114 VARCDHVTGEC-----RCPAGWTGPDQCITSC-----PLGRHGEGC----- 1148
QY 69 FFRKRKHHKTCPLP 88
DB 1149 -----RHSCQCSNGASCDR 1162

RESULT 14
A35356
tumor necrosis factor receptor 2 precursor [validated] - human
N;Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094
R;Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, S.
Science 248, 1019-1023, 1990
A;Title: A receptor for tumor necrosis factor defines an unusual family of cellular and
A;Reference number: A35356; MUID:90260639; PMID:2160731
A;Accession: A35356
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-461 <SMI>
A;Cross-references: UNIPROT:P20333; UNIPARC:UPI000002FAE1; GB:M32315; NID:G189185; PIDN:
R;Kohn, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squire
Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990
A;Title: A second tumor necrosis factor receptor gene product can shed a naturally occur
A;Reference number: A36475; MUID:91045991; PMID:2172983

A;Accession: A36475
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-195,'R',197-461 <KOH>
A;Cross-references: UNIPARC:UPI000003475F; GB:M55994; GB:M38549; NID:G339757; PIDN:AAA36
R;Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, M.
Cytokine 2, 231-237, 1990
A;Title: Two human TNF receptors have similar extracellular, but distinct intracellular,
A;Reference number: A48416; MUID:91370690; PMID:1966549
A;Accession: A48416
A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 23-461 <DEM>
A;Cross-references: UNIPARC:UPI00001736E6; GB:S63368; NID:G235648; PIDN:AA819824.1; PID:
A;Note: sequence extracted from NCBI backbone (NCBIN:63368, NCBI:63371)
R;Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.
Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990
A;Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstra
A;Reference number: A36007; MUID:90349572; PMID:2166946
A;Accession: A36007
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 116-140,'P',142-195,'R',197-362,'T',364-461 <HEL>
A;Cross-references: UNIPARC:UPI00001684D8; GB:M35857; NID:G339751; PIDN:AAA63262.1; PID:
R;Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M.
J. Biol. Chem. 265, 20131-20138, 1990
A;Title: Purification and partial amino acid sequence analysis of two distinct tumor nec
A;Reference number: A23666; MUID:91056048; PMID:2173696
A;Accession: A23666
A;Status: preliminary
A;Molecule type: protein
A;Residues: 23-40,'S',42-136-141;300-306 <LOE>
A;Cross-references: UNIPARC:UPI000002D39D; UNIPARC:UPI00001736E7; UNIPARC:UPI00001736E8;
R;Engelmann, H.; Novick, D.; Wallach, D.
J. Biol. Chem. 265, 1531-1536, 1990
A;Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence
A;Reference number: A35010; MUID:90110215; PMID:2153136
A;Accession: B35010
A;Status: preliminary
A;Molecule type: protein
A;Residues: 27-31 <ENG>
A;Cross-references: UNIPARC:UPI00001736EA
R;Kuhnert, P.; Kemper, O.; Wallach, D.
Gene 150, 381-386, 1994
A;Title: Cloning, sequencing and partial functional characterization of the 5' region of
A;Reference number: I38094; MUID:95121934; PMID:7821811
A;Accession: I38094
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-37 <RES>
A;Cross-references: UNIPARC:UPI0000006D8; EMBL:X80021; NID:G666044; PIDN:CAA56324.1; PI
C;Genetics:
A;Gene: GDB:TNFR2
A;Cross-references: GDB:125914; OMIM:191191
A;Map position: ip36.2-1p36.2
A;Introns: 26/3
A;Note: the list of introns is incomplete
C;Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolo
C;Keywords: duplication; glycoprotein; receptor; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>
F;40-76/Domain: NGF receptor repeat homology <NG1>
F;78-119/Domain: NGF receptor repeat homology <NG2>
F;120-162/Domain: NGF receptor repeat homology <NG3>
F;164-201/Domain: NGF receptor repeat homology <NG4>
F;262-279/Domain: transmembrane #status predicted <TMN>
F;280-461/Domain: intracellular #status predicted <INT>
F;171,193/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 12.4%; Score 73; DB 1; Length 461;
Best Local Similarity 29.5%; Pred. No. 6.4;
Matches 28; Conservative 8; Mismatches 29; Indels 30; Gaps 6;

QY 17 SDCA---VITGACERD-----VQCGAGTCAISLWRLGLRMCTPL-----GREGEF- 59
DB 98 SRCSSDQVETQACTREQNRICTCRFGWYCALSK-OEGCRLCAPLRKCRPGFGVAPGTET 156
QY 60 -----CHPGSHKVPFFRKHKHTCPCLNLLCS 87
DB 157 SDVCKPCAPGT-----FSNTTSSTDICRPHQICN 186
RESULT 15
S14458
laminin alpha-1 chain precursor - human
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: S14458; S14663; A34961
R;Haaparranta, T.; Uitto, J.; Ruoslahti, E.; Engvall, E.
Matrix 11, 151-160, 1991
A;Title: Molecular cloning of the cDNA encoding human laminin A chain.
A;Reference number: S14458; MUID:91333420; PMID:1714537
A;Accession: S14458
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-3075 <HAA>
A;Cross-references: UNIPROT:P25391; UNIPARC:UPI000012E763
R;Nielsen, M.; Vuolteenaho, R.; Boot-Handford, R.; Kallunki, P.; Tryggvason, K.
Biochem. J. 276, 369-379, 1991
A;Title: Primary structure of the human laminin A chain. Limited expression in human ti
A;Reference number: S14663; MUID:91264789; PMID:2049067
A;Accession: S14663
A;Molecule type: mRNA
A;Residues: 1-227,'FE',230-251,'MLP',255-418,'E',420-518,'L',520-1022,'V',1024-1074,'V'
A;Cross-references: UNIPARC:UPI000016ABE4; EMBL:X58531; NID:G34225; PIDN:CAA41418.1; P
R;Olson, D.; Nagayoshi, T.; Fazio, M.; Peltonen, J.; Jaakkola, S.; Sanborn, D.; Sasaki,
Lab. Invest. 60, 772-782, 1989
A;Title: Human laminin: cloning and sequence analysis of cDNAs encoding A, B1 and B2 ch
A;Reference number: A34961; MUID:89280632; PMID:2733383
A;Accession: A34961
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 'W',2397-2745,'L',2747-3053,'L',3055-3072,'PSP' <OLS>
A;Cross-references: UNIPARC:UPI0000177439
A;Note: the authors translated the codon AGA for residue 2692 as Pro
C;Genetics:
A;Gene: GDB:LAMAL1; LAMA
A;Cross-references: GDB:120135; OMIM:150320
A;Map position: 18p11.32-18p11.22
C;Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like
C;Keywords: basement membrane; calcium binding; cell binding; coiled coil; disulfide bo
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-3075/Product: laminin alpha-1 chain #status predicted <MAT>
F;18-269/Domain: VI <DM6>
F;270-516/Domain: V <DM5>
F;270-324/Domain: laminin-type EGF-like homology <LE1>
F;327-394/Domain: laminin-type EGF-like homology <LE2>
F;397-451/Domain: laminin-type EGF-like homology <LE3>
F;454-500/Domain: laminin-type EGF-like homology <LE4>
F;503-512/Domain: laminin-type EGF-like homology #status atypical <LE5>
F;517-708/Domain: IVB <DO4B>
F;709-1159/Domain: IIIB <DO3B>
F;709-739/Domain: laminin-type EGF-like homology #status atypical <LE6>
F;742-788/Domain: laminin-type EGF-like homology <LE7>
F;791-846/Domain: laminin-type EGF-like homology <LE8>
F;849-899/Domain: laminin-type EGF-like homology <LE9>
F;902-948/Domain: laminin-type EGF-like homology <LE10>
F;951-995/Domain: laminin-type EGF-like homology <LE11>
F;998-1041/Domain: laminin-type EGF-like homology <LE12>
F;1044-1087/Domain: laminin-type EGF-like homology <LE13>
F;1050-1109/Domain: laminin-type EGF-like homology #status atypical <LE14>
F;1111-1147/Domain: laminin-type EGF-like homology #status atypical <LE15>
F;1150-1159/Domain: laminin-type EGF-like homology #status atypical <LE16>
F;1160-1361/Domain: IIVa <DO4A>
F;1362-1553/Domain: IIIB <DO3A>
F;1362-1400/Domain: laminin-type EGF-like homology #status atypical <LE17>

Search completed: November 29, 2007, 17:19:40
Job time : 44.3927 secs

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OM protein - protein search, using sw model

Run on: November 29, 2007, 17:18:33 ; Search time 13 Seconds

(without alignments)
656.336 Million cell updates/sec

Title: US-10-692-299-2_COPY_20_105

Perfect score: 498

Sequence: 1 AVITGACERDVQCGAGTCCA.....CSRFPDGYRCMDLKNINP 86

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : PIR_80.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100.5	20.2	350	2 JC71188	REIC protein - hum
2	88.5	17.8	640	2 T08179	LRG5 protein - Chl
3	81	16.3	1964	2 T09059	notch4 - mouse
4	77.5	15.6	473	2 A56175	adhesive plaque pr
5	75	15.1	2531	2 T31070	notch homolog - se
6	73	14.7	112	1 XLHU	collipase precursor
7	72.5	14.6	461	1 A35356	tumor necrosis fac
8	71.5	14.4	1178	1 A39804	thrombospondin pre
9	71.5	14.4	1574	2 T13954	MEGF6 protein - ra
10	71.5	14.4	1854	2 T13576	hypothetical prote
11	71	14.3	112	2 I51909	collipase precursor
12	71	14.3	286	2 S34665	collagen, cuticula
13	71	14.3	593	1 GVHU	granulin precursor
14	70.5	14.2	591	2 I48141	agroganin - guine
15	70.5	14.2	1101	2 T16840	hypothetical prote
16	70.5	14.2	2318	2 S45306	notch 3 protein -
17	70	14.1	251	2 A55035	cysteine-rich prot
18	69	13.9	601	2 B36346	fibulin 1 precursor
19	69	13.9	683	2 C36346	fibulin 1 precursor
20	68.5	13.8	850	2 T14450	serine/threonine k
21	68.5	13.8	1172	2 A42587	thrombospondin 2 p
22	68.5	13.8	1639	1 NMFFB2	laminin gamma-1 ch
23	68	13.7	112	2 A46717	collipase precursor
24	68	13.7	427	1 GQHUN	nerve growth facto
25	68	13.7	547	2 A33901	mannosyl-oligosacc
26	68	13.7	586	1 WMBEDE	65K early nonstruc
27	68	13.7	1150	2 A41641	mannosyl-oligosacc
28	68	13.7	2215	2 T00348	LR11 protein - mou
29	68	13.7	5147	1 IJFFTM	cadherin-related t

30	67.5	13.6	108	2 C88450	protein F21H11.4 [
31	67	13.5	237	2 S45463	probable membrane
32	67	13.5	993	2 I48653	mouse developmenta
33	67	13.5	1620	2 T27283	hypothetical prote
34	67	13.5	2321	2 S78549	notch3 protein - h
35	66.5	13.4	589	2 C38128	epithelin/granulin
36	66.5	13.4	589	2 B38128	epithelin/granulin
37	66.5	13.4	1376	2 G00043	osteonidogen - hum
38	66.5	13.4	4545	1 S25111	alpha-2-macroglobu
39	66	13.3	1172	1 TSHUP2	thrombospondin 2 p
40	66	13.3	1327	2 D70759	probable oteB prot
41	66	13.3	3075	2 S14458	laminin alpha-1 ch
42	66	13.3	3712	2 S18253	laminin alpha-1 ch
43	65.5	13.2	722	2 I48324	DELTA-like 1 - mou
44	65.5	13.2	802	2 T24293	hypothetical prote
45	65.5	13.2	949	2 T24294	hypothetical prote
46	65.5	13.2	1847	2 T18308	probable viteloge
47	65	13.1	3133	2 S52093	hemocytin - silkw
48	64.5	13.0	191	2 H1370	hypothetical prote
49	64.5	13.0	1722	2 S89753	protein FLIC7.4 [l
50	64.5	13.0	3635	2 T10053	laminin alpha 5 ch
51	64	12.9	117	2 H72706	hypothetical prote
52	64	12.9	217	2 A98196	hypothetical prote
53	64	12.9	225	2 A86043	probable transposa
54	64	12.9	425	1 A26431	nerve growth facto
55	64	12.9	587	1 WMBETE	65K early nonstruc
56	64	12.9	1143	2 T22952	hypothetical prote
57	64	12.9	1984	2 T13171	probable viteloge
58	63.5	12.8	728	2 I50719	C-Delta-1 - chicke
59	63.5	12.8	3707	2 S18252	heparan sulfate pr
60	63	12.7	95	1 XLPG2	collipase II precu
61	63	12.7	143	2 B21761	high cysteine chor
62	63	12.7	459	2 I48854	gene murine tumour
63	63	12.7	2825	2 T14271	Doc4 protein, stre
64	63	12.7	2871	2 A55567	fibillin I - bovi
65	62.5	12.6	360	2 AH2272	fructose-bisphosph
66	62.5	12.6	645	2 T22178	hypothetical prote
67	62.5	12.6	895	1 IJXLCF	EP-cadherin precu
68	62.5	12.6	3020	2 A43932	mucin 2 precursor,
69	62	12.4	178	2 A23219	high-cysteine chor
70	62	12.4	491	2 T21421	hypothetical prote
71	62	12.4	998	2 S37627	protein-tyrosine k
72	62	12.4	1113	2 JEO315	low-density lipopr
73	62	12.4	1170	1 TSHUP1	thrombospondin 1 p
74	62	12.4	1170	2 A40558	thrombospondin 1 p
75	62	12.4	1221	2 A49457	fibulin-2 precursor
76	62	12.4	2437	2 S42612	transmembrane prot
77	62	12.4	2555	2 A40043	notch protein homo
78	61.5	12.3	83	2 T26545	hypothetical prote
79	61.5	12.3	277	2 I37552	OX40 homolog - hum
80	61.5	12.3	1111	2 T26972	hypothetical prote
81	61.5	12.3	1687	2 T30176	EGF repeat transme
82	61.5	12.3	2150	2 T32497	hypothetical prote
83	61.5	12.3	2471	2 A49128	cell-fate determin
84	61.5	12.3	2946	2 T15840	hypothetical prote
85	61.5	12.3	5376	2 T42215	zonadhesin - mouse
86	61	12.2	95	2 S63510	pancreatic colipas
87	61	12.2	111	2 I48204	collipase - nutria
88	61	12.2	593	1 S25062	triacylglycerol li
89	61	12.2	685	2 S78040	fibulin, splice fo
90	61	12.2	705	2 S34968	fibulin, splice fo
91	61	12.2	723	2 PN0509	integrin beta-3 ch
92	61	12.2	1251	2 A57293	latent transformin
93	61	12.2	1599	2 T16210	hypothetical prote
94	61	12.2	2476	2 T34022	zonadhesin - pig
95	60.5	12.1	96	2 C86649	hypothetical prote
96	60.5	12.1	129	2 A72606	hypothetical prote
97	60.5	12.1	905	2 T23229	hypothetical prote
98	60.5	12.1	1104	2 I38869	hypothetical prote
99	60.5	12.1	2703	1 A24420	transcription fact
100	60	12.0	451	2 T30603	notch protein - fr
101	60	12.0	734	2 JC4861	perlecan homolog 2
102	60	12.0	735	2 G02937	feritin beta cha
					fertilin beta - cr

103	60	12.0	1295	2	A32901	glp1 protein precu	176	57	11.4	419	2	A59414	metalloproteinase
104	60	12.0	1522	2	H88380	protein T22P7.3 [i	177	57	11.4	468	2	T48686	hypothetical prote
105	60	12.0	1547	2	JQ0096	hypothetical 176K	178	57	11.4	514	2	T10559	PARIS-1 protein -
106	60	12.0	1680	2	A43434	furin (EC 3.4.21.7	179	57	11.4	917	2	JC7799	hypothetical prote
107	60	12.0	1955	1	AGCH	agrin precursor -	180	57	11.4	984	2	T00326	brain-specific ang
108	60	12.0	2918	2	A54105	fibrillin-2 precu	181	57	11.4	1522	2	T00028	serine proteinase
109	60	12.0	4006	2	T09070	probable tenascin	182	57	11.4	1548	2	S34583	fibronectin - bovi
110	59.5	11.9	128	2	S32336	spulation initia	183	57	11.4	2265	1	FNBO	fibronectin - Afri
111	59.5	11.9	589	2	T43210	fibulin-1D precu	184	57	11.4	2386	1	FNHU	giberellin-regula
112	59.5	11.9	689	2	T42760	fibulin 1, splice	185	57	11.4	2481	2	A43908	colicin E1 immunit
113	59.5	11.9	712	2	T42990	probable hormone r	186	56.5	11.3	99	2	S60231	keratin high-sultu
114	59.5	11.9	886	2	A57175	lipoprotein recept	187	56.5	11.3	113	2	RLS332	hypothetical prote
115	59.5	11.9	925	2	T37475	protein T22A3.8 [i	188	56.5	11.3	130	1	KRSH3A	protein F56B3.2 [i
116	59.5	11.9	2823	2	F87908	hypothetical prote	189	56.5	11.3	258	2	T32542	hypothetical prote
117	59.5	11.9	2823	2	T23064	laminin alpha chai	190	56.5	11.3	383	2	D88633	hypothetical prote
118	59.5	11.9	3102	2	T43291	tenascin-X - bovin	191	56.5	11.3	443	2	T08905	Lu-ECAM-1 protein
119	59.5	11.9	4135	2	T42629	alpha-2-macroglobu	192	56.5	11.3	682	2	T12968	hypothetical prote
120	59.5	11.9	4544	1	S02392	hypothetical prote	193	56.5	11.3	905	2	T02205	hypothetical prote
121	59	11.8	96	2	S14018	agglutinin isolect	194	56.5	11.3	1106	2	T44598	gene shuttle craft
122	59	11.8	186	2	A28401	hypothetical prote	195	56.5	11.3	1106	2	T13938	jagged protein pre
123	59	11.8	269	2	T26957	protein Y47D3B.6 [196	56.5	11.3	1220	2	A56136	adult-specific bru
124	59	11.8	283	2	B88597	probable CCH-type	197	56.5	11.3	1458	2	A45665	DNA (cytosine-5)-
125	59	11.8	315	2	B84654	atrolysin A (EC 3.	198	56.5	11.3	1490	2	JC5145	DNA (cytosine-5)-
126	59	11.8	419	2	A1607	tumor necrosis fac	199	56.5	11.3	1495	2	JC4172	brain-specific ang
127	59	11.8	474	2	S38634	hypothetical prote	200	56.5	11.3	1537	2	T00027	DNA (cytosine-5)-
128	59	11.8	616	2	T29234	hypothetical prote	201	56.5	11.3	1572	2	JC5210	DNA (cytosine-5)-
129	59	11.8	907	2	T27317	hypothetical prote	202	56.5	11.3	1612	2	T00027	thyroglobulin prec
130	59	11.8	930	2	T34334	hypothetical prote	203	56.5	11.3	1622	2	JB0378	LDL-receptor-relat
131	59	11.8	1119	2	A8481	protein C16A3.6 [i	204	56.5	11.3	2767	1	U1HU	insulin-like growt
132	59	11.8	1203	2	A49175	Match B protein -	205	56.5	11.3	4753	1	A47437	GATA-binding trans
133	59	11.8	2871	2	A55624	fibrillin-1 precu	206	56	11.2	254	2	T48603	probable endochiti
134	58.5	11.7	308	2	JC7125	epidermal growth f	207	56	11.2	264	2	T52104	hypothetical prote
135	58.5	11.7	325	2	B43692	T2 protein - rabbi	208	56	11.2	265	2	H84867	squamosa promoter
136	58.5	11.7	358	2	T34128	hypothetical prote	209	56	11.2	320	2	T14624	S-receptor kinase
137	58.5	11.7	717	2	S12100	transferrin precu	210	56	11.2	478	2	S47040	protein-tyrosine k
138	58.5	11.7	782	2	A51625	tenascin-like prot	211	56	11.2	491	2	S52920	laminin B1k chain
139	58.5	11.7	884	2	T18649	hypothetical prote	212	56	11.2	643	2	T25473	apoptotic proteina
140	58.5	11.7	895	2	T49010	hypothetical prote	213	56	11.2	801	2	T52605	RNA polymerase (EC
141	58.5	11.7	962	1	TVBE14	106.6K protein kin	214	56	11.2	849	1	T05181	laminin beta-2 cha
142	58.5	11.7	1712	2	A38261	masking protein pr	215	56	11.2	1136	1	S57845	hypothetical prote
143	58.5	11.7	2195	2	T34264	hypothetical prote	216	56	11.2	1170	2	A53612	delta-like homeoti
144	58.5	11.7	4391	2	A38096	perlecan precursor	217	56	11.2	1194	2	T03818	homeotic protein d
145	58	11.6	46	2	A44794	antimicrobial pept	218	56	11.2	1661	2	A55677	preadipocyte facto
146	58	11.6	170	2	H83404	probable ferredoxi	219	56	11.2	1797	2	A55677	cryzain (EC 3.4.22
147	58	11.6	387	2	B49175	Match A protein -	220	56	11.2	106	2	A72581	hypothetical prote
148	58	11.6	574	2	B88465	protein B0244.8 [i	221	55.5	11.1	264	2	A84868	hypothetical prote
149	58	11.6	755	2	A44315	cartilage oligomer	222	55.5	11.1	309	2	T28708	delta-like homeoti
150	58	11.6	798	2	T22793	hypothetical prote	223	55.5	11.1	383	2	S53716	preadipocyte facto
151	58	11.6	869	1	JC4858	LDL receptor prec	224	55.5	11.1	385	2	S53718	hypothetical prote
152	58	11.6	891	2	H86306	F20D23.20 protein	225	55.5	11.1	385	2	A54785	hypothetical prote
153	58	11.6	898	2	T14764	hypothetical prote	226	55.5	11.1	471	1	KHRZOB	urease (EC 3.5.1.5
154	58	11.6	1184	2	A55184	fibulin-2 precu	227	55.5	11.1	503	2	T09026	hypothetical prote
155	58	11.6	1217	1	EGMSMG	epidermal growth f	228	55.5	11.1	569	2	T50711	hypothetical prote
156	58	11.6	1311	2	T37557	hypothetical prote	229	55.5	11.1	674	2	T15524	hypothetical prote
157	58	11.6	1428	2	T08852	lustrin A - Califo	230	55.5	11.1	680	2	T39858	phytochrome B - so
158	58	11.6	1790	1	NMFFB1	laminin beta-1 cha	231	55.5	11.1	1039	2	T14802	hypothetical prote
159	58	11.6	2531	2	A46019	notch-1 protein -	232	55.5	11.1	1296	2	T16859	hypothetical prote
160	58	11.6	2907	2	A57278	fibillin-2 precu	233	55.5	11.1	3570	2	T45025	probable membrane
161	57.5	11.5	458	2	AF0631	probable 4-hydroxy	234	55	11.0	171	2	S66858	chitinase (EC 3.2.
162	57.5	11.5	680	2	FN0510	integrin beta-3 ch	235	55	11.0	268	2	S25311	B cell-associated
163	57.5	11.5	710	2	T46589	ropy-2 protein [im	236	55	11.0	305	2	A46476	follicstatin - mous
164	57.5	11.5	810	2	T10756	Nel-homolog protei	237	55	11.0	323	2	A99211	probable cytochrom
165	57.5	11.5	1356	2	JC1402	protein-tyrosine k	238	55	11.0	343	2	S45321	probable serine/th
166	57.5	11.5	1469	2	B36665	slit protein 2 pre	239	55	11.0	512	2	T06713	choline dehydrogen
167	57.5	11.5	1480	2	A36665	slit protein 1 pre	240	55	11.0	531	2	B83422	beta-galactosidase
168	57.5	11.5	2139	2	A35672	crumbs protein - f	241	55	11.0	599	2	JC8009	thrombospondin 4 P
169	57.5	11.5	2352	2	T30201	Notch homolog prot	242	55	11.0	853	2	B85429	apolipoprotein E r
170	57.5	11.5	3002	2	A47221	fibillin 1 precu	243	55	11.0	961	1	TJ0237	bone morphogenetic
171	57	11.4	92	1	S36658	proteinase inhibit	244	55	11.0	996	2	JB0935	bone morphogenetic
172	57	11.4	175	2	C82686	lactylglutathione	245	55	11.0	1038	2	JC5527	laminin gamma 2 ch
173	57	11.4	212	2	T05936	agglutinin isolect	246	55	11.0	1038	2	JC5527	laminin gamma 2 ch
174	57	11.4	250	1	A49053	CD27 antigen precu	247	55	11.0	1192	2	S69000	laminin gamma 2 ch
175	57	11.4	414	2	T24563	hypothetical prote	248	55	11.0				

249	55	11.0	1357	2	T16860	hypothetical prote	322	53.5	10.7	109	2	S67091	probable membrane
250	55	11.0	1743	2	T26859	hypothetical prote	323	53.5	10.7	202	1	A44247	C4b-binding protei
251	55	11.0	2052	2	T18230	FYF5 finger-contai	324	53.5	10.7	232	2	H69315	cytochrome-c3 hydr
252	55	11.0	2477	2	S14428	fibronectin precu	325	53.5	10.7	266	2	B72532	hypothetical prote
253	55	11.0	2616	2	A57096	nudel protein prec	326	53.5	10.7	273	2	F69199	conserved hypotet
254	55	11.0	3225	2	I52300	giantin - human	327	53.5	10.7	280	2	T33519	hypothetical prote
255	55	11.0	3259	1	A56539	giantin - human	328	53.5	10.7	314	2	T32985	hypothetical prote
256	55	11.0	4660	2	T42737	gp330 protein prec	329	53.5	10.7	346	2	JA0159	cysteine proteinas
257	54.5	10.9	57	2	C46654	growth modulatory	330	53.5	10.7	370	2	AE0289	conserved hypotet
258	54.5	10.9	92	2	D37057	epithelial cell gl	331	53.5	10.7	390	2	S46540	methionine adenosy
259	54.5	10.9	220	2	A95956	hypothetical prote	332	53.5	10.7	424	2	S11676	spore coat protein
260	54.5	10.9	221	2	C34768	ORP2 protein - Orf	333	53.5	10.7	466	2	T06416	cysteine proteinas
261	54.5	10.9	226	2	JC4868	ribonuclease S2 (E	334	53.5	10.7	509	2	T02864	probable Zn finger
262	54.5	10.9	248	2	T19913	hypothetical prote	335	53.5	10.7	568	2	F86291	hypothetical prote
263	54.5	10.9	263	2	T27611	hypothetical prote	336	53.5	10.7	575	2	A49667	interleukin-10 rec
264	54.5	10.9	279	2	C70458	diaminopimelate ep	337	53.5	10.7	584	2	I50419	s-glycerin precuro
265	54.5	10.9	292	2	C98072	protein ZK1240.8 [338	53.5	10.7	753	2	B36268	platelet glycoprot
266	54.5	10.9	310	2	A60967	insulin-like growt	339	53.5	10.7	753	2	G02173	semaphorin III fam
267	54.5	10.9	317	2	I46916	insulin-like growt	340	53.5	10.7	768	2	B41029	integrin beta-8 ch
268	54.5	10.9	318	2	E87929	protein T22H2.6 [i	341	53.5	10.7	773	2	JQ2187	P87 protein - Card
269	54.5	10.9	358	2	T25137	hypothetical prote	342	53.5	10.7	775	2	A61228	collagen alpha 2(I
270	54.5	10.9	386	2	S52035	probable alcohol d	343	53.5	10.7	778	2	A60798	platelet glycoprot
271	54.5	10.9	419	2	E71519	probable ATPase -	344	53.5	10.7	788	2	I77349	platelet glycoprot
272	54.5	10.9	442	2	JC4978	oxidative stress p	345	53.5	10.7	850	2	S56015	gastric mucin MUC5
273	54.5	10.9	530	2	C95334	Tm23a transposase	346	53.5	10.7	863	1	S51789	VLDL receptor prec
274	54.5	10.9	644	2	A36325	epidermal growth f	347	53.5	10.7	952	2	T18900	disintegrin and me
275	54.5	10.9	711	2	S43464	ecdysteroid-induce	348	53.5	10.7	957	2	T15976	hypothetical prote
276	54.5	10.9	761	2	JC5759	brain-specific ser	349	53.5	10.7	1036	2	T17405	scavenger receptor
277	54.5	10.9	788	2	I51530	integrin beta-3 su	350	53.5	10.7	1107	2	T15884	hypothetical prote
278	54.5	10.9	837	2	A29512	LDL receptor precu	351	53.5	10.7	1124	1	I58388	protein-tyrosine k
279	54.5	10.9	938	2	I49071	protein kinase - m	352	53.5	10.7	1193	2	A44018	laminin B2 chain
280	54.5	10.9	948	2	S51605	receptor-like tyro	353	53.5	10.7	1201	2	A57369	anillin - fruit fl
281	54.5	10.9	955	2	A45441	thrombospondin 4 -	354	53.5	10.7	1245	1	MMNSND	nidogen precursor
282	54.5	10.9	984	1	A34076	protein-tyrosine k	355	53.5	10.7	1394	2	A35626	transforming growt
283	54.5	10.9	1143	2	T10636	hypothetical prote	356	53.5	10.7	1678	2	D86481	189.6K hypotetica
284	54.5	10.9	1237	2	A34598	ecdysone-induced p	357	53.5	10.7	1959	1	AGRT	agrin - rat
285	54.5	10.9	1332	2	T23024	hypothetical prote	358	53.5	10.7	2813	1	VWU	von Willebrand fac
286	54.5	10.9	1386	2	T00257	hypothetical prote	359	53.5	10.7	3507	2	T34513	hypothetical prote
287	54.5	10.9	1443	2	S05979	hypothetical prote	360	53	10.6	47	2	B58319	gamma-zeathionin 2
288	54.5	10.9	2647	2	A37098	steroid hormone re	361	53	10.6	77	2	S29563	endothelin 2 precu
289	54.5	10.9	7962	2	I38346	gelatin factor AB	362	53	10.6	141	2	T08790	hypothetical prote
290	54	10.8	63	2	S08572	elastin titin - hu	363	53	10.6	216	2	B71682	probable ubiquinol
291	54	10.8	132	1	T1HUSP	chymotrypsin/elast	364	53	10.6	216	2	JX0265	platelet aggregati
292	54	10.8	148	2	G82223	antileukoproteinas	365	53	10.6	309	2	T22402	hypothetical prote
293	54	10.8	212	2	S09623	pi1B-related prote	366	53	10.6	343	2	I49067	zinc finger protei
294	54	10.8	213	1	AEWT2	agglutinin isolect	367	53	10.6	396	1	KXBOZ	plasma protein Z -
295	54	10.8	236	2	T05695	pathogenesis-relat	368	53	10.6	424	2	T39524	hypothetical prote
296	54	10.8	287	2	A41257	apoptosis protein	369	53	10.6	502	2	T20130	hypothetical prote
297	54	10.8	335	2	S03212	hypothetical prote	370	53	10.6	551	2	S51941	prunin 1 precursor
298	54	10.8	341	2	AE2445	hypothetical prote	371	53	10.6	578	2	S50446	VAC8 protein - yea
299	54	10.8	496	1	ALPGP	alpha-amylase [EC	372	53	10.6	605	2	JC5673	receptor tyrosine
300	54	10.8	571	2	A17230	alpha-amylase [EC	373	53	10.6	610	2	I48612	developmental kina
301	54	10.8	571	2	S24789	jaraahagin C.precu	374	53	10.6	613	2	A88448	protein C45G9.6 [i
302	54	10.8	609	2	S55270	catrocollastatin p	375	53	10.6	626	2	I48614	developmental kina
303	54	10.8	732	2	JC4194	lanosterol synthas	376	53	10.6	636	2	H64429	DNA-directed RNA p
304	54	10.8	737	2	S65758	nitrate reductase	377	53	10.6	670	2	T49510	fibroin-3 related
305	54	10.8	748	2	S66129	disintegrin (EC 3.	378	53	10.6	686	2	S43562	KO8E5.3 protein -
306	54	10.8	790	2	A39627	disintegrin (EC 3.	379	53	10.6	711	1	A47136	macrophage-scimula
307	54	10.8	794	2	F88508	protein Hi412.6 [380	53	10.6	738	2	S40992	hypothetical prote
308	54	10.8	823	2	S18968	cytorestin precurs	381	53	10.6	739	2	B88553	protein KO4H4.2b [
309	54	10.8	977	2	T00014	DAP-1-alpha protei	382	53	10.6	838	2	T20125	hypothetical prote
310	54	10.8	1052	2	B49120	protein-tyrosine k	383	53	10.6	874	2	B70914	probable dnaB prot
311	54	10.8	1142	2	T30272	hypothetical prote	384	53	10.6	964	2	JC5545	integrin beta-4 pr
312	54	10.8	1364	2	T51920	probable xanthine	385	53	10.6	998	2	JC5672	receptor tyrosine
313	54	10.8	1364	2	T00250	MEGF2 protein - hu	386	53	10.6	1360	2	T33922	hypothetical prote
314	54	10.8	1429	2	S06434	homeotic protein 1	387	53	10.6	1875	2	A36429	integrin beta-4 ch
315	54	10.8	1584	2	T22674	hypothetical prote	388	53	10.6	2017	1	A36014	myosin II heavy ch
316	54	10.8	2531	2	S18188	notch protein homo	389	53	10.6	2057	2	S61477	myosin II precurs
317	54	10.8	2652	1	VF1HB2	genome polypeptin	390	52.5	10.5	170	2	A55824	drosomyacin precurs
318	54	10.8	3051	2	S42373	hypothetical prote	391	52.5	10.5	154	2	A86086	hypothetical prote
319	54	10.8	3175	1	RRWVEV	genome polypeptin	392	52.5	10.5	163	2	E91238	hypothetical prote
320	54	10.8	4351	2	T00252	MEGF1 protein - ra	393	52.5	10.5	203	2	T02696	probable disease r
321	53.5	10.7	57	2	A46654	growth modulatory	394	52.5	10.5	250	2	T01779	trypsin (EC 3.4.21

395	52.5	10.5	250	2	S31384	trypsin (EC 3.4.21	468	51.5	10.3	252	2	T46247	hypothetical prote
396	52.5	10.5	255	2	T44991	oxidoreductase [im	469	51.5	10.3	261	2	A55242	MHC class II histo
397	52.5	10.5	261	2	S17889	class II histocomp	470	51.5	10.3	282	2	A48516	surfactant protein
398	52.5	10.5	268	2	AF0195	4-amino-4-deoxycho	471	51.5	10.3	284	1	JC7686	activator of CAMP-
399	52.5	10.5	280	2	D82017	hypothetical prote	472	51.5	10.3	287	1	S75925	DNA-formamidopyrim
400	52.5	10.5	287	2	T09035	hypothetical prote	473	51.5	10.3	289	2	A84812	probable aquaporin
401	52.5	10.5	288	2	D81002	conserved hypotet	474	51.5	10.3	297	2	H69609	hypothetical prote
402	52.5	10.5	288	1	A41927	insulin-like growt	475	51.5	10.3	317	2	AF2129	hypothetical prote
403	52.5	10.5	349	2	S47093	hypothetical prote	476	51.5	10.3	323	2	T27450	hypothetical prote
404	52.5	10.5	354	2	T22274	hypothetical prote	477	51.5	10.3	334	2	AF0295	conserved hypotet
405	52.5	10.5	362	2	G96735	probable prolone-r	478	51.5	10.3	384	2	T24860	hypothetical prote
406	52.5	10.5	370	2	AE3479	alcohol dehydrogen	479	51.5	10.3	409	2	A86240	protein F20B24.10
407	52.5	10.5	370	2	T34126	hypothetical prote	480	51.5	10.3	410	2	T47926	hypothetical prote
408	52.5	10.5	387	2	I38449	extracellular prot	481	51.5	10.3	435	2	S40993	hypothetical prote
409	52.5	10.5	397	2	T26731	neuro-D4 protein -	482	51.5	10.3	435	2	S36772	E-selectin - bovin
410	52.5	10.5	403	2	T26326	hypothetical prote	483	51.5	10.3	488	2	T47697	Regulator of chrom
411	52.5	10.5	431	2	T37621	hypothetical prote	484	51.5	10.3	497	2	T27012	hypothetical prote
412	52.5	10.5	431	2	C85073	probable transposo	485	51.5	10.3	518	2	T23120	hypothetical prote
413	52.5	10.5	747	2	T39744	conserved hypotet	486	51.5	10.3	523	2	F71302	asparagine-tRNA li
414	52.5	10.5	788	2	A26547	platelet glycoprot	487	51.5	10.3	562	2	T49386	hypothetical prote
415	52.5	10.5	788	2	A37057	integrin beta-6 ch	488	51.5	10.3	585	2	S43572	hypothetical prote
416	52.5	10.5	941	1	A55195	chordin precursor	489	51.5	10.3	595	2	E88571	protein C05B5.5 [i
417	52.5	10.5	1106	2	T04015	hypothetical prote	490	51.5	10.3	591	2	T48596	ankyrin-like prote
418	52.5	10.5	1373	2	JE0095	gastric mucin MUC5	491	51.5	10.3	592	2	T21536	hypothetical prote
419	52.5	10.5	1531	2	T42218	elit-1 protein hom	492	51.5	10.3	685	2	C56591	EVS B steroid rece
420	52.5	10.5	1607	2	T43212	insulin-like growt	493	51.5	10.3	765	2	T15447	hypothetical prote
421	52.5	10.5	1650	2	S53457	dominant autoantig	494	51.5	10.3	865	2	B69074	hypothetical prote
422	52.5	10.5	1712	1	CGHU2B	collagen alpha 2(I	495	51.5	10.3	899	2	G02428	probable formate d
423	52.5	10.5	1737	1	T00209	MEGF8 protein - hu	496	51.5	10.3	915	2	JC6148	subtilisin-like pr
424	52.5	10.5	1801	1	MMRTS	laminin beta-2 cha	497	51.5	10.3	981	2	A41401	mineralocorticoid
425	52.5	10.5	3566	1	A40701	tenascin-X precurs	498	51.5	10.3	984	2	A29513	mineralocorticoid
426	52.5	10.4	77	2	S47158	metallothionein II	499	51.5	10.3	1165	2	S27809	GRPase-activating
427	52.5	10.4	107	2	T49527	hypothetical prote	500	51.5	10.3	1299	2	T43251	furin (EC 3.4.21.7
428	52.5	10.4	151	2	T20071	hypothetical prote	501	51.5	10.3	1321	2	JE0352	mucin MUC5B, trach
429	52.5	10.4	181	1	MXRRD	nonstructural prot	502	51.5	10.3	1786	1	MMMSB1	laminin beta-1 cha
430	52.5	10.4	189	2	JC6084	RNA-binding protei	503	51.5	10.3	2023	2	TJ1354	polycomb protein e
431	52.5	10.4	191	2	T50306	hypothetical prote	504	51.5	10.2	84	2	UN0469	85K MKR-20 recogni
432	52.5	10.4	213	1	D70416	phosphoglycolate p	505	51.5	10.2	87	2	SN0670	Na+-channel-blocki
433	52.5	10.4	221	2	G69420	hydrogenase expres	506	51.5	10.2	102	2	S26409	protein 108 precu
434	52.5	10.4	227	1	LNKZ	lectin precursor -	507	51.5	10.2	120	2	TJ1740	hypothetical 12.7K
435	52.5	10.4	281	2	T39199	C2H2-150 - human	508	51.5	10.2	142	2	A71097	hypothetical prote
436	52.5	10.4	289	2	ATP128	ATP-binding protei	509	51.5	10.2	169	2	T03033	probable cytochrom
437	52.5	10.4	302	2	S65021	chitinase (EC 3.2.	510	51.5	10.2	187	2	H69956	5-formyltetrahydro
438	52.5	10.4	375	1	S62640	alcohol dehydrogen	511	51.5	10.2	205	2	T27278	hypothetical prote
439	52.5	10.4	393	2	D86168	hypothetical prote	512	51.5	10.2	226	2	E71478	probable phosphogl
440	52.5	10.4	435	2	I54182	tumor necrosis fac	513	51.5	10.2	229	2	T34325	hypothetical prote
441	52.5	10.4	456	1	KXBO	protein C (activat	514	51.5	10.2	233	2	B69202	endonuclease III -
442	52.5	10.4	467	2	D86485	protein F28J9.13 [515	51.5	10.2	240	2	T47864	GATA transcription
443	52.5	10.4	513	2	D88991	protein apx-1 [imp	516	51.5	10.2	243	2	T31144	hypothetical prote
444	52.5	10.4	541	2	T48811	hypothetical prote	517	51.5	10.2	260	2	S11562	probable MASH-1 pr
445	52.5	10.4	601	2	D89711	protein F40E10.4 [518	51.5	10.2	261	2	S51678	chitinase (EC 3.2.
446	52.5	10.4	601	2	T22025	hypothetical prote	519	51.5	10.2	284	2	A28008	troponin T, cardia
447	52.5	10.4	610	2	T16761	hypothetical prote	520	51.5	10.2	319	2	D97081	ketopantoate reduc
448	52.5	10.4	635	2	C81861	hypothetical prote	521	51.5	10.2	333	2	T27800	hypothetical prote
449	52.5	10.4	656	2	S49745	probable membrane	522	51.5	10.2	353	2	A53142	hypothetical prote
450	52.5	10.4	716	1	JC5061	macrophage-stimula	523	51.5	10.2	374	1	S35669	alcohol dehydrogen
451	52.5	10.4	737	2	PQ0219	RNA-2 polyprotein	524	51.5	10.2	375	1	DSHOAL	alcohol dehydrogen
452	52.5	10.4	786	2	T31793	hypothetical prote	525	51.5	10.2	388	2	A82045	cystathionine gamm
453	52.5	10.4	893	2	H95953	probable bifunctio	526	51.5	10.2	413	2	T34123	hypothetical prote
454	52.5	10.4	961	2	A53380	faciogenital dyspl	527	51.5	10.2	417	2	T45857	hypothetical prote
455	52.5	10.4	1064	2	T40136	fibropellin Ia - S	528	51.5	10.2	429	2	T21113	coagulation factor
456	52.5	10.4	1106	2	T18739	hypothetical prote	529	51.5	10.2	452	1	A30351	hypothetical prote
457	52.5	10.4	1300	2	A36502	insulin receptor-r	530	51.5	10.2	525	2	T35084	hypothetical prote
458	52.5	10.4	1358	1	XOCHDH	xanthine dehydroge	531	51.5	10.2	548	2	T16642	hypothetical prote
459	52.5	10.4	1513	2	A54895	mucin 2, intestina	532	51.5	10.2	651	2	JC7705	death receptor-6 -
460	52.5	10.4	1557	2	T28811	hypothetical prote	533	51.5	10.2	675	1	KXMS	plasma protein S p
461	51.5	10.3	77	2	AF2564	hypothetical prote	534	51.5	10.2	714	2	S77385	nitrate reductase
462	51.5	10.3	103	4	S59331	hypothetical prote	535	51.5	10.2	736	2	S57961	dimethylamine dehy
463	51.5	10.3	131	1	KRSHA3	keratin high-sulfu	536	51.5	10.2	780	2	A34102	von Willebrand fac
464	51.5	10.3	132	1	KRG7J7	keratin high-sulfu	537	51.5	10.2	873	1	I48952	VLDL receptor prec
465	51.5	10.3	135	2	AU2100	hypothetical prote	538	51.5	10.2	934	1	A34372	complement C6 prec
466	51.5	10.3	221	2	S59832	hypothetical prote	539	51.5	10.2	1345	2	B71608	DNA-directed RNA p
467	51.5	10.3	251	2	G96006	probable SUR1-like	540	51.5	10.2	1379	2	T37752	hypothetical serin

541	51	10.2	1408	2	S16148	gene serrate prote	614	50	10.0	249	2	E89546	conserved hypothet
542	51	10.2	1700	2	S08167	Balbani ring 3 pr	615	50	10.0	256	2	T06649	hypothetical prote
543	51	10.2	1798	2	S33869	laminin beta-2 cha	616	50	10.0	268	1	G71271	probable ABC trans
544	51	10.2	1820	2	A55494	latent transformin	617	50	10.0	281	2	AE0671	N-hydroxyarylamine
545	51	10.2	3106	1	S53868	laminin alpha-2 ch	618	50	10.0	281	2	A38090	N-hydroxyarylamine
546	51	10.2	3191	2	T22945	hypothetical prote	619	50	10.0	282	1	YPD011	prestalk D11 prote
547	51	10.2	4543	1	A53102	alpha-2-macroglobu	620	50	10.0	288	2	S46536	chitinase (EC 3.2.
548	51	10.2	13288	2	T03099	mucin, submaxillar	621	50	10.0	294	2	T23916	hypothetical prote
549	50.5	10.1	47	2	S69145	gamma-thionin SI-a	622	50	10.0	297	2	T46590	probable regulator
550	50.5	10.1	118	2	S38491	ig heavy chain - h	623	50	10.0	298	2	T33046	hypothetical prote
551	50.5	10.1	122	2	T28977	hypothetical prote	624	50	10.0	302	1	TPCHTC	troponin T, cardia
552	50.5	10.1	151	2	T34245	hypothetical prote	625	50	10.0	306	2	S38251	foliistatin-relate
553	50.5	10.1	154	2	E87530	isouinolone 1-oxi	626	50	10.0	306	2	S51361	foliistatin-relate
554	50.5	10.1	201	2	T07011	proteinase inhibit	627	50	10.0	308	2	S51362	foliistatin-relate
555	50.5	10.1	214	2	T19930	hypothetical prote	628	50	10.0	332	2	T25138	hypothetical prote
556	50.5	10.1	230	2	T34854	hypothetical prote	629	50	10.0	353	2	D96596	hypothetical prote
557	50.5	10.1	247	2	D75027	dihydrocorotate deh	630	50	10.0	356	2	A25918	thrombomodulin - b
558	50.5	10.1	260	1	A46517	CD27 antigen precu	631	50	10.0	359	2	T02833	threonine aldolase
559	50.5	10.1	272	2	H95314	probable transposa	632	50	10.0	372	2	A33184	alcohol dehydrogen
560	50.5	10.1	283	2	T23785	hypothetical prote	633	50	10.0	384	2	T19513	hypothetical prote
561	50.5	10.1	284	2	T29715	hypothetical prote	634	50	10.0	393	1	A48357	nonstructural prot
562	50.5	10.1	308	2	T37286	collagen 40 - Caen	635	50	10.0	415	2	T32467	hypothetical prote
563	50.5	10.1	323	1	SYECAC	cysteine synthase	636	50	10.0	427	2	E84966	serine-tRNA ligase
564	50.5	10.1	323	2	F91039	cysteine synthase	637	50	10.0	449	2	B28002	conserved hypothet
565	50.5	10.1	323	2	A85884	cysteine synthase	638	50	10.0	450	2	T14352	WD-repeat protein
566	50.5	10.1	324	2	T25154	hypothetical prote	639	50	10.0	460	2	B74555	DNA repair protein
567	50.5	10.1	348	1	S32484	L-Iditol 2-dehydro	640	50	10.0	481	2	JC4342	fibrinolytic prote
568	50.5	10.1	372	2	A42778	agglutinin precurs	641	50	10.0	481	2	S43125	trimucin precursor
569	50.5	10.1	390	2	S49491	methionine adenosy	642	50	10.0	503	2	A49431	activin/TGF-beta-1
570	50.5	10.1	390	2	G84785	probable s-adenosy	643	50	10.0	558	2	T17324	hypothetical prote
571	50.5	10.1	398	2	A35281	integumentary muc	644	50	10.0	573	2	JC4335	hypothetical prote
572	50.5	10.1	428	2	S45361	LRR47 protein - fr	645	50	10.0	581	2	B54665	anti-mullerian hor
573	50.5	10.1	473	2	H84550	probable obtusifol	646	50	10.0	604	2	D71377	phenylalanine-tRNA
574	50.5	10.1	484	2	T25944	hypothetical prote	647	50	10.0	642	2	D69085	transcription cont
575	50.5	10.1	513	1	RGBYC6	cell division cont	648	50	10.0	647	2	T43952	hypothetical prote
576	50.5	10.1	538	2	E84863	hypothetical prote	649	50	10.0	666	2	F13110	probable periplasm
577	50.5	10.1	603	2	JC5063	prosteglandin-endo	650	50	10.0	669	2	T06702	hypothetical prote
578	50.5	10.1	604	2	F87936	protein M01G12.12	651	50	10.0	684	2	B39595	phospholipase C -
579	50.5	10.1	604	2	T23669	hypothetical prote	652	50	10.0	686	2	B5267	prolyl endopeptida
580	50.5	10.1	618	2	D71055	probable indolepyr	653	50	10.0	686	2	T25987	hypothetical prote
581	50.5	10.1	657	2	D71351	probable primosoma	654	50	10.0	704	2	T03478	probable DNA-direc
582	50.5	10.1	664	1	JX0336	succinate dehydrog	655	50	10.0	759	2	T44142	DR1 protein (impor
583	50.5	10.1	686	2	JC7569	Delta-4 protein -	656	50	10.0	775	2	S28284	hypothetical prote
584	50.5	10.1	758	2	S51748	lethal(2)denticlel	657	50	10.0	780	2	T27941	hypothetical prote
585	50.5	10.1	769	1	IJHULM	leukocyte adhesion	658	50	10.0	782	2	E88556	protein B0464.5a [
586	50.5	10.1	769	2	A41029	integrin beta-8 ch	659	50	10.0	792	2	T42963	hypothetical prote
587	50.5	10.1	814	2	A95206	glycosyl transfera	660	50	10.0	887	2	S57430	hypothetical prote
588	50.5	10.1	856	2	T52415	polycarb protein E	661	50	10.0	889	2	T23299	probable formate d
589	50.5	10.1	898	2	T01503	hypothetical prote	662	50	10.0	962	2	JC5571	hypothetical prote
590	50.5	10.1	955	2	S56649	pyruvate, phosphat	663	50	10.0	975	2	JC5570	subtilisin-like pr
591	50.5	10.1	1019	1	A56318	enteropeptidase (E	664	50	10.0	1053	2	S46199	probable calcium t
592	50.5	10.1	1087	2	S28282	hypothetical prote	665	50	10.0	1054	2	A61221	hypothetical prote
593	50.5	10.1	1164	2	T06144	disease resistance	666	50	10.0	1069	2	T42681	hypothetical prote
594	50.5	10.1	1237	2	T46609	calcium-activated	667	50	10.0	1093	2	F88556	protein B0464.5a [
595	50.5	10.1	1297	2	T30274	proteolialisin - se	668	50	10.0	1108	2	JC4037	alpha-mannosidase
596	50.5	10.1	1384	2	T02748	hypothetical prote	669	50	10.0	1391	2	S73652	RNA polymerase bet
597	50.5	10.1	1551	1	A43364	M polyprotein prec	670	50	10.0	1481	1	O2D093	pyrimidine synthe
598	50.5	10.1	1627	2	S65464	pregnancy-associat	671	50	10.0	2027	2	S60123	hypothetical prote
599	50.5	10.1	1745	1	S19694	tenascin precursor	672	50	10.0	2056	2	G88564	hypothetical prote
600	50.5	10.1	1761	2	T13990	collagen type IV a	673	50	10.0	2120	2	T30243	protein R10E11.1 [
601	50.5	10.1	2180	2	T29764	hypothetical prote	674	50	10.0	2910	2	T42214	alpha tectorin - c
602	50.5	10.1	2225	2	T26063	hypothetical prote	675	50	10.0	3005	2	T08841	otogelin - mouse
603	50.5	10.1	2599	2	A96616	unknown protein F1	676	49.5	9.9	61	2	C81079	polypeptide - dour
604	50.5	10.1	3084	1	MMWSA	laminin alpha-1 ch	677	49.5	9.9	74	2	S05594	hypothetical prote
605	50.5	10.1	4307	2	T20721	hypothetical prote	678	49.5	9.9	142	2	H72600	hypothetical prote
606	50	10.0	87	2	JN0669	Na+-channel-blocki	679	49.5	9.9	156	2	T43957	hypothetical prote
607	50	10.0	96	1	XLHOB	collipase B precurs	680	49.5	9.9	163	2	B83445	probable oxidoredu
608	50	10.0	98	2	AG3416	hypothetical prote	681	49.5	9.9	170	2	T51042	hypothetical prote
609	50	10.0	103	2	T25294	hypothetical prote	682	49.5	9.9	176	2	T48699	hypothetical prote
610	50	10.0	176	2	T31796	hypothetical prote	683	49.5	9.9	213	2	E71212	hypothetical prote
611	50	10.0	193	2	T16566	hypothetical prote	684	49.5	9.9	256	2	JC4627	fibroblast growth
612	50	10.0	204	2	T35410	probable DNA-bindi	685	49.5	9.9	274	2	G84353	hypothetical prote
613	50	10.0	233	2	T47136	hypothetical prote	686	49.5	9.9	291	1	JN0064	insulin-like growt

687	49.5	9.9	305	2	I48601	760	49	9.8	415	2	S60078	Runt domain contai
688	49.5	9.9	322	1	S37344	761	49	9.8	468	2	B40228	neurexin I-beta pr
689	49.5	9.9	349	2	A85303	762	49	9.8	469	2	G86638	cationic amino aci
690	49.5	9.9	349	2	T04272	763	49	9.8	474	2	T07297	hypothetical prote
691	49.5	9.9	357	2	C72022	764	49	9.8	490	2	T06714	probable cytochrom
692	49.5	9.9	357	2	F86603	765	49	9.8	493	2	JC5486	membrane glycoprot
693	49.5	9.9	357	2	T32881	766	49	9.8	500	2	H96570	hypothetical prote
694	49.5	9.9	369	2	S72734	767	49	9.8	524	2	T41663	probable aminopept
695	49.5	9.9	375	1	DEM5AA	768	49	9.8	525	2	T04329	probable transcrip
696	49.5	9.9	379	1	F64633	769	49	9.8	537	2	JC5629	importin alpha - t
697	49.5	9.9	381	2	A71882	770	49	9.8	568	2	H96744	mullerian-inhibiti
698	49.5	9.9	397	2	T22932	771	49	9.8	573	2	B83231	probable cytosolic
699	49.5	9.9	416	2	T32458	772	49	9.8	593	2	S45281	probable short-cha
700	49.5	9.9	416	2	T25101	773	49	9.8	603	2	A38630	coagulation factor
701	49.5	9.9	483	2	T06711	774	49	9.8	606	2	A54665	prostaglandin-endo
702	49.5	9.9	483	2	T06712	775	49	9.8	640	1	A30452	netrin-1 precursor
703	49.5	9.9	554	2	B85072	776	49	9.8	640	1	A30452	uromodulin precurs
704	49.5	9.9	608	2	T02684	777	49	9.8	642	1	A38283	plasma protein S p
705	49.5	9.9	642	1	S52111	778	49	9.8	663	1	A38283	arachidonate 12-li
706	49.5	9.9	646	2	JN0473	779	49	9.8	685	2	JC7570	Delta-4 protein -
707	49.5	9.9	661	2	T42754	780	49	9.8	685	2	T12170	NADH2 dehydrogenas
708	49.5	9.9	689	2	T52060	781	49	9.8	715	2	JC2222	major surface glyc
709	49.5	9.9	741	2	T13042	782	49	9.8	727	2	B84847	probable CCH-type
710	49.5	9.9	741	2	T13658	783	49	9.8	736	2	A99279	hypothetical prote
711	49.5	9.9	744	2	T13757	784	49	9.8	739	2	H85245	VPI like protein (
712	49.5	9.9	756	2	S60966	785	49	9.8	754	2	T05163	hypothetical prote
713	49.5	9.9	853	2	T04600	786	49	9.8	754	2	AH3004	hypothetical prote
714	49.5	9.9	861	2	A48825	787	49	9.8	774	2	RVETC	vgg protein [limpo
715	49.5	9.9	874	2	T30398	788	49	9.8	790	2	H71509	RNA-directed RNA p
716	49.5	9.9	915	1	A48225	789	49	9.8	816	2	B98196	phenylalanine-trna
717	49.5	9.9	926	1	A35905	790	49	9.8	816	2	QRHYLD	hypothetical prote
718	49.5	9.9	1188	2	T05846	791	49	9.8	854	1	QRHYLD	vgg protein [limpo
719	49.5	9.9	1191	2	S65068	792	49	9.8	862	1	QRMSLD	RNA-directed RNA p
720	49.5	9.9	1221	2	T23472	793	49	9.8	873	2	A49729	hypothetical prote
721	49.5	9.9	1255	1	B44213	794	49	9.8	873	1	QRMSLD	phenylalanine-trna
722	49.5	9.9	1367	2	A41228	795	49	9.8	875	2	F96027	hypothetical prote
723	49.5	9.9	1523	2	T13953	796	49	9.8	910	2	A34721	LDL receptor precu
724	49.5	9.9	1607	1	MMWSE2	797	49	9.8	911	2	B34721	LDL receptor precu
725	49.5	9.9	1614	2	T29861	798	49	9.8	925	2	JC2033	LDL receptor precu
726	49.5	9.9	1614	2	A35326	799	49	9.8	949	2	T44577	LDL receptor precu
727	49.5	9.9	1745	2	A46431	800	49	9.8	951	2	T45726	VLDL receptor prec
728	49.5	9.9	1748	1	JN0786	801	49	9.8	973	2	T01862	VLDL receptor prec
729	49.5	9.9	1807	2	JC6319	802	49	9.8	976	2	A36355	probable maltoolig
730	49.5	9.9	2025	2	T30884	803	49	9.8	988	2	I58351	androgen receptor
731	49.5	9.9	2156	1	RVUNE	804	49	9.8	1019	2	T13039	G protein-coupled
732	49.5	9.9	2406	2	A54148	805	49	9.8	1081	2	T15692	G protein-coupled
733	49.5	9.9	2415	1	A39086	806	49	9.8	1133	1	EGRT	epidermal growth f
734	49.5	9.9	2515	2	S47008	807	49	9.8	1176	2	C26427	period clock prote
735	49.5	9.9	3229	2	S27852	808	49	9.8	1176	2	S40899	VP88 protein - yea
736	49.5	9.9	3512	2	T17121	809	49	9.8	1292	2	T09229	galactose binding
737	49.5	9.9	3562	2	A47171	810	49	9.8	1343	2	T20718	hypothetical prote
738	49	9.8	62	2	I51538	811	49	9.8	1343	2	T20718	E2 glycoprotein pr
739	49	9.8	65	2	S03858	812	49	9.8	1353	1	JQ2168	surface glycoprote
740	49	9.8	67	2	PC4008	813	49	9.8	1361	2	S29998	surface glycoprote
741	49	9.8	72	2	A42325	814	49	9.8	1362	2	A37474	E2 glycoprotein pr
742	49	9.8	93	2	S72363	815	49	9.8	1363	1	VGTHOU	E2 glycoprotein pr
743	49	9.8	93	2	JR0159	816	49	9.8	1363	1	VGTHOU	E2 glycoprotein pr
744	49	9.8	96	2	S43910	817	49	9.8	1363	1	VGTHOU	E2 glycoprotein pr
745	49	9.8	117	2	A24178	818	49	9.8	1363	1	VGTHOU	E2 glycoprotein pr
746	49	9.8	127	1	NBOK2	819	49	9.8	1363	1	VGTHOU	E2 glycoprotein pr
747	49	9.8	145	1	PKF2U	820	49	9.8	1363	1	VGTHOU	surface protein -
748	49	9.8	193	2	PQ0503	821	49	9.8	1363	1	VGTHOU	hypothetical prote
749	49	9.8	239	2	PQ0504	822	49	9.8	1526	2	T19473	carbamoyl-phosphat
750	49	9.8	257	2	F83366	823	49	9.8	1645	2	T31339	WD-40 repeat prote
751	49	9.8	278	2	H96611	824	49	9.8	1770	2	S56221	hypothetical prote
752	49	9.8	300	2	T49748	825	49	9.8	1786	1	MMHUB1	laminin beta-1 cha
753	49	9.8	302	2	T26513	826	49	9.8	2019	1	JQ1322	tenascin precursor
754	49	9.8	329	2	T07000	827	49	9.8	2524	2	A35844	Xotch protein - Af
755	49	9.8	329	2	T06999	828	49	9.8	2588	2	T14342	NSD1 protein - mou
756	49	9.8	329	2	S05390	829	49	9.8	4302	2	A38971	polycystic kidney
757	49	9.8	375	2	JC7508	830	49	9.8	54	1	S23075	protein PMP-D1 - m
758	49	9.8	386	2	JQ0189	831	48.5	9.7	79	2	T06381	proteinase inhibit
759	49	9.8	388	2	JQ0189	832	48.5	9.7	79	2	T06381	proteinase inhibit

833	48.5	9.7	99	2	S60230	gibberellin-regula	906	48	9.6	67	2	B69830	hypothetical prote
834	48.5	9.7	112	2	S54832	gip1 protein - gar	907	48	9.6	74	2	AF3436	hypothetical prote
835	48.5	9.7	118	1	PK8712	phospholipase A2 (908	48	9.6	107	1	WBEL2	latency-related pr
836	48.5	9.7	120	2	PH1650	ig heavy chain v r	909	48	9.6	134	1	WTBO	seminal fluid prot
837	48.5	9.7	135	2	G83671	hypothetical prote	910	48	9.6	147	2	T30616	hypothetical prote
838	48.5	9.7	150	2	T46301	hypothetical prote	911	48	9.6	170	2	A64347	conserved hypotet
839	48.5	9.7	165	2	I39626	nicotine dehydrog	912	48	9.6	192	2	AF2851	hypothetical prote
840	48.5	9.7	177	1	CYDPAA	alpha-crystallin c	913	48	9.6	197	2	S56662	proteinase inhibit
841	48.5	9.7	190	2	S21130	vascular endotheli	914	48	9.6	201	2	T31492	hypothetical prote
842	48.5	9.7	202	2	T24524	hypothetical prote	915	48	9.6	204	2	S63145	probable membrane
843	48.5	9.7	203	2	S54800	nitrile hydratase	916	48	9.6	229	2	D97628	ubiquinol-cytochro
844	48.5	9.7	203	2	S19714	nitrile hydratase	917	48	9.6	237	2	I47031	insulin-like growt
845	48.5	9.7	207	2	B83523	hypothetical prote	918	48	9.6	237	2	S08073	cyclic nucleotide
846	48.5	9.7	232	2	A11551	hypothetical prote	919	48	9.6	240	2	A39842	insulin-like growt
847	48.5	9.7	250	2	T30124	hypothetical prote	920	48	9.6	245	2	T49889	zinc finger trans
848	48.5	9.7	267	2	F87665	hypothetical prote	921	48	9.6	250	2	S30157	osmotin precursor
849	48.5	9.7	274	2	T18768	hypothetical prote	922	48	9.6	251	2	B71298	hypothetical prote
850	48.5	9.7	297	2	T45705	hypothetical prote	923	48	9.6	260	2	T47391	hypothetical prote
851	48.5	9.7	298	2	T27644	hypothetical prote	924	48	9.6	268	2	B42424	chitinase (EC 3.2.
852	48.5	9.7	304	2	A33274	insulin-like growt	925	48	9.6	272	1	G69587	L-arabinose operon
853	48.5	9.7	305	2	UN0508	hypothetical prote	926	48	9.6	302	2	T39146	hypothetical prote
854	48.5	9.7	306	2	E37471	insulin-like growt	927	48	9.6	303	2	T46715	hypothetical prote
855	48.5	9.7	307	2	F71294	hypothetical prote	928	48	9.6	326	2	S14266	uracil-DNA glycosy
856	48.5	9.7	317	2	A36066	trans-activator of	929	48	9.6	332	2	T19150	hypothetical prote
857	48.5	9.7	317	2	D86070	regulator for metE	930	48	9.6	334	2	H69076	hypothetical prote
858	48.5	9.7	317	2	F91223	regulator for metE	931	48	9.6	334	2	D70918	hypothetical prote
859	48.5	9.7	346	2	T34129	hypothetical prote	932	48	9.6	335	2	H75518	probable cytochrom
860	48.5	9.7	350	2	T37511	probable phosphopr	933	48	9.6	344	2	I57698	folliculin - rat
861	48.5	9.7	354	1	S04243	proteoglycan link	934	48	9.6	348	2	A34705	collagen - Caenorh
862	48.5	9.7	355	1	LKCH	proteoglycan link	935	48	9.6	356	2	C70398	hypothetical prote
863	48.5	9.7	357	2	S09267	ig alpha chain C r	936	48	9.6	363	2	G82070	3-beta-hydroxy-Delt
864	48.5	9.7	369	2	T48612	hypothetical prote	937	48	9.6	369	2	S41971	probable cytochrom
865	48.5	9.7	396	1	W2BE8	dutp diphosphatase	938	48	9.6	374	2	A95960	matrix protein - m
866	48.5	9.7	400	2	T46383	hypothetical prote	939	48	9.6	375	1	A60004	probable cytochrom
867	48.5	9.7	433	2	B82965	hypothetical prote	940	48	9.6	375	1	MFNZMS	matrix protein - m
868	48.5	9.7	448	2	S41725	hypothetical prote	941	48	9.6	390	2	S20336	probable alcohol d
869	48.5	9.7	455	2	S33033	integrase - Saccha	942	48	9.6	404	2	C86396	hypothetical prote
870	48.5	9.7	462	2	T40420	probable acid phos	943	48	9.6	414	2	H95843	hypothetical prote
871	48.5	9.7	470	2	A12188	hypothetical prote	944	48	9.6	431	2	S56228	alpha-factor recep
872	48.5	9.7	476	2	S57963	methyl CpG binding	945	48	9.6	442	2	S50062	cell wall glycopro
873	48.5	9.7	489	2	T067115	probable cytochrom	946	48	9.6	455	1	GQHUT1	tumor necrosis fac
874	48.5	9.7	521	2	I51693	XPolycarb - Africa	947	48	9.6	457	2	S20662	glycine receptor a
875	48.5	9.7	559	1	C9HU	complement C9 prec	948	48	9.6	487	2	C47080	copper resistance
876	48.5	9.7	605	2	H69581	transcription acti	949	48	9.6	495	2	S32179	tniQ protein homol
877	48.5	9.7	614	2	S42526	finger protein unk	950	48	9.6	513	2	S28358	prespore vesicle p
878	48.5	9.7	634	1	S35574	transcription fact	951	48	9.6	552	2	E70731	probable pitB prot
879	48.5	9.7	640	2	T19346	hypothetical prote	952	48	9.6	561	2	E70610	hypothetical prote
880	48.5	9.7	702	2	E72775	probable helicase	953	48	9.6	580	2	D84772	probable sugar tra
881	48.5	9.7	726	2	H82774	phage-related DNA	954	48	9.6	594	1	A46758	glutamate decarbox
882	48.5	9.7	779	2	H71301	probable membrane-	955	48	9.6	594	2	UC4065	glutamate decarbox
883	48.5	9.7	786	2	AG2375	WD-40 repeat-prote	956	48	9.6	600	2	I49281	fertilin alpha pre
884	48.5	9.7	809	2	S55344	outer envelope mem	957	48	9.6	606	2	D86443	probable PPR-repea
885	48.5	9.7	810	2	B33048	plasmin (EC 3.4.21	958	48	9.6	615	1	KFHU12	coagulation factor
886	48.5	9.7	860	2	T39502	hypothetical prote	959	48	9.6	616	2	T32131	hypothetical prote
887	48.5	9.7	917	2	T48950	telencephalin prec	960	48	9.6	621	2	I38467	low density lipopr
888	48.5	9.7	932	2	T45894	hypothetical prote	961	48	9.6	624	2	T00044	vacuolar sorting r
889	48.5	9.7	958	2	H84783	probable PHD-type	962	48	9.6	634	2	T02594	hypothetical prote
890	48.5	9.7	977	2	S49004	tyrosine kinase Mp	963	48	9.6	651	2	A39372	potassium channel
891	48.5	9.7	1021	2	T05108	hypothetical prote	964	48	9.6	690	2	G84638	hypothetical prote
892	48.5	9.7	1207	2	T21557	hypothetical prote	965	48	9.6	698	2	T23469	hypothetical prote
893	48.5	9.7	1262	1	EGHU	epidermal growth f	966	48	9.6	706	2	T49899	zinc finger trans
894	48.5	9.7	1247	1	MMHUND	nidogen precursor	967	48	9.6	724	2	B71404	hypothetical prote
895	48.5	9.7	1328	2	T43060	agrin - electric r	968	48	9.6	729	2	AH2857	anthranilate synth
896	48.5	9.7	1391	2	T20406	hypothetical prote	969	48	9.6	739	2	T21431	hypothetical prote
897	48.5	9.7	1490	2	E87351	nonstructural poly	970	48	9.6	748	2	S41050	fibroblast growth
898	48.5	9.7	1508	2	B76966	glutamate synthase	971	48	9.6	750	2	S41051	fibroblast growth
899	48.5	9.7	1895	2	T15881	hypothetical prote	972	48	9.6	786	2	A35466	progesterone recep
900	48.5	9.7	2182	2	T14320	calcineurin inhibi	973	48	9.6	818	2	T32154	hypothetical prote
901	48.5	9.7	2643	2	T29149	hypothetical prote	974	48	9.6	822	2	T25866	hypothetical prote
902	48.5	9.7	3005	1	GNVSTV	genome polyprotein	975	48	9.6	824	2	T23923	hypothetical prote
903	48.5	9.7	3672	2	T23433	hypothetical prote	976	48	9.6	834	2	S13442	hemocyanin type A
904	48.5	9.7	3704	2	T37316	probable laminin a	977	48	9.6	840	2	AG0526	penicillin-binding
905	48	9.6	66	2	S59621	metallothionein is	978	48	9.6				

979	48	9.6	832	2	F87325	hypothetical prote	1052	47.5	9.5	416	1	JN0006	nerve growth facto
980	48	9.6	923	2	A39596	progesterone recep	1053	47.5	9.5	418	2	E90925	probable enzyme EC
981	48	9.6	923	2	I53280	progesterone recep	1054	47.5	9.5	418	2	A85774	hypothetical prote
982	48	9.6	930	2	A25923	progesterone recep	1055	47.5	9.5	418	2	B64924	vascular endotheli
983	48	9.6	933	1	QRHUP	progesterone recep	1056	47.5	9.5	419	2	S69207	nucleosid prote
984	48	9.6	948	2	AD0790	sensor protein Rcs	1057	47.5	9.5	429	1	VHVUV	hypothetical prote
985	48	9.6	965	2	S62935	hypothetical prote	1058	47.5	9.5	451	2	T20798	similar to phospho
986	48	9.6	972	2	A30363	glycoprotein GP330	1059	47.5	9.5	454	2	A97048	zinc finger protei
987	48	9.6	1013	2	I50615	receptor-type prot	1060	47.5	9.5	455	2	T32189	probable lipopolys
988	48	9.6	1019	2	A38738	coagulation factor	1061	47.5	9.5	473	2	C81984	4-carboxy-2-hydrox
989	48	9.6	1068	2	T04112	pol protein homolo	1062	47.5	9.5	475	2	T39359	4-carboxy-2-hydrox
990	48	9.6	1076	2	F96831	hypothetical prote	1063	47.5	9.5	484	2	JC5779	thioglucoosidase (E
991	48	9.6	1100	2	G83376	probable trehalose	1064	47.5	9.5	505	2	T31272	amine oxidase (fla
992	48	9.6	1146	2	A38587	collagen, cornea-s	1065	47.5	9.5	524	2	S57621	hypothetical prote
993	48	9.6	1193	2	A86193	hypothetical prote	1066	47.5	9.5	527	2	S13763	hypothetical prote
994	48	9.6	1352	2	G84473	hypothetical prote	1067	47.5	9.5	535	2	S62437	CAMP protein alpha
995	48	9.6	1416	2	B88550	protein ZC84.1 [im	1068	47.5	9.5	537	2	D86299	conserved hypothet
996	48	9.6	1433	2	A46053	bullous pemphigoid	1069	47.5	9.5	558	2	S57953	protein-tyrosine k
997	48	9.6	1532	2	A61262	collagen alpha 1(X	1070	47.5	9.5	587	2	AG3169	calnexin-t - mouse
998	48	9.6	1609	1	MMHUB2	laminin gamma-1 ch	1071	47.5	9.5	602	2	JU0215	protein-tyrosine k
999	48	9.6	1767	2	T00458	hypothetical prote	1072	47.5	9.5	611	2	A54086	hypothetical prote
1000	48	9.6	1808	2	T15099	hypothetical prote	1073	47.5	9.5	630	1	T01380	succinate dehydrog
1001	48	9.6	1959	1	A33977	myosin heavy chain	1074	47.5	9.5	631	2	E71933	hypothetical prote
1002	48	9.6	2214	2	T16305	hypothetical prote	1075	47.5	9.5	665	1	A42792	xeroderma pigmento
1003	48	9.6	2339	2	A45597	DNA-directed RNA p	1076	47.5	9.5	817	2	T21336	protein R3F9.18 [i
1004	48	9.6	2470	2	I50726	cation-independent	1077	47.5	9.5	900	2	S70630	hypothetical prote
1005	48	9.6	2610	2	T20968	hypothetical prote	1078	47.5	9.5	919	2	A96812	hypothetical prote
1006	48	9.6	2809	2	T30213	G-cadherin - sea u	1079	47.5	9.5	922	2	T23573	receptor protein k
1007	48	9.6	2844	2	S28291	hemocyanin G-type	1080	47.5	9.5	987	2	T50850	hypothetical prote
1008	48	9.6	2896	2	T30939	polyprotein - deng	1081	47.5	9.5	1042	2	T26644	hypothetical prote
1009	48	9.6	3391	2	JS0219	metallothionein A	1082	47.5	9.5	1045	2	S55253	sucrose-phosphate
1010	47.5	9.5	64	2	A25775	neurotoxin 3 - bar	1083	47.5	9.5	1119	2	T16720	probable rho GDP-
1011	47.5	9.5	65	1	NTSR3C	Ig heavy chain V r	1084	47.5	9.5	1158	2	T50454	DNA-directed RNA p
1012	47.5	9.5	97	2	S26890	hypothetical prote	1085	47.5	9.5	1210	2	S35548	nonstructural poly
1013	47.5	9.5	108	2	PH1651	Ig heavy chain V r	1086	47.5	9.5	1224	2	A25884	nonstructural poly
1014	47.5	9.5	113	2	D75583	hypothetical prote	1087	47.5	9.5	2492	1	C44213	filamin, Muller ce
1015	47.5	9.5	120	2	T31000	cysteine-rich prot	1088	47.5	9.5	2492	1	MNVWD	seven-pass transme
1016	47.5	9.5	125	2	S24831	hypothetical prote	1089	47.5	9.5	2567	2	A49551	hypothetical prote
1017	47.5	9.5	143	2	B84128	cell wall hydrolas	1090	47.5	9.5	3034	2	T14119	trithorax protein
1018	47.5	9.5	152	1	A56939	isoquinoline 1-oxi	1091	47.5	9.5	3228	2	T21381	hypothetical prote
1019	47.5	9.5	172	1	KRSHHA	keratin high-sulfu	1092	47.5	9.5	3759	2	A35085	polyprotein - fava
1020	47.5	9.5	186	2	T32656	hypothetical prote	1093	47.5	9.5	3765	2	T29165	probable small sec
1021	47.5	9.5	207	2	F95966	probable aldehyde	1094	47.5	9.5	5825	2	T12117	Gibberellin-regula
1022	47.5	9.5	209	2	T02394	hypothetical prote	1095	47.5	9.5	88	2	T36927	T cell leukemia/ly
1023	47.5	9.5	220	2	JC7972	hypothetical prote	1096	47.5	9.5	97	2	S71371	hypothetical prote
1024	47.5	9.5	230	2	B30691	hypothetical prote	1097	47.5	9.5	114	2	T19716	metalloproteinase
1025	47.5	9.5	231	2	D64774	ybaX protein - Esc	1098	47.5	9.5	131	1	ZYSMN	keratin high-sulfu
1026	47.5	9.5	231	2	D64774	hypothetical prote	1099	47.5	9.5	131	1	KXGTJM	hypothetical prote
1027	47.5	9.5	231	2	F85541	conserved hypothet	1100	47.5	9.5	138	2	AG5215	hypothetical prote
1028	47.5	9.5	236	2	H71287	lymphocyte activat	1101	47.5	9.5	144	2	C71252	hypothetical prote
1029	47.5	9.5	255	2	I38426	hypothetical prote	1102	47.5	9.5	150	2	D87652	hypothetical prote
1030	47.5	9.5	264	2	T16271	protein P58F6.1 [i	1103	47.5	9.5	155	2	T25845	conserved hypothet
1031	47.5	9.5	281	2	C88638	hypothetical prote	1104	47.5	9.5	157	2	C87659	hypothetical prote
1032	47.5	9.5	304	2	T30716	hypothetical prote	1105	47.5	9.5	158	2	AB1045	Fxa protein (impo
1033	47.5	9.5	308	2	T05297	hypothetical prote	1106	47.5	9.5	158	2	AG0223	hypothetical prote
1034	47.5	9.5	312	2	T25048	hypothetical prote	1107	47.5	9.5	158	2	T42700	conserved hypothet
1035	47.5	9.5	317	2	AD0461	lysoR-family transc	1108	47.5	9.5	167	1	JC1102	endothelin 3 precu
1036	47.5	9.5	323	1	SVBAC	cysteine synthase	1109	47.5	9.5	168	2	T81110	thi protein - Rhiz
1037	47.5	9.5	323	2	AD0810	cysteine synthase	1110	47.5	9.5	169	2	JQ1599	hypothetical prote
1038	47.5	9.5	324	2	S20981	chitinase (EC 3.2.	1111	47.5	9.5	176	2	B85355	hypothetical prote
1039	47.5	9.5	324	2	S20981	Fas antigen precu	1112	47.5	9.5	176	2	T22273	conserved hypothet
1040	47.5	9.5	325	2	T02455	hypothetical prote	1113	47.5	9.5	180	2	AB1010	hypothetical prote
1041	47.5	9.5	325	2	T24783	hypothetical prote	1114	47.5	9.5	200	2	F69047	GTP cyclohydrolase
1042	47.5	9.5	329	2	T20436	hypothetical prote	1115	47.5	9.5	208	2	P97570	GTP cyclohydrolase
1043	47.5	9.5	333	2	T24783	hypothetical prote	1116	47.5	9.5	208	2	A27291	hypothetical prote
1044	47.5	9.5	342	2	T18993	hypothetical prote	1117	47.5	9.5	219	2	H85358	ribosomal protein
1045	47.5	9.5	347	2	T34131	hypothetical prote	1118	47.5	9.5	230	2	S25964	hypothetical prote
1046	47.5	9.5	354	2	T19856	hypothetical prote	1119	47.5	9.5	232	2	T22977	hypothetical prote
1047	47.5	9.5	370	2	F86236	protein F14N23.9 [1120	47.5	9.5	233	2	T22977	hypothetical prote
1048	47.5	9.5	375	2	A81227	conserved hypothet	1121	47.5	9.5	236	2	A53853	apolipoprotein B m
1049	47.5	9.5	375	2	F81999	probable integral	1122	47.5	9.5	242	2	T31174	hypothetical prote
1050	47.5	9.5	397	2	A32370	cyclin B1 - Africa	1123	47.5	9.5				
1051	47.5	9.5	411	2	T19728	hypothetical prote	1124	47.5	9.5				

1125	47	9.4	250	2	E70104	1198	47	9.4	788	1	JDLVHH	DNA-directed DNA p
1126	47	9.4	258	2	D85550	1199	47	9.4	861	2	I39714	cellulose synthase
1127	47	9.4	258	2	A30700	1200	47	9.4	907	2	B75182	DNA-directed RNA p
1128	47	9.4	266	2	T08059	1201	47	9.4	916	2	G75417	SNF2/Rad54 helicas
1129	47	9.4	271	2	S12787	1202	47	9.4	969	1	A39490	subtilisin-like pr
1130	47	9.4	271	2	J45484	1203	47	9.4	988	2	I50611	protein-tyrosine k
1131	47	9.4	274	2	T36489	1204	47	9.4	1086	2	T05407	hypothetical prote
1132	47	9.4	279	2	C75538	1205	47	9.4	1168	2	I56985	kalinin B1 - mouse
1133	47	9.4	280	2	A24224	1206	47	9.4	1219	2	H84464	probable helicase
1134	47	9.4	283	2	J65531	1207	47	9.4	1324	2	S06187	RNA2 polyprotein -
1135	47	9.4	309	2	B49878	1208	47	9.4	1354	2	T13363	phosphoribosylform
1136	47	9.4	332	2	D70605	1209	47	9.4	1356	2	A45445	janusin precursor,
1137	47	9.4	338	2	A18116	1210	47	9.4	1372	2	T25933	hypothetical prote
1138	47	9.4	350	2	T39795	1211	47	9.4	1375	2	T18961	FAB1 protein homol
1139	47	9.4	350	2	S00337	1212	47	9.4	1474	2	D88550	DNA (cytosine-5-) -
1140	47	9.4	351	2	S20078	1213	47	9.4	1545	2	T14288	protein Zc84.6 [im
1141	47	9.4	353	1	ROECA	1214	47	9.4	1611	2	G84493	probable retroelem
1142	47	9.4	353	2	AH0843	1215	47	9.4	1961	1	A61231	myosin heavy chain
1143	47	9.4	353	2	D91073	1216	47	9.4	2201	2	A32160	tenascin-C - human
1144	47	9.4	353	2	D91073	1217	47	9.4	4151	2	T13734	groovin gene prote
1145	47	9.4	354	2	S31481	1218	46.5	9.3	58	2	AD0841	hypothetical prote
1146	47	9.4	356	2	S37586	1219	46.5	9.3	65	1	NTSR1C	neurotoxin 1 - bar
1147	47	9.4	356	2	AG0401	1220	46.5	9.3	98	2	I47086	BI11B4 high-sulfur
1148	47	9.4	358	2	T26281	1221	46.5	9.3	118	1	PSKPT3	phospholipase A2 (
1149	47	9.4	367	1	S24935	1222	46.5	9.3	130	2	T08584	hypothetical prote
1150	47	9.4	369	2	A34614	1223	46.5	9.3	137	2	T15609	hypothetical prote
1151	47	9.4	380	2	G01639	1224	46.5	9.3	141	2	A64751	hypothetical prote
1152	47	9.4	387	2	B38302	1225	46.5	9.3	147	2	G31586	hypothetical prote
1153	47	9.4	404	2	H84593	1226	46.5	9.3	164	2	J01551	V3 protein - Panic
1154	47	9.4	410	2	S26669	1227	46.5	9.3	182	1	KRSHMD	keratin high-sulfu
1155	47	9.4	434	2	T19205	1228	46.5	9.3	188	1	S35524	adrenodoxin precur
1156	47	9.4	438	2	E86924	1229	46.5	9.3	198	2	S56510	hypothetical prote
1157	47	9.4	444	2	T27234	1230	46.5	9.3	202	2	T10358	thiol-endopeptidas
1158	47	9.4	446	2	A34418	1231	46.5	9.3	210	2	T10590	hypothetical prote
1159	47	9.4	448	2	D41727	1232	46.5	9.3	235	2	S43513	hemoglobin linker
1160	47	9.4	448	2	T36114	1233	46.5	9.3	252	2	H82574	phage-related prot
1161	47	9.4	451	2	A1651	1234	46.5	9.3	259	1	PMWBM	bisphosphoglycerat
1162	47	9.4	461	1	KXHU	1235	46.5	9.3	272	2	E70548	probable bpoC prot
1163	47	9.4	478	2	JQ1301	1236	46.5	9.3	274	2	T52103	GATA-binding trans
1164	47	9.4	479	2	T16130	1237	46.5	9.3	277	2	JC7903	collectin liver 1
1165	47	9.4	486	2	T06770	1238	46.5	9.3	279	1	HLMSG	class II histocomp
1166	47	9.4	490	2	T06710	1239	46.5	9.3	282	2	S27769	NAD glycohydrolase
1167	47	9.4	493	2	JC5621	1240	46.5	9.3	292	2	T50710	hypothetical prote
1168	47	9.4	499	2	A86468	1241	46.5	9.3	305	2	S76401	hypothetical prote
1169	47	9.4	500	2	S26688	1242	46.5	9.3	312	2	D97552	lipid A biosynthes
1170	47	9.4	520	2	I84718	1243	46.5	9.3	312	2	A52772	lipid A biosynthes
1171	47	9.4	522	2	D96764	1244	46.5	9.3	313	2	T22828	hypothetical prote
1172	47	9.4	527	2	J80373	1245	46.5	9.3	316	2	S65020	chitinase (EC 3.2.
1173	47	9.4	533	2	S37781	1246	46.5	9.3	320	2	S22450	3-oxoacyl-(acyl-ca
1174	47	9.4	541	2	T47290	1247	46.5	9.3	320	2	S22450	cell adhesion glyco
1175	47	9.4	551	1	VGNZPG	1248	46.5	9.3	328	2	B81724	conserved hypothet
1176	47	9.4	555	2	I53869	1249	46.5	9.3	332	2	F85058	hypothetical prote
1177	47	9.4	555	2	T40294	1250	46.5	9.3	332	2	S83263	dihydroxotatate deh
1178	47	9.4	581	2	F82723	1251	46.5	9.3	342	2	A83263	hypothetical prote
1179	47	9.4	585	2	T47364	1252	46.5	9.3	347	2	T32768	hypothetical prote
1180	47	9.4	606	2	S43118	1253	46.5	9.3	356	2	T32827	hypothetical prote
1181	47	9.4	612	2	JH0799	1254	46.5	9.3	359	2	A43532	B-cell surface ant
1182	47	9.4	621	2	JC1346	1255	46.5	9.3	367	2	G71076	probable hydrogena
1183	47	9.4	635	2	S36718	1256	46.5	9.3	369	1	TVCHTB	thyroid hormone re
1184	47	9.4	647	2	B82579	1257	46.5	9.3	369	2	S58211	beta-thyroid hormo
1185	47	9.4	651	2	B85024	1258	46.5	9.3	371	2	T32692	hypothetical prote
1186	47	9.4	676	2	A40363	1259	46.5	9.3	377	2	C83372	hypothetical prote
1187	47	9.4	693	2	JN0673	1260	46.5	9.3	390	2	D70849	probable aminotran
1188	47	9.4	704	2	B84685	1261	46.5	9.3	391	2	H70640	probable pqqE prot
1189	47	9.4	716	1	A40332	1262	46.5	9.3	394	2	T21013	hypothetical prote
1190	47	9.4	724	2	C49423	1263	46.5	9.3	403	2	C75405	streptomycin biosy
1191	47	9.4	735	2	T08140	1264	46.5	9.3	419	2	JQ2254	farnesyl-diphospha
1192	47	9.4	735	2	AE1858	1265	46.5	9.3	421	2	E86184	hypothetical prote
1193	47	9.4	743	2	B84639	1266	46.5	9.3	437	2	B70540	probable adenosylm
1194	47	9.4	756	2	S47656	1267	46.5	9.3	446	2	T31644	hypothetical prote
1195	47	9.4	759	2	T43031	1268	46.5	9.3	449	2	C84458	hypothetical prote
1196	47	9.4	763	2	D86326	1269	46.5	9.3	459	2	T19991	hypothetical prote
1197	47	9.4	775	2	A48644	1270	46.5	9.3	465	2	H86482	protein F575.11 [i

1271	46.5	9.3	1	NMIV27	1344	46	9.2	62	2	H81791	hypothetical prote
1272	46.5	9.3	2	C81039	1345	46	9.2	66	2	A55869	crustacean-specifi
1273	46.5	9.3	2	T46067	1346	46	9.2	81	4	B49316	hypothetical prote
1274	46.5	9.3	2	S09489	1347	46	9.2	95	2	T42112	hypothetical prote
1275	46.5	9.3	2	JC7189	1348	46	9.2	98	1	KRSHH4	keratin high-sulfu
1276	46.5	9.3	2	I80182	1349	46	9.2	113	2	S56647	trypsin inhibitor
1277	46.5	9.3	2	JM0056	1350	46	9.2	123	2	S18470	wnt protein homolo
1278	46.5	9.3	2	T19390	1351	46	9.2	124	2	AE2874	hypothetical prote
1279	46.5	9.3	2	S10772	1352	46	9.2	125	2	E72716	hypothetical prote
1280	46.5	9.3	2	E42902	1353	46	9.2	127	2	T44119	hypothetical prote
1281	46.5	9.3	2	I80183	1354	46	9.2	135	2	H72531	hypothetical prote
1282	46.5	9.3	2	A41907	1355	46	9.2	137	2	AI0575	conserved hypothet
1283	46.5	9.3	2	S51568	1356	46	9.2	143	2	QJ1448	hypothetical 16K p
1284	46.5	9.3	2	S00336	1357	46	9.2	150	1	OKBYS1	cell division cont
1285	46.5	9.3	2	T23003	1358	46	9.2	151	2	AE2352	hypothetical prote
1286	46.5	9.3	2	I83558	1359	46	9.2	156	2	H69455	tungsten formylmet
1287	46.5	9.3	2	T16408	1360	46	9.2	160	2	C86458	unknown protein, 6
1288	46.5	9.3	2	G70366	1361	46	9.2	163	1	H83499	hypothetical prote
1289	46.5	9.3	2	A32545	1362	46	9.2	174	2	T15176	ferredoxin protein
1290	46.5	9.3	2	T00859	1363	46	9.2	180	2	AG0796	hypothetical prote
1291	46.5	9.3	2	T23271	1364	46	9.2	180	2	F85868	NADH2 dehydrogenas
1292	46.5	9.3	2	T18635	1365	46	9.2	180	2	G64999	NADH2 dehydrogenas
1293	46.5	9.3	2	C42125	1366	46	9.2	180	2	E91024	NADH2 dehydrogenas
1294	46.5	9.3	2	T30620	1367	46	9.2	180	2	AB0311	NADH2 dehydrogenas
1295	46.5	9.3	2	G95364	1368	46	9.2	184	2	AC3427	transposase BME114
1296	46.5	9.3	2	B71379	1369	46	9.2	188	2	G95889	probable oxidoredu
1297	46.5	9.3	2	T06088	1370	46	9.2	191	2	G90088	40S ribosomal prot
1298	46.5	9.3	2	S52390	1371	46	9.2	193	2	T35847	probable carbonic
1299	46.5	9.3	2	C82548	1372	46	9.2	193	2	D97157	stage III sporulat
1300	46.5	9.3	2	JC7501	1373	46	9.2	203	2	T17972	hypothetical prote
1301	46.5	9.3	2	B71972	1374	46	9.2	204	2	E84443	probable disease r
1302	46.5	9.3	2	D64534	1375	46	9.2	205	2	G82563	autolytic lysozyme
1303	46.5	9.3	2	A71141	1376	46	9.2	207	2	S28510	E6 protein - multi
1304	46.5	9.3	2	T12627	1377	46	9.2	209	2	T30698	hypothetical prote
1305	46.5	9.3	2	T13585	1378	46	9.2	210	1	QZMCA	hypothetical prote
1306	46.5	9.3	2	F87789	1379	46	9.2	210	2	I40540	vsd protein - Pse
1307	46.5	9.3	2	S32659	1380	46	9.2	214	2	AF0779	glutathione-S-tran
1308	46.5	9.3	2	S28084	1381	46	9.2	215	2	A29318	ubiquinol-cytochro
1309	46.5	9.3	2	E82227	1382	46	9.2	219	2	E82825	hypothetical prote
1310	46.5	9.3	2	A36811	1383	46	9.2	220	2	S44808	hypothetical prote
1311	46.5	9.3	2	T52569	1384	46	9.2	226	2	I59173	glutamate decarbox
1312	46.5	9.3	2	Q43084	1385	46	9.2	226	2	D81741	phosphoglycerate m
1313	46.5	9.3	2	SRXLH2	1386	46	9.2	231	1	RDNCUF	ubiquinol-cytochro
1314	46.5	9.3	2	T40771	1387	46	9.2	243	2	D97237	phosphoglycerate m
1315	46.5	9.3	2	G90459	1388	46	9.2	249	2	T24604	hypothetical prote
1316	46.5	9.3	2	AB1398	1389	46	9.2	254	2	I48599	insulin-like growt
1317	46.5	9.3	2	AB1773	1390	46	9.2	254	2	JC1464	insulin-like growt
1318	46.5	9.3	2	T30257	1391	46	9.2	256	2	T28106	hypothetical prote
1319	46.5	9.3	2	A53663	1392	46	9.2	257	2	T12961	hypothetical prote
1320	46.5	9.3	2	G86342	1393	46	9.2	269	2	T36639	probable substrate
1321	46.5	9.3	2	A26838	1394	46	9.2	269	2	S75243	hypothetical prote
1322	46.5	9.3	2	D96798	1395	46	9.2	270	2	T16968	hypothetical prote
1323	46.5	9.3	2	S18555	1396	46	9.2	286	2	S61199	hypothetical prote
1324	46.5	9.3	2	I48378	1397	46	9.2	287	2	B72387	deoxyribonuclease
1325	46.5	9.3	2	T33754	1398	46	9.2	289	2	AH3113	shikimate 5-dehydr
1326	46.5	9.3	2	D86236	1399	46	9.2	289	2	E98173	hypothetical prote
1327	46.5	9.3	2	A53183	1400	46	9.2	308	2	T46026	hypothetical prote
1328	46.5	9.3	2	JQ1978	1401	46	9.2	312	2	E30803	alcohol dehydrogen
1329	46.5	9.3	2	VHVVVE	1402	46	9.2	312	2	C98203	probable adhE prot
1330	46.5	9.3	2	VHVVVT	1403	46	9.2	319	2	A53502	follicistatin - Afri
1331	46.5	9.3	2	D44213	1404	46	9.2	320	1	G72061	probable phosphoes
1332	46.5	9.3	2	JH0675	1405	46	9.2	320	1	G86562	probable phosphoes
1333	46.5	9.3	2	T33236	1406	46	9.2	325	1	VMUT17	VSG expression sit
1334	46.5	9.3	2	T15276	1407	46	9.2	325	1	C70673	probable gpdA2 pro
1335	46.5	9.3	2	GNVYE7	1408	46	9.2	334	2	E95279	UDP-glucose 4-epim
1336	46.5	9.3	2	T16743	1409	46	9.2	334	2	E95279	probable imported
1337	46.5	9.3	2	S58870	1410	46	9.2	338	2	S75089	UDP-glucose 4-epim
1338	46.5	9.3	2	JC2554	1411	46	9.2	343	2	S55369	follicistatin - chic
1339	46	9.2	44	I48942	1412	46	9.2	346	2	A64448	hypothetical prote
1340	46	9.2	48	S68952	1413	46	9.2	361	2	T30743	hypothetical prote
1341	46	9.2	60	B27490	1414	46	9.2	366	1	A46704	aryl-alcohol dehyd
1342	46	9.2	60	B27490	1415	46	9.2	366	1	D70351	probable hexosyltr
1343	46	9.2	60	AE3099	1416	46	9.2	367	2	T29752	hypothetical prote

1417 46 9.2 368 2 S67507 morphogen lefty pr
1418 46 9.2 369 1 B64921 conserved hypothet
1419 46 9.2 369 2 AC2157 alcohol dehydrogen
1420 46 9.2 369 2 A85771 hypothetrical prote
1421 46 9.2 369 2 E90922 hypothetrical prote
1422 46 9.2 370 2 JC7591 spinal cord-derive
1423 46 9.2 372 2 S23936 L-selectin precurs
1424 46 9.2 376 2 D95370 probable oxidoredu
1425 46 9.2 377 2 AB1552 N-acetylglucosamin
1426 46 9.2 377 2 AD1194 APX-1 protein homo
1427 46 9.2 379 2 T16213 F420-nonreducing h
1428 46 9.2 383 2 S49928 polygalacturonase
1429 46 9.2 383 2 S24156 45K WW domain-cont
1430 46 9.2 383 2 JC7507 hypothetrical prote
1431 46 9.2 389 2 T30454 hypothetrical prote
1432 46 9.2 440 2 F70792 hypothetrical prote
1433 46 9.2 443 2 S59771 hypothetrical 49.3K
1434 46 9.2 450 2 E98303 nitrioltriactate
1435 46 9.2 450 2 AH2979 hypothetrical prote
1436 46 9.2 453 2 T04828 hypothetrical prote
1437 46 9.2 453 2 T01114 hypothetrical prote
1438 46 9.2 457 2 S38296 gamma-aminobutyric
1439 46 9.2 461 1 S18994 protein C (activat
1440 46 9.2 462 2 T36848 probable glutamine
1441 46 9.2 474 2 T29336 hypothetrical prote
1442 46 9.2 480 1 A30065 trigramin precursor
1443 46 9.2 484 2 JE0261 N-acetylglucosamin
1444 46 9.2 490 1 C57150 NADP-reducing hydr
1445 46 9.2 490 2 A5141 GlcNAc beta-1,4-N-
1446 46 9.2 492 2 T38156 citrate lyase - fi
1447 46 9.2 509 2 T04688 hypothetrical prote
1448 46 9.2 511 2 T34359 hypothetrical prote
1449 46 9.2 531 2 S75997 asparagine-tRNA li
1450 46 9.2 531 2 T14640 cytochrome P450 CY
1451 46 9.2 539 2 A35052 interleukin-2 rece
1452 46 9.2 540 2 B37844 probable oxidoredu
1453 46 9.2 553 2 T04683 hypothetrical prote
1454 46 9.2 556 1 S12602 60K cysteine-rich
1455 46 9.2 556 2 A86560 60 kDa Cysteine-ri
1456 46 9.2 570 2 T46011 hypothetrical prote
1457 46 9.2 576 2 A48157 renal transcriptio
1458 46 9.2 593 1 A41367 glutamate decarbox
1459 46 9.2 604 2 F69802 ABC transporter (A
1460 46 9.2 610 2 S64126 cell division cont
1461 46 9.2 632 2 E69407 NADH oxidase (noxB
1462 46 9.2 632 2 G69306 NADH oxidase (noxB
1463 46 9.2 675 1 KBOS plasma protein S p
1464 46 9.2 679 2 I52822 leukemia virus rec
1465 46 9.2 679 2 I48084 gibbon ape leukemi
1466 46 9.2 692 2 T47493 hypothetrical prote
1467 46 9.2 698 1 TFHUP transferrin precur
1468 46 9.2 700 2 A96690 hypothetrical prote
1469 46 9.2 729 2 I52481 PEPT 2 - human
1470 46 9.2 752 1 C2HU complement C2 prec
1471 46 9.2 769 1 JC1121 leukocyte adhesion
1472 46 9.2 772 2 T02805 chloride channel p
1473 46 9.2 781 2 T49472 hormone-sensitive
1474 46 9.2 825 2 S55060 ferritin alpha-II
1475 46 9.2 827 2 A29917 tRNA ligase (EC 6.
1476 46 9.2 834 2 JQ1965 hypothetrical 94K p
1477 46 9.2 836 2 AD2565 hypothetrical prote
1478 46 9.2 837 2 A42112 mucin-like peptide
1479 46 9.2 845 2 H71317 probable methyl-ac
1480 46 9.2 855 2 A48168 proliferating-cell
1481 46 9.2 874 2 S55602 Glycoprotein B - e
1482 46 9.2 882 1 IJHUCE cadherin 1 precurs
1483 46 9.2 882 2 F86164 hypothetrical prote
1484 46 9.2 886 1 GNLJSP pol polyprotein -
1485 46 9.2 897 2 S67283 hypothetrical prote
1486 46 9.2 899 2 F84477 probable retroelem
1487 46 9.2 905 2 S55059 ferritin alpha-I -
1488 46 9.2 907 2 H71031 probable DNA-dirc
1489 46 9.2 908 2 T50695 secA protein [impo

1490 46 9.2 919 2 A39248 androgen receptor
1491 46 9.2 939 2 AF2503 hypothetrical prote
1492 46 9.2 949 2 D84487 probable retroelem
1493 46 9.2 1004 2 JC2221 major surface glyc
1494 46 9.2 1016 2 G86295 hypothetrical prote
1495 46 9.2 1038 2 T13177 sog protein - frui
1496 46 9.2 1045 2 T16275 hypothetrical prote
1497 46 9.2 1047 2 A12002 hypothetrical prote
1498 46 9.2 1069 2 A81050 exodeoxyribonuclea
1499 46 9.2 1069 2 D81826 exodeoxyribonuclea
1500 46 9.2 1092 2 T12520 hypothetrical prote

ALIGNMENTS

RESULT 1

JC7188
REIC protein - human
C:Species: Homo sapiens (man)
C>Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 11-May-2000
C:Accession: JC7188
R:Tsugi, T.; Miyazaki, M.; Sakaguchi, M.; Inoue, Y.; Namba, M.
Biochem. Biophys. Res. Commun. 268, 20-24, 2000
A:Title: A REIC gene shows down-regulation in human immortalized cells and human tumor
A:Reference number: JC7188; MUID:20119095; PMID:10652205
A:Accession: JC7188
A:Molecule type: mRNA
A:Residues: 1-350 <TSU>
A:Cross-references: UNIPARC:UPI00000179471; DBJ:AB034203
A:Experimental source: heart
A:Comment: This protein is a secreted glycoprotein for head induction in amphibian embryo
C:Genetics:
A:Gene: reic
C:Superfamily: human REIC protein
C:Keywords: cardiac muscle; coiled coil; glycoprotein; heart; tumor

Query Match 20.2%; Score 100.5; DB 2; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.0035;
Matches 26; Conservative 3; Mismatches 29; Indels 11; Gaps 4;

Qy 7 CERDVQCGAGTCCAIISLWRLG--RMCTPLRGEGECH-PGSHKVPFFRKRH-----HT 58
Db 208 CDNQDCQPGLCGCAFAQ---RGLLFPVCTPLPVEGELCHDPASRLDLLITWELEPDGALDR 264

Qy 59 CPCPLNLLC 67

Db 265 CPCASGLLC 273

RESULT 2

T08179
LRGS protein - Chlamydomonas reinhardtii
C:Species: Chlamydomonas reinhardtii
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: T08179
R:Gloeckner, G.; Beck, C.F.
submitted to the EMBL Data Library, October 1996
A:Description: Molecular characterization of a gene (LRG5) involved in blue light signal
A:Reference number: Z16399
A:Accession: T08179
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-640 <GLO>
A:Cross-references: UNIPROT:Q96397; UNIPARC:UPI000009E362; EMBL:U73817; NID:gl1644369; P

Query Match 17.8%; Score 88.5; DB 2; Length 640;
Best Local Similarity 31.6%; Pred. No. 0.11;
Matches 24; Conservative 5; Mismatches 24; Indels 23; Gaps 4;

Qy 13 CGAGTCCAISLWRLGRLMCTPLRGEGECHPGSHKVPFFRKRHHTCPCLNLLCSRF-- 70

```
Db 488 CTAGRC-----NW-----TCLPWGSGGTWPRPLMT-----SRTACALPTPCCSRWLR 533
Qy 71 -----PDGRYRCSM 79
Db 534 RWRGWAPEGGRWCSL 549

RESULT 3
T09059
notch4 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T09059
R;Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; S.
submitted to the EMBL Data Library, October 1997
A;Description: Sequence of the mouse major histocompatibility locus class III region.
A;Reference number: Z16543
A;Accession: T09059
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1964 <ROW>
A;Cross-references: UNIPROT:P31695; UNIPARC:UPI000016C7F1; EMBL:AF030001; NID:g2564945;
C;Genetics:
A;Gene: notch4
A;Map position: 17
A;Intons: 22/1; 49/2; 148/1; 264/1; 305/1; 384/1; 436/1; 501/1; 539/1; 577/1; 618/1; 67
1679/3; 1729/1; 1761/3
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology
C;Keywords: receptor; signal transduction
F;514-545/Domain: EGF homology <EGF>

Query Match 16.3%; Score 81; DB 2; Length 1964;
Best Local Similarity 30.4%; Pred. No. 1.8;
Matches 24; Conservative 7; Mismatches 22; Indels 26; Gaps 5;

Qy 7 CERDVO-----CGAGTCATSLWRLGLRMC-TPLGREGECHPGSHKVPFRKHH 57
Db 188 CERDINECFLEPGPCPGQTSCHNTL---GSYQCLCPVQGEQPC-----KLRKG 233

Qy 58 TCP---CLPNLCSRFPDG 73
Db 234 ACPGSGCLNGTCLQVPEG 252

RESULT 4
A56175
adhesive plaque protein Mgfp2 precursor - Mediterranean mussel
C;Species: Mytilus galloprovincialis (Mediterranean mussel)
C;Date: 27-Apr-1995 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004
C;Accession: A56175
R;Inoue, K.; Takeuchi, Y.; Miki, D.; Odo, S.
J. Biol. Chem. 270, 6698-6701, 1995
A;Title: Mussel adhesive plaque protein gene is a novel member of epidermal growth facto
A;Reference number: A56175; MUID:95204464; PMID:7896812
A;Accession: A56175
A;Molecule type: mRNA
A;Residues: 1-473 <INO>
A;Cross-references: UNIPROT:Q25464; UNIPARC:UPI000012AB7B; GB:D43794; NID:g602767; PIDN:
C;Keywords: duplication
F;1-17/Domain: signal sequence #status predicted <SIG>
F;387-419/Domain: EGF homology <EGF1>
F;429-460/Domain: EGF homology <EGF>
F;23,36,43,56,75,382,424,455,468,473/Modified site: 3',4'-dihydroxyphenylalanine (Tyr) #

Query Match 15.6%; Score 77.5; DB 2; Length 473;
Best Local Similarity 31.2%; Pred. No. 1.2;
Matches 24; Conservative 11; Mismatches 23; Indels 19; Gaps 7;

Qy 7 CERDVQCCAGTCCATSLWRLGLRMC-TPLGREGECH-PGSHKVPFRKHHKC---PCL 62
Db 117 CEKNV-CSPNFC-----KNGKCSPLGKGTGKTCGSGYTG---RCEVHACKPNCK 165

us-10-692-299-2_copy_20_105.spdi.rpr

Qy 63 PNLLCSRFPDGR--YRC 77
Db 166 NKGRC--FPDGKGYKC 180

RESULT 5
T31070
notch homolog - sea urchin (Lytechinus variegatus)
C;Species: Lytechinus variegatus (variegated urchin)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 31-Jan-2000
C;Accession: T31070
R;Sherwood, D.R.; McClay, D.R.
Development 124, 3363-3374, 1997
A;Title: Identification and localization of a sea urchin Notch homologue: insights into
A;Reference number: Z20966; MUID:97454256; PMID:9310331
A;Accession: T31070
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-2531 <SHE>
A;Cross-references: UNIPARC:UPI000007E31C; EMBL:AF000634; NID:g2570350; PID:g2570351; P
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology

Query Match 15.1%; Score 75; DB 2; Length 2531;
Best Local Similarity 29.9%; Pred. No. 9.4;
Matches 23; Conservative 8; Mismatches 32; Indels 14; Gaps 5;

Qy 3 ITGACERDVOCAGTCCAI--SLWRLGLRMC-TPLGREGECHPGSHKVPFRKHHKHTCP 60
Db 120 VDNVCKLEEPQNGGTCLRTTSLMDYEC-FCTP-ANTGENTCTDDNHCV-----SNP 168

Qy 61 CLPNLCSRFPDGRYRC 77
Db 169 CLNGAVCTSSSDG-YSC 184

RESULT 6
XLHU
colipase precursor [validated] - human
N;Alternate names: procolipase
C;Species: Homo sapiens (man)
C;Date: 04-Dec-1986 #sequence_revision 19-May-1995 #text_change 09-Jul-2004
C;Accession: A42568; A33949; A03163
R;Sims, H.F.; Lowe, M.E.
Biochemistry 31, 7120-7125, 1992
A;Title: The human colipase gene: isolation, chromosomal location, and tissue-specific
A;Reference number: A42568; MUID:92353041; PMID:1643046
A;Accession: A42568
A;Molecule type: DNA
A;Residues: 1-112 <SIM>
A;Cross-references: UNIPROT:P04118; UNIPARC:UPI0000127E78; GB:M95529; NID:g180842; PIDN:
A;Note: sequence extracted from NCBI backbone (NCBIN:110576, NCBIN:110578, NCBIP:110580
R;Lowe, M.E.; Rosenblum, J.L.; McEwen, P.; Strauss, A.W.
Biochemistry 29, 823-828, 1990
A;Title: Cloning and characterization of the human colipase cDNA.
A;Reference number: A33949; MUID:90248429; PMID:2337598
A;Accession: A33949
A;Molecule type: mRNA
A;Residues: 1-112 <LOW>
A;Cross-references: UNIPARC:UPI0000127E78; GB:J02883; NID:g180885; PIDN:AAAS2054.1; PII:
A;Note: evidence of partial N-glycosylation, possibly at Asn-43
R;Starnby, B.; Engstrom, A.; Hellman, U.; Vihernt, A.M.; Sternby, N.H.; Borgstrom, B.
Biochim. Biophys. Acta 784, 75-80, 1984
A;Title: The primary sequence of human pancreatic colipase.
A;Reference number: A30652; MUID:84104937; PMID:6691986
A;Accession: A03163
A;Molecule type: protein
A;Residues: 23-108 <STE>
A;Cross-references: UNIPARC:UPI0000174141
C;Comment: Colipase, a cofactor of triacylglycerol lipase (EC 3.1.1.3), forms a 1:1 st
se the enzyme is washed off by bile salts, which are known to have an inhibitory effect
C;Genetics:
A;Gene: GDB:CLPS
A;Cross-references: GDB:127277; OMIM:120105
```


F:658-697/Domain: EGF homology <EGF>

Query Match 14.4%; Score 71.5; DB 1; Length 1178;
Best Local Similarity 21.8%; Pred. No. 11;
Matches 27; Conservative 8; Mismatches 32; Indels 57; Gaps 5;

QY 11 VQCGAGTCCALSLW-----LRGLRMCTPLRGEGECHPGSHKV-----PF----- 50
DB 457 VTCGVGNITRIILNSPIPOGKGNKCVNGRETEKCEKAPCPVNGQWPSPWACTVTC 516

QY 51 ----FRKR-----KHHC-----PCLPNLCSRPDQ 73
DB 517 GGGIRSRILNSPEPOYGKPKCVGDTKQHDMCNKRDPCIDGCLNSPFCGAECSNPDG 576

QY 74 RYRC 77
DB 577 SWSC 580

RESULT 9
T13954
MEGF6 protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T13954
R;Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
A;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A;Reference number: Z14126; MUID:98360089; PMID:9693030
A;Accession: T13954
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1574 <NAK>
A;Cross-references: UNIPROT:O88281; UNIPARC:UPI0000043BEE; EMBL:AB011532; NID:93449293;
A;Experimental source: strain Sprague-Dawley; brain
C;Genetics:
A;Gene: MEGF6

Query Match 14.4%; Score 71.5; DB 2; Length 1574;
Best Local Similarity 28.4%; Pred. No. 14;
Matches 23; Conservative 6; Mismatches 31; Indels 21; Gaps 4;

QY 3 ITGAC-----ERDVQCGAGTCCALSLRLGLRMCTPLRGEGECHPGSHKVPPFRKRAKH 57
DB 758 VTGELCPPGKTGBDDCAD--CPGRMGLGCQBIQACEHASCNP-----ETG 804

QY 58 TCPCPLNLCSRPDPGRYRCS 78
DB 805 TCLCLPGFVGRCD---TCS 822

RESULT 10
T13576
hypothetical protein 52C10.5 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Accession: T13576
R;Benos, P.
submitted to the EMBL Data Library, February 1999
A;Description: Sequencing the distal X chromosome of Drosophila melanogaster.
A;Reference number: Z17690
A;Accession: T13576
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1854 <BEN>
A;Cross-references: UNIPROT:O96838; UNIPARC:UPI000008354E; EMBL:AL035311; NID:e1373062;
C;Genetics:
A;Cross-references: FlyBase:FBgn0026309
A;Introns: 4/3; 53/3; 209/3; 962/1; 1632/1; 1686/2; 1739/1; 1793/1
A;Note: EG:52C10.5

Query Match 14.4%; Score 71.5; DB 2; Length 1854;
Best Local Similarity 36.4%; Pred. No. 17;

Matches 20; Conservative 6; Mismatches 22; Indels 7; Gaps 3;

QY 37 EGEECHPGSHKVPFRKRKHHTCPLPNLLCSR-----FPDGRVRCSDMLKNINF 86
DB 228 KAKECYDCSQKFSTFR-RKHH-CRLCGQIFCSKCCNVVPGMIIRCDGLKVCNY 280

RESULT 11
I51909
collipase precursor - rat
N;Alternate names: procollipase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: I51909; A34623
R;Payne, R.M.; Sims, H.F.; Jennens, M.L.; Lowe, M.E.
Am. J. Physiol. 266, G914-G921, 1994
A;Title: Rat pancreatic lipase and two related proteins: enzymatic properties and mRNA
A;Reference number: I51909; MUID:94262798; PMID:8203536
A;Accession: I51909
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-112 <PAV>
A;Cross-references: UNIPROT:P17084; UNIPARC:UPI00001708E5; GB:M33333; NID:9203502; PIDN:AAA40943.1; PIDN:
R;Wicker, C.; Puigserver, A.
Biochem. Biophys. Res. Commun. 167, 130-136, 1990
A;Title: Rat pancreatic collipase mRNA: nucleotide sequence of a cDNA clone and nutritional
A;Reference number: A34623; MUID:90179738; PMID:2129524
A;Accession: A34623
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-17, 'V', '19-112 <WIC>
A;Cross-references: UNIPARC:UPI00001708E5; GB:M33333; NID:9203502; PIDN:AAA40943.1; PIDN:
C;Superfamily: collipase
C;Keywords: lipid digestion, lipid hydrolysis; pancreas
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-112/Product: collipase #status predicted <MAR>

Query Match 14.3%; Score 71; DB 2; Length 112;
Best Local Similarity 31.1%; Pred. No. 1.6;
Matches 19; Conservative 5; Mismatches 29; Indels 8; Gaps 3;

QY 7 CERDVQCGAGTCCALSLRLGLRMCTPLRGEGECHPGSHKVPPFRKRAKHHTCPLPNLL 66
DB 34 CVNSMQC-KSRCCQHDITL-GIARCTHKAMENSECPTLYGIYYR-----CPCERGT 85

QY 67 C 67
DB 86 C 86

RESULT 12
S34665
collagen, cuticular - root-knot nematode (Meloidogyne incognita)
C;Species: Meloidogyne incognita
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S34665
R;van der Eycken, W.V.; de Almeida Engler, J.; van Montagu, M.; Gheysen, G.
submitted to the EMBL Data Library, July 1993
A;Description: Identification and analysis of a cuticular collagen gene from the plant
A;Reference number: S34665
A;Accession: S34665
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-286 <VAN>
A;Cross-references: UNIPROT:Q25467; UNIPARC:UPI000016BF3F; EMBL:Z24734; NID:g395144; PIDN:

Query Match 14.3%; Score 71; DB 2; Length 286;
Best Local Similarity 40.5%; Pred. No. 3.7;
Matches 15; Conservative 2; Mismatches 20; Indels 0; Gaps 0;

QY 33 PLRGEGECHPGSHKVPFRKRKHHTCPLPNLLCSR 69
DB 234 PSGKFGAPGPGPHGPPGQDQAYCFCPPRSLCSR 270

A;Status: preliminary; translated from GE/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1101 <GEI>
A;Cross-references: UNIPROT:Q22378; UNIPARC:UPI000017BB8F; EMBL:U39644; NID:G10493339; PF
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CESP:T10E10.4
A;Introns: 93/2; 152/2; 191/3; 209/2; 283/3; 303/1; 399/3; 421/1; 440/1; 465/1; 547/3; 7
Query Match 14.2%; Score 70.5; DB 2; Length 1101;
Best Local Similarity 22.9%; Pred. No. 13;
Matches 27; Conservative 6; Mismatches 36; Indels 49; Gaps 5;
QY 7 CERDVQCGAGTCCAISLWLRG-----LRMCTPLGR-- 36
Db 761 CPPGNQCENGVCCEPMCMSSGSIASSVCGMANSCPIGYICEGRCCCLEPLPLCPNGGRAS 820
QY 37 -----EGEECHFG-----SHKVPFFFRKHKHTCPCLPNLLCSRFDPDGRYRCSM 79
Db 821 MRCYRGAECPGYGCTPLGGCCLLSMEFVCPTRSNVAVCQSPNNVC---PSGA-SCTM 874

Search completed: November 29, 2007, 17:19:47
Job time : 19.6073 secs

OM protein - protein search, using sw model
Run on: November 29, 2007, 17:14:38 ; Search time 358 Seconds
(without alignments)
143.348 Million cell updates/sec

Title: US-10-692-299-2

Perfect score: 589

Sequence: 1 MRGATRVSIMLLLVTVSDCA.....CSRFPDGRYRCMDLKNINF 105

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

2782304 seqs, 48933398 residues

2782304 seqs satisfying chosen parameters: 2782304

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

A_Geneseq_200701.*

1: Geneseq1980s.*

2: Geneseq1990s.*

3: Geneseq2000s.*

4: Geneseq2001s.*

5: Geneseq2002s.*

6: Geneseq2003as.*

7: Geneseq2003bs.*

8: Geneseq2004s.*

11: Geneseq2007s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
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RESULT 1

ID AAV6745 standard; protein; 105 AA.

DE Membrane-bound protein PRO1186.

PN WO9963088-A2.

PD 09-DEC-1999.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 589; DB 3; Length 105;

Best Local Similarity 100.0%; Pred. No. 4.3e-54;

RESULT 2

ID AAB18453 standard; protein; 105 AA.

DE A human TANGO 266 polypeptide.

PN WO200052022-A1.

PD 08-SEP-2000.

PA (MILL-) MILLENNIUM PHARM INC.

Query Match 100.0%; Score 589; DB 3; Length 105;

Best Local Similarity 100.0%; Pred. No. 4.3e-54;

RESULT 3

ID AAB70148 standard; protein; 105 AA.

DE Human G protein-coupled receptor protein-related sequence #4.

PN WO200116309-A1.

PD 08-MAR-2001.

PA (TAKE) TAKEDA CHEM IND LTD.

Query Match 100.0%; Score 589; DB 4; Length 105;

Best Local Similarity 100.0%; Pred. No. 4.3e-54;

RESULT 4

ID AAB68427 standard; protein; 105 AA.

DE Amino acid sequence of a human Zven2 polypeptide.

PN WO200136465-A2.

PD 25-MAY-2001.

PA (ZYMO) ZYMOGENETICS INC.

Query Match 100.0%; Score 589; DB 4; Length 105;

Best Local Similarity 100.0%; Pred. No. 4.3e-54;

RESULT 5

ID AAU12406 standard; protein; 105 AA.

DE Human PRO1186 polypeptide sequence.

PN WO200140466-A2.

PD 07-JUN-2001.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 589; DB 4; Length 105;

Best Local Similarity 100.0%; Pred. No. 4.3e-54;

RESULT 6

ID AAB53096 standard; protein; 105 AA.

DE Human prokineticin 1 precursor protein.

PN WO200140466-A2.

PD 07-JUN-2001.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 589; DB 4; Length 105;

Best Local Similarity 100.0%; Pred. No. 4.3e-54;

DE Human angiogenesis-associated protein PRO1186, SEQ ID NO:165.
PN WO200053753-A2.
PD 14-SEP-2000.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 589; DB 4; Length 105;

Best Local Similarity 100.0%; Pred. No. 4.3e-54;

RESULT 7

ID AAB65268 standard; protein; 105 AA.

DE Human PRO1186 (UNQ600) protein sequence SEQ ID NO:371.

PN WO200073454-A1.

PD 07-DEC-2000.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 589; DB 4; Length 105;

Best Local Similarity 100.0%; Pred. No. 4.3e-54;

RESULT 8

ID AAB48175 standard; protein; 105 AA.

DE Human PRO1186 polypeptide.

PN WO200075327-A1.

PD 14-DEC-2000.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 589; DB 4; Length 105;

Best Local Similarity 100.0%; Pred. No. 4.3e-54;

RESULT 9

ID AAB48067 standard; protein; 105 AA.

DE Human extracellular signaling molecule (EXCS) (ID 2006548CD1).

PN WO200070049-A2.

PD 23-NOV-2000.

PA (INCY-) INCYTE GENOMICS INC.

Query Match 100.0%; Score 589; DB 4; Length 105;

Best Local Similarity 100.0%; Pred. No. 4.3e-54;

RESULT 10

ID AAM50773 standard; protein; 105 AA.

DE Endocrine gland-derived vascular endothelial growth factor.

PN WO200200711-A2.

PD 03-JAN-2002.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 589; DB 5; Length 105;

Best Local Similarity 100.0%; Pred. No. 4.3e-54;

RESULT 11

ID AAU83674 standard; protein; 105 AA.

DE Human PRO protein, Seq ID No 166.

PN WO200208288-A2.

PD 31-JAN-2002.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 589; DB 5; Length 105;

Best Local Similarity 100.0%; Pred. No. 4.3e-54;

RESULT 12

ID ABB84902 standard; protein; 105 AA.

DE Human PRO1186 protein sequence SEQ ID NO:172.

PN WO200200690-A2.

PD 03-JAN-2002.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 589; DB 5; Length 105;

Best Local Similarity 100.0%; Pred. No. 4.3e-54;

RESULT 13

ID AAO15527 standard; protein; 105 AA.

DE Human physiologically-active ZAQ ligand-related protein 3.

PN WO200257443-A1.

PD 25-JUL-2002.

PA (TAKE) TAKEDA CHEM IND LTD.

Query Match 100.0%; Score 589; DB 5; Length 105;

Best Local Similarity 100.0%; Pred. No. 4.3e-54;

RESULT 14

ID ABB06308 standard; protein; 105 AA.

DE Human G protein-coupled receptor ZAQ ligand protein SEQ ID NO:23.

PN WO200206483-A1.

PD 24-JAN-2002.

PA (TAKE) TAKEDA CHEM IND LTD.

Query Match 100.0%; Score 589; DB 5; Length 105;

Best Local Similarity 100.0%; Pred. No. 4.3e-54;

RESULT 15

ID AAE24382 standard; protein; 105 AA.

DE Human prokineticin 1 precursor protein.

PN WO200140466-A2.

PD 07-JUN-2001.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 589; DB 5; Length 105;

Best Local Similarity 100.0%; Pred. No. 4.3e-54;

PN WO200236625-A2.
 PD 10-MAY-2002.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 100.0%; Score 589; DB 5; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 16
 ID ABB95508 standard; protein; 105 AA.
 DE Human angiogenesis related protein PRO1186 SEQ ID NO: 172.
 PN WO200208284-A2.
 PD 31-JAN-2002.
 PA (GETH) GENENTECH INC.
 PA (BAKE/) BAKER K P.
 PA (FERR/) FERRARA N.
 PA (GERB/) GERBER H.
 PA (GERR/) GERRITSEN M E.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GURN/) GURNEY A L.
 PA (HILL/) HILLAN K J.
 PA (MARS/) MARSTERS S A.
 PA (PANJ/) PAN J.
 PA (PAON/) PAONI N F.
 PA (STEP/) STEPHAN J F.
 PA (WATA/) WATANABE C K.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.
 Query Match 100.0%; Score 589; DB 5; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 17
 ID ADY31906 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN WO200193983-A1.
 PD 13-DEC-2001.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 5; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 18
 ID ABUS8083 standard; protein; 105 AA.
 DE Human PRO polypeptide #115.
 PN US2003027163-A1.
 PD 06-FEB-2003.
 Query Match 100.0%; Score 589; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 19
 ID ABUS9161 standard; protein; 105 AA.
 DE Novel human secreted or transmembrane protein PRO1186.
 PN US200212252-A1.
 PD 19-SEP-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 20
 ID ABUS2673 standard; protein; 105 AA.
 DE Human secreted/transmembrane protein PRO1186.
 PN US2003032023-A1.
 PD 13-FEB-2003.
 Query Match 100.0%; Score 589; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 21
 ID AB017850 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003032156-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 22
 ID ABUS0592 standard; protein; 105 AA.
 DE Human secreted/transmembrane protein, #151.
 PN US2002160384-A1.
 PD 31-OCT-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 6; Length 105;

Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 23
 ID ARU80821 standard; protein; 105 AA.
 DE Human PRO polypeptide #83.
 PN US2003036635-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 24
 ID ABO33787 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003045687-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 25
 ID ABU13974 standard; protein; 105 AA.
 DE Human PRO1186 polypeptide.
 PN US2002103125-A1.
 PD 01-AUG-2002.
 PA (GETH) GENENTECH LTD.
 Query Match 100.0%; Score 589; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 26
 ID ABUS8800 standard; protein; 105 AA.
 DE Human endocrine gland-derived vascular endothelial growth factor.
 PN US2002192634-A1.
 PD 19-DEC-2002.
 PA (PERR/) FERRARA N.
 PA (WATA/) WATANABE C.
 PA (WOOD/) WOOD W I.
 PA (SHEK/) SHEK T.
 Query Match 100.0%; Score 589; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 27
 ID ABUS1104 standard; protein; 105 AA.
 DE Human PRO polypeptide #235.
 PN US2003004311-A1.
 PD 02-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 28
 ID ABUS7603 standard; protein; 105 AA.
 DE Human ZVEN2.
 PN US6485938-B1.
 PD 26-NOV-2002.
 PA (ZYMO) ZYMOGENETICS INC.
 Query Match 100.0%; Score 589; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 29
 ID ABUS7559 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003003531-A1.
 PD 02-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 30
 ID ABUS6804 standard; protein; 105 AA.
 DE Human PRO polypeptide #235.
 PN US2003036180-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 31
 ID ABUS9885 standard; protein; 105 AA.
 DE Novel secreted and transmembrane protein PRO1186.
 PN US2003017563-A1.
 PD 23-JAN-2003.

PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 32
 ID ABU59308 standard; protein; 105 AA.
 DE Human secreted/transmembrane protein, #151.
 PN US2003027162-A1.
 PD 06-FEB-2003.
 Query Match 100.0%; Score 589; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 33
 ID ABO26005 standard; protein; 105 AA.
 DE Human PRO1186 polypeptide.
 PN US2002127576-A1.
 PD 12-SEP-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 34
 ID ABO25075 standard; protein; 105 AA.
 DE Human secreted/transmembrane protein (PRO) #235.
 PN US2003036179-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 35
 ID ABU82130 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003088063-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 36
 ID ABU59014 standard; protein; 105 AA.
 DE Human secreted/transmembrane protein, #151.
 PN US2002142961-A1.
 PD 03-OCT-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 37
 ID ABU92392 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003022187-A1.
 PD 30-JAN-2003.
 Query Match 100.0%; Score 589; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 38
 ID ABU59457 standard; protein; 105 AA.
 DE Novel human secreted or transmembrane protein PRO1198.
 PN US2003027985-A1.
 PD 06-FEB-2003.
 Query Match 100.0%; Score 589; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 39
 ID ABU67080 standard; protein; 105 AA.
 DE Human secreted/transmembrane, PRO, protein SEQ ID 470.
 PN US2003032155-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 40
 ID ABU92223 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003017476-A1.
 PD 23-JAN-2003.
 Query Match 100.0%; Score 589; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 41
 ID ABU10929 standard; protein; 105 AA.

DE Human PRO polypeptide #115.
 PN US2002123463-A1.
 PD 05-SEP-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 42
 ID ABU81681 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2002177164-A1.
 PD 28-NOV-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 43
 ID ABU88620 standard; protein; 105 AA.
 DE Human secreted and transmembrane polypeptide PRO1186.
 PN US2002197615-A1.
 PD 26-DEC-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 44
 ID ABO34134 standard; protein; 105 AA.
 DE Human PRO1186 polypeptide.
 PN US2003017981-A1.
 PD 23-JAN-2003.
 Query Match 100.0%; Score 589; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 45
 ID ADA45989 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003023238-A1.
 PD 30-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 46
 ID ADA76420 standard; protein; 105 AA.
 DE Human PRO polypeptide #235.
 PN US2003073212-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 47
 ID ABU72310 standard; protein; 105 AA.
 DE Human PRO1186 protein.
 PN US2003050448-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 48
 ID ADA19070 standard; protein; 105 AA.
 DE Human PRO polypeptide #235.
 PN US2003054517-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 49
 ID ADA61693 standard; protein; 105 AA.
 DE Homo sapiens.
 PN US2003049816-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 50
 ID ADB19478 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003068796-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 51
ID ADB28019 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 52
ID ADA86498 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 53
ID ADB16062 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 54
ID ADA37882 standard; protein; 105 AA.
DE Human secreted/transmembrane protein PRO1186.
PN US200308297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 55
ID ADA47848 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 56
ID ADA21568 standard; protein; 105 AA.
DE Human secreted/transmembrane polypeptide PRO1186.
PN US2003054404-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 57
ID ADA10355 standard; protein; 105 AA.
DE Human secreted/transmembrane protein, PRO1186.
PN US2003059831-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 58
ID ADA67643 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 59
ID ADB30650 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;

Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 60
ID ADA85946 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 61
ID ADA17899 standard; protein; 105 AA.
DE Human PRO1186 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 62
ID ADA97158 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 63
ID ADA79462 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 64
ID ADA87601 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 65
ID ADB16803 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 66
ID ADA28007 standard; protein; 105 AA.
DE Human secreted/transmembrane protein PRO1186.
PN US2003054359-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 67
ID ADA91895 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 68
ID ADB14958 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 69
ID ADB18919 standard; protein; 105 AA.

DE Novel human secreted and transmembrane protein PRO1186.
PN US2003073211-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 70
ID ADA94134 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 71
ID ADB20030 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 72
ID ADB13342 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 73
ID ABO43383 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 74
ID ADA94587 standard; protein; 105 AA.
DE Human secreted/transmembrane protein PRO1186.
PN US2003059832-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 75
ID ADA74596 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 76
ID ADB24829 standard; protein; 105 AA.
DE Human PRO polypeptide SEQ ID NO 470.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 77
ID ADA82353 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 78
ID ADA75316 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003073216-A1.

PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 79
ID ADA85394 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082895-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 80
ID ADA84842 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 81
ID ADB30098 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 82
ID ADA80626 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 83
ID ADA75868 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 84
ID ADA38812 standard; protein; 105 AA.
DE Human secreted/transmembrane protein PRO1186.
PN US2003059780-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 85
ID ADA47093 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 86
ID ADB25389 standard; protein; 105 AA.
DE Human PRO polypeptide SEQ ID NO 470.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 87
ID ADA93565 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 88
ID ADB26915 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 89
ID ADB31202 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 90
ID ABJ72438 standard; protein; 105 AA.
DE Human PRO1186 protein.
PN US2003027988-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 91
ID ADA92933 standard; protein; 105 AA.
DE Human secreted/transmembrane protein PRO1186.
PN US2003060407-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 92
ID ADA61130 standard; protein; 105 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 93
ID ADB24277 standard; protein; 105 AA.
DE Human PRO polypeptide SEQ ID NO 470.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 94
ID ADA96606 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 95
ID ADA81178 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 96
ID ADA96054 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;

RESULT 97
ID ADB26363 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 98
ID ADB21848 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 99
ID ABO34333 standard; protein; 105 AA.
DE Human secreted/transmembrane polypeptide PRO 1186.
PN US2003044934-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 100
ID ADA77627 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 101
ID ADB18367 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 102
ID ADA87050 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 103
ID ADA88153 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 104
ID ADA46541 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 105
ID ADB28571 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 106
ID ADB28571 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;

ID ADB29123 standard; protein; 105 AA.
 DE Human PRO polypeptide #235.
 PN US2003082706-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 107
 ID ABO53220 standard; protein; 105 AA.
 DE Human secreted/transmembrane protein PRO1186.
 PN US2003044806-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 108
 ID ADA77075 standard; protein; 105 AA.
 DE Human PRO polypeptide #235.
 PN US2003059909-A1.
 PD 27-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 109
 ID ADA22494 standard; protein; 105 AA.
 DE Human secreted/transmembrane polypeptide PRO1186.
 PN US2003040473-A1.
 PD 27-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 110
 ID ADA88705 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003073213-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 111
 ID ADA97710 standard; protein; 105 AA.
 DE Human PRO polypeptide #235.
 PN US2003082686-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 112
 ID ADB27467 standard; protein; 105 AA.
 DE Human PRO polypeptide #235.
 PN US2003022239-A1.
 PD 30-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 113
 ID ADB22400 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003087344-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 114
 ID ABO22590 standard; protein; 105 AA.
 DE Human secreted/transmembrane protein PRO1186.
 PN US2003017982-A1.
 PD 23-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 115
 ID ADA06660 standard; protein; 105 AA.
 DE Human secreted/transmembrane PRO polypeptide #115.
 PN US2003049638-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 116
 ID ADB72140 standard; protein; 105 AA.
 DE Human membrane bound receptor/protein PRO1186 amino acid sequence.
 PN US2003065147-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 117
 ID ADA39353 standard; protein; 105 AA.
 DE Human secreted/transmembrane protein PRO1186.
 PN US2003059782-A1.
 PD 27-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 118
 ID ADA67091 standard; protein; 105 AA.
 DE Human PRO polypeptide #235.
 PN US2003068793-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 119
 ID ADB22952 standard; protein; 105 AA.
 DE Human PRO polypeptide #235.
 PN US2003077711-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 120
 ID ADB23725 standard; protein; 105 AA.
 DE Human PRO polypeptide SEQ ID NO 470.
 PN US2003077712-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 121
 ID ADA92447 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003082712-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 122
 ID ADB15510 standard; protein; 105 AA.
 DE Human PRO polypeptide #235.
 PN US2003087352-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 123
 ID ADB83656 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003073814-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 124
 ID ADB80762 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003088068-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 125
 ID ADB73303 standard; protein; 105 AA.

DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003096968-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 126
 ID ADB38762 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003082766-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 127
 ID ADB96379 standard; protein; 105 AA.
 DE Human PRO polypeptide #115.
 PN US2003054403-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 128
 ID ADB78385 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003092889-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 129
 ID ADB38210 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003087347-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 130
 ID ADB66682 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003082689-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 131
 ID ADB85033 standard; protein; 105 AA.
 DE Human PRO polypeptide #83.
 PN US2003073817-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 132
 ID ADB89762 standard; protein; 105 AA.
 DE Human PRO polypeptide #235.
 PN US2003082698-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 133
 ID ADB90494 standard; protein; 105 AA.
 DE Human PRO polypeptide #235.
 PN US2003082762-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 134
 ID ADB39595 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003082764-A1.

PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 135
 ID ADB78139 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003092886-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 136
 ID ADB87205 standard; protein; 105 AA.
 DE Human PRO polypeptide #83.
 PN US2003088067-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 137
 ID ADB84787 standard; protein; 105 AA.
 DE Human PRO polypeptide #83.
 PN US2003092890-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 138
 ID ADB47218 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003082687-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 139
 ID ADB83902 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003069397-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 140
 ID ADB86825 standard; protein; 105 AA.
 DE Human PRO polypeptide #235.
 PN US2003082697-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 141
 ID ADB73057 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003092887-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 142
 ID ADB77430 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003082696-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 143
 ID ADB34587 standard; protein; 105 AA.
 DE Human PRO polypeptide SEQ ID NO 470.
 PN US2003077717-A1.
 PD 24-APR-2003.

PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 589; DB 7; Length 105;
 RESULT 144
 ID ADB35691 standard; protein; 105 AA.
 DE Human PRO polypeptide SEQ ID NO 470.
 PN US2003077719-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 589; DB 7; Length 105;
 RESULT 145
 ID ADB34035 standard; protein; 105 AA.
 DE Human PRO polypeptide SEQ ID NO 470.
 PN US2003077716-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 589; DB 7; Length 105;
 RESULT 146
 ID ADB35139 standard; protein; 105 AA.
 DE Human PRO polypeptide SEQ ID NO 470.
 PN US2003077718-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 589; DB 7; Length 105;
 RESULT 147
 ID ADB36243 standard; protein; 105 AA.
 DE Human PRO polypeptide SEQ ID NO 470.
 PN US2003077720-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 589; DB 7; Length 105;
 RESULT 148
 ID ADB46638 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003082692-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 589; DB 7; Length 105;
 RESULT 149
 ID ADC57851 standard; protein; 105 AA.
 DE Human PRO polypeptide #115.
 PN US2003027754-A1.
 PD 06-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 589; DB 7; Length 105;
 RESULT 150
 ID ADC55215 standard; protein; 105 AA.
 DE Human PRO polypeptide #115.
 PN US2003045463-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 589; DB 7; Length 105;
 RESULT 151
 ID ADC12082 standard; protein; 105 AA.
 DE Human secreted/transmembrane protein PRO1186.
 PN US2003049681-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 589; DB 7; Length 105;
 RESULT 152
 ID ADC56504 standard; protein; 105 AA.
 DE Human PRO polypeptide #115.
 PN US2003064375-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 589; DB 7; Length 105;
 RESULT 153
 ID ADC07559 standard; protein; 105 AA.

DE Human secreted/transmembrane protein PRO1186.
 PN US2003068447-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 589; DB 7; Length 105;
 RESULT 154
 ID ADC11549 standard; protein; 105 AA.
 DE Human secreted/transmembrane protein PRO1186.
 PN US2003069403-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 589; DB 7; Length 105;
 RESULT 155
 ID ADC36895 standard; protein; 105 AA.
 DE Human PRO polypeptide #83.
 PN US200308065-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 589; DB 7; Length 105;
 RESULT 156
 ID ADC21885 standard; protein; 105 AA.
 DE Human PRO polypeptide #83.
 PN US2003096969-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 589; DB 7; Length 105;
 RESULT 157
 ID ADC50511 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003092106-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 589; DB 7; Length 105;
 RESULT 158
 ID ADC72058 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003092107-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 589; DB 7; Length 105;
 RESULT 159
 ID ADC60037 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003092105-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 589; DB 7; Length 105;
 RESULT 160
 ID ADC49916 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003088064-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 589; DB 7; Length 105;
 RESULT 161
 ID ADC49115 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003088070-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 589; DB 7; Length 105;
 RESULT 162
 ID ADC49632 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003088071-A1.
 PD 08-MAY-2003.

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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 163
ID ADC47493 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003088072-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 164
ID ADC53044 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein Seq ID470.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 165
ID ADC5398 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein Seq ID470.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 166
ID ADC60589 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 167
ID ADC51064 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 168
ID ADC65591 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 169
ID ADC54689 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein Seq ID470.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 170
ID ADC53650 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein Seq ID470.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 171
ID ADC59173 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein Seq ID470.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.

PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 172
ID ADC56051 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein Seq ID470.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 173
ID ADC58621 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein Seq ID470.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 174
ID ADC14671 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 175
ID ADC47238 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003105288-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 176
ID ADD08203 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003068623-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 177
ID AD003295 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 178
ID ADC90287 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 179
ID ADC82028 standard; protein; 105 AA.
DE Human PRO polypeptide #115.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 180
ID ADC69706 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 181
ID ADC48595 standard; protein; 105 AA.

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DE Human PRO polypeptide #235.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 182
ID ADD10124 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 183
ID ADD07670 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 184
ID ADC78113 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003096972-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 185
ID ADD04699 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 186
ID ADC82561 standard; protein; 105 AA.
DE Human PRO polypeptide #115.
PN US2003059833-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 187
ID ADD06348 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003073816-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 188
ID ADC80655 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 189
ID ADD11162 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 190
ID ADD10461 standard; protein; 105 AA.
DE Human secreted/transmembrane PRO polypeptide #86.
PN US2003105011-A1.

PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 191
ID ADC48043 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 192
ID ADD08741 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003073090-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 193
ID ADC77867 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003088066-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 194
ID ADC80103 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 195
ID ADD06990 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 196
ID ADD11421 standard; protein; 105 AA.
DE Human secreted/transmembrane PRO polypeptide #86.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 197
ID ADD09572 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 198
ID ADC83237 standard; protein; 105 AA.
DE Human PRO polypeptide #115.
PN US2003059783-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 199
ID ADD50830 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003105291-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;

Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 200
 ID ADD41285 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003203438-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 201
 ID ADD52424 standard; protein; 105 AA.
 DE Human PRO polypeptide #235.
 PN US2003194769-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 202
 ID ADD51076 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003105290-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 203
 ID ADD53164 standard; protein; 105 AA.
 DE Human PRO polypeptide #235.
 PN US2003194792-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 204
 ID ADD53716 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003203437-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 205
 ID ADD55344 standard; protein; 105 AA.
 DE Human PRO polypeptide #115.
 PN US2003077593-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 206
 ID ADD69106 standard; protein; 105 AA.
 DE Human ZAQ-related protein - SEQ ID 84.
 PN WO200306860-A1.
 PD 14-AUG-2003.
 PA (TAKE) TAKEDA CHEM IND LTD.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 207
 ID ADD37214 standard; protein; 105 AA.
 DE Human secreted/transmembrane PRO polypeptide #86.
 PN US2003105012-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 208
 ID ADD56302 standard; protein; 105 AA.
 DE Human PRO polypeptide #115.
 PN US2003077594-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 209
 ID ADD51872 standard; protein; 105 AA.

DE Human PRO polypeptide #235.
 PN US2003194779-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 210
 ID ADD02671 standard; protein; 105 AA.
 DE Human PRO polypeptide #235.
 PN US2003203431-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 211
 ID ADD50557 standard; protein; 105 AA.
 DE Human PRO polypeptide #83.
 PN US2003096971-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 212
 ID ADD02105 standard; protein; 105 AA.
 DE Human PRO polypeptide #235.
 PN US2003203430-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 213
 ID ADD54287 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003203432-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 214
 ID ADD54740 standard; protein; 105 AA.
 DE Human PRO polypeptide #115.
 PN US2002132253-A1.
 PD 19-SEP-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 215
 ID ADD50311 standard; protein; 105 AA.
 DE Human PRO polypeptide #83.
 PN US2003096970-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 216
 ID ADD51322 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003105289-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 217
 ID ADD92604 standard; protein; 105 AA.
 DE Human PRO polypeptide #235.
 PN US2003199030-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 218
 ID ADD91500 standard; protein; 105 AA.
 DE Human PRO polypeptide #235.

PA US2003199055-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 219
 ID ADE04114 standard; protein; 105 AA.
 DE Human PRO polypeptide #235.
 PN US2003199057-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 220
 ID ABE26894 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003087304-A1.
 PD 08-MAY-2003.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 221
 ID ABE32411 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003194765-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 222
 ID ADE22343 standard; protein; 105 AA.
 DE Human PRO polypeptide #235.
 PN US2003199056-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 223
 ID ADD79567 standard; protein; 105 AA.
 DE Human PRO polypeptide #235.
 PN US2003203428-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 224
 ID ADE42103 standard; protein; 105 AA.
 DE Human PRO polypeptide #235.
 PN US2003194772-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 225
 ID ABE17920 standard; protein; 105 AA.
 DE Human PRO polypeptide #235.
 PN US2003199023-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 226
 ID ADD92052 standard; protein; 105 AA.
 DE Human PRO polypeptide #235.
 PN US2003199053-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 227
 ID ABE33515 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003194767-A1.
 PD 16-OCT-2003.

PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 228
 ID ADE34067 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003194791-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 229
 ID AD080119 standard; protein; 105 AA.
 DE Human PRO polypeptide #235.
 PN US2003207417-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 230
 ID ADD93156 standard; protein; 105 AA.
 DE Human PRO polypeptide #235.
 PN US2003194768-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 231
 ID ADE19576 standard; protein; 105 AA.
 DE Human PRO polypeptide #235.
 PN US2003199025-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 232
 ID ADE19024 standard; protein; 105 AA.
 DE Human PRO polypeptide #235.
 PN US2003199026-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 233
 ID ADE43220 standard; protein; 105 AA.
 DE Human PRO polypeptide #235.
 PN US2003199033-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 234
 ID ADD96009 standard; protein; 105 AA.
 DE Human PRO polypeptide #235.
 PN US2003199059-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 235
 ID ADE22895 standard; protein; 105 AA.
 DE Human PRO polypeptide #235.
 PN US2003199064-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 236
 ID ADD79013 standard; protein; 105 AA.
 DE Human PRO polypeptide #235.
 PN US2003203429-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.

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Query Match      100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 237
ID ADE2361 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match      100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 238
ID ADE32963 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 239
ID ADE42655 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 240
ID ADE40671 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 241
ID ADD89699 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 242
ID ADE40983 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 243
ID ADE04782 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 244
ID ADE92911 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 245
ID ADE67298 standard; protein; 105 AA.
DE Human PRO1186 amino acid sequence SEQ ID NO:371.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 246
ID ADF28070 standard; protein; 105 AA.
DE Human Zven 2.
PN US2003148317-A1.
PD 07-AUG-2003.
PA (ZYMO ) ZYMOGENETICS INC.
Query Match      100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 247
ID ADG21620 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 248
ID ADG23261 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 249
ID ADF97596 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 250
ID ABG75089 standard; protein; 105 AA.
DE Prokineticin 1 (PROK1).
PN WO2003083073-A2.
PD 09-OCT-2003.
PA (FARB ) BAYER PHARM CORP.
Query Match      100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 251
ID ABG75086 standard; protein; 105 AA.
DE Human prokineticin 1 (PROK1).
PN WO2003083073-A2.
PD 09-OCT-2003.
PA (FARB ) BAYER PHARM CORP.
Query Match      100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 252
ID ADG80660 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 253
ID ADG80108 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 254
ID ADH54400 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 589; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 255

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ID ADH5952 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 7; Length 105;
RESULT 256
ID ADI35552 standard; protein; 105 AA.
DE Human PRO polypeptide #115.
PN US2003050457-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 589; DB 7; Length 105;
RESULT 257
ID ADI64171 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 7; Length 105;
RESULT 258
ID ADI65120 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 7; Length 105;
RESULT 259
ID ADI63619 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 7; Length 105;
RESULT 260
ID ADH82033 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 7; Length 105;
RESULT 261
ID ADI00045 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003049682-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 589; DB 7; Length 105;
RESULT 262
ID ADH81481 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 7; Length 105;
RESULT 263
ID ADJ71810 standard; protein; 105 AA.
DE Human prokineticin 1 protein.
PN WO2003040326-A2.
PD 15-MAY-2003.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 7; Length 105;
RESULT 264
ID ADM82650 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003087355-A1.

PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 7; Length 105;
RESULT 265
ID ADN16049 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 7; Length 105;
RESULT 266
ID ADN1678 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 7; Length 105;
RESULT 267
ID ADN15497 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 7; Length 105;
RESULT 268
ID ADN14945 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 7; Length 105;
RESULT 269
ID ADC48869 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003092888-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 8; Length 105;
RESULT 270
ID ADC81207 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 8; Length 105;
RESULT 271
ID ADE21040 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 8; Length 105;
RESULT 272
ID ADE05884 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 8; Length 105;
RESULT 273
ID ADD76655 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003100087-A1.
PD 29-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 274
ID ADD75113 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 275
ID ADD75859 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 276
ID ADD85091 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 277
ID ADD86917 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 278
ID ADE20794 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 279
ID ADE39091 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003096362-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 280
ID ADH8019 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 281
ID ADH6423 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 282
ID ADE05638 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 589; DB 8; Length 105.
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 283
ID ADD73623 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
FN US2003100711-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 284
ID ADE75971 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
FN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 285
ID ADD78463 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
FN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 286
ID ADE41422 standard; protein; 105 AA.
DE Human secreted/transmembrane PRO polypeptide #86.
FN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 287
ID ADE23447 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
FN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 288
ID ADE21286 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
FN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 289
ID ADD77401 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
FN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 290
ID ADE20548 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
FN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 291
ID ADD75613 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
FN US2003100064-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 292
ID ADD75613 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
FN US2003100064-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;

Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 292
ID ADD74129 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 293
ID ADD74375 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 294
ID ADD76105 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 295
ID ADD85597 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100721-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 296
ID ADE23999 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 297
ID ADE24642 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 298
ID ADD87467 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 299
ID ADE05146 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 300
ID ADD75359 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;

RESULT 301
ID ADD76903 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 302
ID ADD86671 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 303
ID ADE89333 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 304
ID ADD78139 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 305
ID ADE18472 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 306
ID ADE88781 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 307
ID ADD77647 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 308
ID ADD77893 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 309
ID ADD85351 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 310
ID ADD85351 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;

ID ADD73883 standard; protein; 105 AA.
 DE Human PRO polypeptide #83.
 PN US2003100710-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 8; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 311
 ID ADD74621 standard; protein; 105 AA.
 DE Human PRO polypeptide #83.
 PN US2003100713-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 8; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 312
 ID ADD77149 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003100716-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 8; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 313
 ID ADD85843 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003100720-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 8; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 314
 ID ADR05392 standard; protein; 105 AA.
 DE Human PRO polypeptide #83.
 PN US2003100723-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 8; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 315
 ID ADR74867 standard; protein; 105 AA.
 DE Human PRO polypeptide #83.
 PN US2003100724-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 8; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 316
 ID ADE94801 standard; protein; 105 AA.
 DE Human PRO polypeptide #235.
 PN US2003199027-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 8; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 317
 ID ADE91212 standard; protein; 105 AA.
 DE Human PRO polypeptide #235.
 PN US2003199061-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 8; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 318
 ID ADF35497 standard; protein; 105 AA.
 DE Human PRO polypeptide #235.
 PN US2003194760-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 8; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 319
 ID ADE95353 standard; protein; 105 AA.
 DE Human PRO polypeptide #235.

PN US2003199052-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 8; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 320
 ID ADE93463 standard; protein; 105 AA.
 DE Human PRO polypeptide #235.
 PN US2003199060-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 8; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 321
 ID ADF35044 standard; protein; 105 AA.
 DE Human PRO polypeptide #235.
 PN US2003199029-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 8; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 322
 ID ADE92359 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003199051-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 8; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 323
 ID ADE90660 standard; protein; 105 AA.
 DE Human PRO polypeptide #235.
 PN US2003199063-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 8; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 324
 ID ADE91807 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003199058-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 8; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 325
 ID ADG11747 standard; protein; 105 AA.
 DE Human PRO1186 polypeptide.
 PN US2003228655-A1.
 PD 11-DEC-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 8; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 326
 ID ADG05679 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003096959-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 8; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 327
 ID ADG27233 standard; protein; 105 AA.
 DE Human PRO polypeptide #83.
 PN US2003096962-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 589; DB 8; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.3e-54;
 RESULT 328
 ID ADG02386 standard; protein; 105 AA.
 DE Human PRO polypeptide #235.
 PN US2003207352-A1.

PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 329
ID ADG22172 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 330
ID ADG20242 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 331
ID ADF98148 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 332
ID ADG24365 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 333
ID ADF98719 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 334
ID ADG03550 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 335
ID ADF99271 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 336
ID ADG16856 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 337
ID ADG05315 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207375-A1.
PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 338
ID ADG19582 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 339
ID ADG11296 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003096967-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 340
ID ADG13419 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 341
ID ADG08476 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 342
ID ADG15646 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 343
ID ADG12075 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 344
ID ADF97044 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 345
ID ADG06229 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 346
ID ADG23813 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

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Query Match
Best Local Similarity 100.0%; Score 589; DB 8; Length 105;
RESULT 347
ID ADG04102 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 8; Length 105;
RESULT 348
ID ADG25003 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 8; Length 105;
RESULT 349
ID ADF94632 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003096964-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 8; Length 105;
RESULT 350
ID ADG07300 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 8; Length 105;
RESULT 351
ID ADG07852 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 8; Length 105;
RESULT 352
ID ADG06728 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003096966-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 8; Length 105;
RESULT 353
ID ADG55347 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 8; Length 105;
RESULT 354
ID ADG61011 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 8; Length 105;
RESULT 355
ID ADG62115 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 8; Length 105;
RESULT 356
ID ADG82316 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 8; Length 105;
RESULT 357
ID ADG57555 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 8; Length 105;
RESULT 358
ID ADG57003 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 8; Length 105;
RESULT 359
ID ADG55899 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 8; Length 105;
RESULT 360
ID ADG58659 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 8; Length 105;
RESULT 361
ID ADG71025 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 8; Length 105;
RESULT 362
ID ADH39072 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003096965-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 8; Length 105;
RESULT 363
ID ADG58107 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 8; Length 105;
RESULT 364
ID ADG53691 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 8; Length 105;
RESULT 365
ID ADG62115 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 8; Length 105;
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RESULT 365
ID ADG71577 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 366
ID ADG81764 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 367
ID ADH19617 standard; protein; 105 AA.
DE Human secreted/transmembrane protein PRO1186.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 368
ID ADH30726 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 369
ID ADH12093 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 370
ID ADG52515 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 371
ID ADG54243 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 372
ID ADG81212 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 373
ID ADG56451 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 374
ID ADH12717 standard; protein; 105 AA.

DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 375
ID ADH21110 standard; protein; 105 AA.
DE Human secreted/transmembrane protein PRO1186.
PN US2003224358-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 376
ID ADG61563 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 377
ID ADH20150 standard; protein; 105 AA.
DE Human secreted/transmembrane protein PRO1186.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 378
ID ADH28650 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 379
ID ADG54795 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 380
ID ADG59835 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 381
ID ADH43605 standard; protein; 105 AA.
DE Human PRO polypeptide #86.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 382
ID ADG34162 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2004006206-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 383
ID ADI81259 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207361-A1.

PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 384
ID ADI33632 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 385
ID ADH69726 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 386
ID ADG10002 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 387
ID ADI15473 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 388
ID ADG09350 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 389
ID ADI14805 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 390
ID ADI29887 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003096961-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 391
ID ADI18400 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 392
ID ADM27284 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2004044179-A1.
PD 04-MAR-2004.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 393
ID ADJ63681 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 394
ID ADJ77576 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 395
ID ADK82950 standard; protein; 105 AA.
DE Human PRO polypeptide #86.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 396
ID ADK66642 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2004044180-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 397
ID ADJ65698 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 398
ID ADM27834 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 399
ID ADL66891 standard; protein; 105 AA.
DE Human extracellular signaling molecule (EXCS) -11 protein.
PN US2004048244-A1.
PD 11-MAR-2004.
PA (TANG/) TANG Y T.
PA (YUEH/) YUE H.
PA (LALP/) LAL P.
PA (BURF/) BURFORD N.
PA (BAND/) BANDMAN O.
PA (BAUG/) BAUGHN M.R.
PA (AZIM/) AZIMZAI Y.
PA (LUDA/) LU D A M.
PA (ARVI/) ARVIZU C.
Query Match 100.0%; Score 589; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 400
ID ADN08155 standard; protein; 105 AA.
DE Human endocrine gland vascular endothelial growth factor.
PN DE10229379-A1.
PD 29-JAN-2004.
PA (SCHD) SCHERING AG.

Query Match
Best Local Similarity 100.0%; Score 589; DB 8; Length 105;
RESULT 401
ID ADM42558 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 8; Length 105;
RESULT 402
ID ADM41842 standard; protein; 105 AA.
DE Amino acid sequence of a human Zven2 polypeptide.
PN WO2004032850-A2.
PD 22-APR-2004.
PA (ZYMO) ZYMOGENETICS INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 8; Length 105;
RESULT 403
ID ADM28420 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 8; Length 105;
RESULT 404
ID ADI95902 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 8; Length 105;
RESULT 405
ID ADI96454 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 8; Length 105;
RESULT 406
ID ADS86960 standard; protein; 105 AA.
DE Human Zven2 protein.
PN WO2004031367-A2.
PD 15-APR-2004.
PA (ZYMO) ZYMOGENETICS INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 8; Length 105;
RESULT 407
ID ADS00464 standard; protein; 105 AA.
DE Human EG-VEGF, SEQ ID 8.
PN WO2004081229-A2.
PD 23-SEP-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 8; Length 105;
RESULT 408
ID ADS86475 standard; protein; 105 AA.
DE Human ZAQ ligand protein related to eating disorders & obesity Seq 7.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match
Best Local Similarity 100.0%; Score 589; DB 8; Length 105;
RESULT 409
ID ADS75493 standard; protein; 105 AA.
DE Human prokineticin 2 receptor protein.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match
Best Local Similarity 100.0%; Score 589; DB 8; Length 105;

Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 410
ID ADS32406 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2004203125-A1.
PD 14-OCT-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 8; Length 105;
RESULT 411
ID ADT03390 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2004214269-A1.
PD 28-OCT-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 8; Length 105;
RESULT 412
ID ADY86164 standard; protein; 105 AA.
DE Human EG-VEGF, SEQ ID NO:2.
PN US2005064522-A1.
PD 24-MAR-2005.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 9; Length 105;
RESULT 413
ID ADZ03441 standard; protein; 105 AA.
DE Human secreted/transmembrane PRO1186 protein.
PN US2005074837-A1.
PD 07-APR-2005.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 9; Length 105;
RESULT 414
ID ADZ8922 standard; protein; 105 AA.
DE Human prokineticin 1 isoform.
PN WO2005042717-A2.
PD 12-MAY-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match
Best Local Similarity 100.0%; Score 589; DB 9; Length 105;
RESULT 415
ID AEA38601 standard; protein; 105 AA.
DE Human secreted/transmembrane protein, #183.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 589; DB 9; Length 105;
RESULT 416
ID AEB14187 standard; protein; 105 AA.
DE Cancer cell diagnosis method-related human protein - SEQ ID 470.
PN US2005153396-A1.
PD 14-JUL-2005.
PA (BAKE) BAKER K P.
PA (BERE) BERSINI M.
PA (DEFO) DEFOGE L.
PA (DESN) DESNOYERS L.
PA (FILV) FILVAROPF E.
PA (GAOW) GAO W.
PA (GERR) GERRITSEN M E.
PA (GODD) GODDARD A.
PA (GODO) GODOWSKI P J.
PA (GURN) GURNEY A L.
PA (SHER) SHERWOOD S.
PA (SMIT) SMITH V.
PA (STEW) STEWART T A.
PA (TUMA) TUMAS D.
PA (WATA) WATANABE C K.
PA (WOOD) WOOD W I.
PA (ZHAN) ZHANG Z.
Query Match
Best Local Similarity 100.0%; Score 589; DB 9; Length 105;

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RESULT 417
ID AEB4588 standard; protein; 105 AA.
DE Human Zven2 protein, SEQ ID NO: 5.
PN US2005153322-A1.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 100.0%; Score 589; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 418
ID AEC06124 standard; protein; 105 AA.
DE Human EG-VEGF protein.
PN WO2005076972-A2.
PA (OHIS) UNIV OHIO STATE RES FOUND.
Query Match 100.0%; Score 589; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 419
ID AED08088 standard; protein; 105 AA.
DE Human Zven2 protein.
PN US2005214800-A1.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 100.0%; Score 589; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 420
ID AED86385 standard; protein; 105 AA.
DE Human PRO amino acid sequence, seq id 470.
PN US2005245730-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 421
ID AEG58332 standard; protein; 105 AA.
DE Human PRO1186 polypeptide SEQ ID NO: 470.
PN US2006073568-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 10; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 422
ID AEH49352 standard; protein; 105 AA.
DE Human secreted polypeptide PRO1136, SEQ ID NO:166.
PN EPI659177-A2.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 10; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 423
ID AEI43977 standard; protein; 105 AA.
DE Human cancer-related PRO protein amino acid sequence - SEQ ID 470.
PN US2006040351-A1.
PA (BAKE/) BAKER K P.
PA (BERE/) BERESINI M.
PA (DEFO/) DEFOURGE L.
PA (DESN/) DESNOYERS L.
PA (FILV/) FILVAROFF E.
PA (GAOW/) GAO W.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (SHER/) SHERWOOD S.
PA (SMIT/) SMITH V.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
PA (ZHAN/) ZHANG Z.
Query Match 100.0%; Score 589; DB 10; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 424
ID AEI24060 standard; protein; 105 AA.
DE Human secreted/transmembrane protein PRO1186, SEQ ID NO:470.
PN EPI672070-A2.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 10; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 425
ID AEK48387 standard; protein; 105 AA.
DE Human PRO1186 amino acid sequence.
PN EPI686174-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 10; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 426
ID AEL62980 standard; protein; 105 AA.
DE Human PRO1186 polypeptide, SEQ ID NO: 166.
PN EPI700867-A2.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 10; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 427
ID AEL17020 standard; protein; 105 AA.
DE Human secreted polypeptide PRO1136, SEQ ID NO:166.
PN EPI702928-A2.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 589; DB 10; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
RESULT 428
ID AAB70147 standard; protein; 105 AA.
DE Human G protein-coupled receptor protein-related sequence #3.
PN WO200116309-A1.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 99.8%; Score 588; DB 4; Length 105;
Best Local Similarity 99.0%; Pred. No. 5.4e-54;
RESULT 429
ID AAM79066 standard; protein; 105 AA.
DE Human protein SEQ ID NO 1728.
PN WO200157190-A2.
PA (HYSE-) HYSEQ INC.
Query Match 99.8%; Score 588; DB 4; Length 105;
Best Local Similarity 99.0%; Pred. No. 5.4e-54;
RESULT 430
ID AAG79596 standard; protein; 105 AA.
DE GSP4 sequence.
PN WO200269689-A2.
PA (GEST) GENSET.
Query Match 99.8%; Score 588; DB 5; Length 105;
Best Local Similarity 99.0%; Pred. No. 5.4e-54;
RESULT 431
ID AAO15526 standard; protein; 105 AA.
DE Human physiologically-active ZAQ ligand-related protein 2.
PN WO200257443-A1.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 99.8%; Score 588; DB 5; Length 105;
Best Local Similarity 99.0%; Pred. No. 5.4e-54;
RESULT 432
ID ABB06307 standard; protein; 105 AA.
DE Human G protein-coupled receptor ZAQ ligand protein SEQ ID NO:22.
PN WO200206483-A1.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 99.8%; Score 588; DB 5; Length 105;
Best Local Similarity 99.0%; Pred. No. 5.4e-54;
RESULT 433
ID ABP75987 standard; protein; 105 AA.
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DE Human GENSET protein SEQ ID 194.
 PN WO200283898-A1.
 PD 24-OCT-2002.
 PA (GENSET) GENSET.
 Query Match 99.8%; Score 588; DB 6; Length 105;
 Best Local Similarity 99.0%; Pred. No. 5.4e-54;
 RESULT 434
 ID AED69105 standard; protein; 105 AA.
 DE Human ZAQ-related protein - SEQ ID 83.
 PN WO2003066860-A1.
 PD 14-AUG-2003.
 PA (TAKE) TAKEDA CHEM IND LTD.
 Query Match 99.8%; Score 588; DB 7; Length 105;
 Best Local Similarity 99.0%; Pred. No. 5.4e-54;
 RESULT 435
 ID A886473 standard; protein; 105 AA.
 DE Human ZAQ ligand protein related to eating disorders & obesity Seq 5.
 PN WO2004084945-A1.
 PD 07-OCT-2004.
 PA (TAKE) TAKEDA CHEM IND LTD.
 Query Match 99.8%; Score 588; DB 8; Length 105;
 Best Local Similarity 99.0%; Pred. No. 5.4e-54;
 RESULT 436
 ID AED00619 standard; protein; 105 AA.
 DE Human prokineticin 1 (PK1).
 PN WO2005091925-A2.
 PD 06-OCT-2005.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 99.8%; Score 588; DB 9; Length 105;
 Best Local Similarity 99.0%; Pred. No. 5.4e-54;
 RESULT 437
 ID AAB18475 standard; protein; 105 AA.
 DE A human TANGO 266 polypeptide clone.
 PN WO200502022-A1.
 PD 08-SEP-2000.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 99.5%; Score 586; DB 3; Length 105;
 Best Local Similarity 99.0%; Pred. No. 8.8e-54;
 RESULT 438
 ID AAB18473 standard; protein; 105 AA.
 DE A human TANGO 266 polypeptide clone.
 PN WO200502022-A1.
 PD 08-SEP-2000.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 99.5%; Score 586; DB 3; Length 105;
 Best Local Similarity 99.0%; Pred. No. 8.8e-54;
 RESULT 439
 ID AAB18474 standard; protein; 105 AA.
 DE A human TANGO 266 polypeptide clone.
 PN WO200502022-A1.
 PD 08-SEP-2000.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 99.5%; Score 586; DB 3; Length 105;
 Best Local Similarity 99.0%; Pred. No. 8.8e-54;
 RESULT 440
 ID ABP76151 standard; protein; 105 AA.
 DE Human GENSET protein SEQ ID 477.
 PN WO200283898-A1.
 PD 24-OCT-2002.
 PA (GENSET) GENSET.
 Query Match 99.8%; Score 582; DB 6; Length 105;
 Best Local Similarity 98.1%; Pred. No. 2.3e-53;
 RESULT 441
 ID ABP75986 standard; protein; 105 AA.
 DE Human GENSET protein SEQ ID 193.
 PN WO200283898-A1.
 PD 24-OCT-2002.
 PA (GENSET) GENSET.
 Query Match 98.8%; Score 582; DB 6; Length 105;
 Best Local Similarity 98.1%; Pred. No. 2.3e-53;
 RESULT 442
 ID AED00616 standard; protein; 105 AA.
 DE Rhesus monkey prokineticin 1 (PK1) SEQ ID NO 28.

PN WO2005091925-A2.
 PD 06-OCT-2005.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 98.1%; Score 578; DB 9; Length 105;
 Best Local Similarity 98.1%; Pred. No. 6.1e-53;
 RESULT 443
 ID AEL00448 standard; protein; 113 AA.
 DE Recombinant N-terminal FLAG-tagged human prokineticin-1.
 PN WO2006104713-A1.
 PD 05-OCT-2006.
 PA (JANC) JANSSEN PHARM NV.
 PA (MISK/) MISKOWSKI T A.
 Query Match 97.6%; Score 575; DB 10; Length 113;
 Best Local Similarity 92.9%; Pred. No. 1.4e-52;
 RESULT 444
 ID ADZ8921 standard; protein; 105 AA.
 DE Rhesus monkey prokineticin 2.
 PN WO2005042717-A2.
 PD 12-MAY-2005.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 97.1%; Score 572; DB 9; Length 105;
 Best Local Similarity 97.1%; Pred. No. 2.6e-52;
 RESULT 445
 ID AEX60511 standard; protein; 114 AA.
 DE Human prokineticin 1 (N-terminally FLAG tagged).
 PN WO2006102112-A2.
 PD 28-SEP-2006.
 PA (JANC) JANSSEN PHARM NV.
 Query Match 95.8%; Score 564.5; DB 10; Length 114;
 Best Local Similarity 92.1%; Pred. No. 1.8e-51;
 RESULT 446
 ID AB99151 standard; protein; 105 AA.
 DE Rat ZAQ protein.
 PN WO200262996-A1.
 PD 15-AUG-2002.
 PA (TAKE) TAKEDA CHEM IND LTD.
 Query Match 92.5%; Score 545; DB 5; Length 105;
 Best Local Similarity 89.5%; Pred. No. 1.8e-49;
 RESULT 447
 ID AB06956 standard; protein; 105 AA.
 DE Rat G protein-coupled receptor ZAQ ligand protein SEQ ID NO:43.
 PN WO200216607-A1.
 PD 28-FEB-2002.
 PA (TAKE) TAKEDA CHEM IND LTD.
 Query Match 92.5%; Score 545; DB 5; Length 105;
 Best Local Similarity 89.5%; Pred. No. 1.8e-49;
 RESULT 448
 ID ADB69154 standard; protein; 105 AA.
 DE Rat ZAQ-related protein - SEQ ID 132.
 PN WO2003066860-A1.
 PD 14-AUG-2003.
 PA (TAKE) TAKEDA CHEM IND LTD.
 Query Match 92.5%; Score 545; DB 7; Length 105;
 Best Local Similarity 89.5%; Pred. No. 1.8e-49;
 RESULT 449
 ID ADS86487 standard; protein; 105 AA.
 DE Rat ZAQ ligand protein related to eating disorders & obesity Seq 19.
 PN WO2004084945-A1.
 PD 07-OCT-2004.
 PA (TAKE) TAKEDA CHEM IND LTD.
 Query Match 92.5%; Score 545; DB 8; Length 105;
 Best Local Similarity 89.5%; Pred. No. 1.8e-49;
 RESULT 450
 ID AB99153 standard; protein; 105 AA.
 DE Rat ZAQ protein.
 PN WO200262996-A1.
 PD 15-AUG-2002.
 PA (TAKE) TAKEDA CHEM IND LTD.
 Query Match 91.9%; Score 541; DB 5; Length 105;
 Best Local Similarity 88.6%; Pred. No. 4.9e-49;
 RESULT 451
 ID AB06958 standard; protein; 105 AA.
 DE Rat G protein-coupled receptor ZAQ ligand protein SEQ ID NO:47.

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PD WO200216607-A1.
PD 28-FEB-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 91.9%; Score 541; DB 5; Length 105;
Best Local Similarity 88.6%; Pred. No. 4.9e-49;
RESULT 452
ID ADD69158 standard; protein; 105 AA.
DE Rat ZAQ-related protein - SEQ ID 136.
PD WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 91.9%; Score 541; DB 7; Length 105;
Best Local Similarity 88.6%; Pred. No. 4.9e-49;
RESULT 453
ID ADS86491 standard; protein; 105 AA.
DE Rat ZAQ ligand protein related to eating disorders & obesity Seq 23.
PD WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 91.9%; Score 541; DB 8; Length 105;
Best Local Similarity 88.6%; Pred. No. 4.9e-49;
RESULT 454
ID ABB99152 standard; protein; 105 AA.
DE Rat ZAQ protein.
PD WO200262996-A1.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 91.5%; Score 539; DB 5; Length 105;
Best Local Similarity 88.6%; Pred. No. 7.9e-49;
RESULT 455
ID ABB6957 standard; protein; 105 AA.
DE Rat G protein-coupled receptor ZAQ ligand protein SEQ ID NO:45.
PD WO200216607-A1.
PD 28-FEB-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 91.5%; Score 539; DB 5; Length 105;
Best Local Similarity 88.6%; Pred. No. 7.9e-49;
RESULT 456
ID ADD69156 standard; protein; 105 AA.
DE Rat ZAQ-related protein - SEQ ID 134.
PD WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 91.5%; Score 539; DB 7; Length 105;
Best Local Similarity 88.6%; Pred. No. 7.9e-49;
RESULT 457
ID ADS86489 standard; protein; 105 AA.
DE Rat ZAQ ligand protein related to eating disorders & obesity Seq 21.
PD WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 91.5%; Score 539; DB 8; Length 105;
Best Local Similarity 88.6%; Pred. No. 7.9e-49;
RESULT 458
ID ABB99148 standard; protein; 105 AA.
DE Mouse ZAQ protein.
PD WO200262996-A1.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 88.5%; Score 521; DB 5; Length 105;
Best Local Similarity 84.8%; Pred. No. 6.2e-47;
RESULT 459
ID ADP69129 standard; protein; 105 AA.
DE Murine ZAQ-related protein - SEQ ID 107.
PD WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 88.5%; Score 521; DB 7; Length 105;
Best Local Similarity 84.8%; Pred. No. 6.2e-47;
RESULT 460
ID ADS00466 standard; protein; 105 AA.
DE Murine EG-VEGF, SEQ ID 10.
PD WO2004081229-A2.

PD 23-SEP-2004.
PA (GETH) GENENTECH INC.
Query Match 88.5%; Score 521; DB 8; Length 105;
Best Local Similarity 84.8%; Pred. No. 6.2e-47;
RESULT 461
ID ADS86479 standard; protein; 105 AA.
DE Murine ZAQ ligand protein related to eating disorders & obesity Seq 11.
PD WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 88.5%; Score 521; DB 8; Length 105;
Best Local Similarity 84.8%; Pred. No. 6.2e-47;
RESULT 462
ID ABJ05340 standard; protein; 125 AA.
DE Target fusion peptide production method-related protein #3.
PD WO200236762-A1.
PD 10-MAY-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 85.1%; Score 501; DB 5; Length 125;
Best Local Similarity 98.9%; Pred. No. 9.6e-45;
RESULT 463
ID ABJ05339 standard; protein; 130 AA.
DE Human PTH(1-34)-ZAQ ligand fusion protein.
PD WO200236762-A1.
PD 10-MAY-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 85.1%; Score 501; DB 5; Length 130;
Best Local Similarity 98.9%; Pred. No. 1e-44;
RESULT 464
ID AAB70146 standard; protein; 86 AA.
DE Human G protein-coupled receptor protein-related sequence #2.
PD WO200116309-A1.
PD 08-MAR-2001.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 84.6%; Score 498; DB 4; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.3e-44;
RESULT 465
ID ABB76801 standard; protein; 86 AA.
DE Human ZAQ-1.
PD WO200208417-A1.
PD 31-JAN-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 84.6%; Score 498; DB 5; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.3e-44;
RESULT 466
ID ABJ05338 standard; protein; 86 AA.
DE Human ZAQ protein ligand.
PD WO200236762-A1.
PD 10-MAY-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 84.6%; Score 498; DB 5; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.3e-44;
RESULT 467
ID AAO15529 standard; protein; 86 AA.
DE Human physiologically-active ZAQ ligand-related protein 4.
PD WO200257443-A1.
PD 25-JUL-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 84.6%; Score 498; DB 5; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.3e-44;
RESULT 468
ID ABB06306 standard; protein; 86 AA.
DE Human G protein-coupled receptor ZAQ ligand protein SEQ ID NO:21.
PD WO200206483-A1.
PD 24-JAN-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 84.6%; Score 498; DB 5; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.3e-44;
RESULT 469
ID AAE24383 standard; protein; 86 AA.
DE Human prokineticin 1 mature protein.
PD WO200236625-A2.
PD 10-MAY-2002.

PA (REGC) UNIV CALIFORNIA.
 Query Match 84.6%; Score 498; DB 5; Length 86;
 Best Local Similarity 100.0%; Pred. No. 1.3e-44;
 RESULT 470
 ID AED00599 standard; protein; 86 AA.
 DE Partial human prokineticin 1 (PK1) SEQ ID NO 11.
 PN WO2005091925-A2.
 PD 06-OCT-2005.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 84.6%; Score 498; DB 9; Length 86;
 Best Local Similarity 100.0%; Pred. No. 1.3e-44;
 RESULT 471
 ID ADO05360 standard; protein; 86 AA.
 DE Human prokineticin 1 (PK1), SEQ ID NO:9.
 PN WO2003088904-A2.
 PD 30-OCT-2003.
 PA (TAKE) TAKEDA CHEM IND LTD.
 Query Match 84.6%; Score 498; DB 7; Length 86;
 Best Local Similarity 100.0%; Pred. No. 1.3e-44;
 RESULT 472
 ID ADR24003 standard; protein; 86 AA.
 DE Human ZAQ-1 ligand protein #1.
 PN WO2004065419-A1.
 PD 05-AUG-2004.
 PA (TAKE) TAKEDA CHEM IND LTD.
 Query Match 84.6%; Score 498; DB 8; Length 86;
 Best Local Similarity 100.0%; Pred. No. 1.3e-44;
 RESULT 473
 ID ADR24003 standard; protein; 86 AA.
 DE Human ZAQ-1 ligand protein #1.
 PN WO2004065419-A1.
 PD 05-AUG-2004.
 PA (TAKE) TAKEDA CHEM IND LTD.
 Query Match 84.6%; Score 498; DB 8; Length 86;
 Best Local Similarity 100.0%; Pred. No. 1.3e-44;
 RESULT 474
 ID ADS86471 standard; protein; 86 AA.
 DE Human ZAQ ligand protein related to eating disorders & obesity Seq 3.
 PN WO2004084945-A1.
 PD 07-OCT-2004.
 PA (TAKE) TAKEDA CHEM IND LTD.
 Query Match 84.6%; Score 498; DB 8; Length 86;
 Best Local Similarity 100.0%; Pred. No. 1.3e-44;
 RESULT 475
 ID ADS75494 standard; protein; 86 AA.
 DE Human prokineticin 1 receptor protein.
 PN WO2004087054-A2.
 PD 14-OCT-2004.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 84.6%; Score 498; DB 8; Length 86;
 Best Local Similarity 100.0%; Pred. No. 1.3e-44;
 RESULT 476
 ID ADM00759 standard; protein; 86 AA.
 DE Amino acid sequence of human prokineticin 1 (PK1).
 PN WO2004113361-A2.
 PD 29-DEC-2004.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 84.6%; Score 498; DB 9; Length 86;
 Best Local Similarity 100.0%; Pred. No. 1.3e-44;
 RESULT 477
 ID ADZ58575 standard; protein; 86 AA.
 DE Human ZAQ-1 amino acid sequence - SEQ ID 2.
 PN WO2005037870-A1.
 PD 28-APR-2005.
 PA (TAKE) TAKEDA PHARM CO LTD.
 Query Match 84.6%; Score 498; DB 9; Length 86;
 Best Local Similarity 100.0%; Pred. No. 1.3e-44;
 RESULT 478
 ID AEB45594 standard; protein; 86 AA.
 DE Human Zven2 protein fragment.
 PN US2005153322-A1.
 PD 14-JUL-2005.
 PA (ZYMO) ZYMOGENETICS INC.

Query Match 84.6%; Score 498; DB 9; Length 86;
 Best Local Similarity 100.0%; Pred. No. 1.3e-44;
 RESULT 479
 ID AED00599 standard; protein; 86 AA.
 DE Partial human prokineticin 1 (PK1) SEQ ID NO 11.
 PN WO2005091925-A2.
 PD 06-OCT-2005.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 84.6%; Score 498; DB 9; Length 86;
 Best Local Similarity 100.0%; Pred. No. 1.3e-44;
 RESULT 480
 ID AEJ43367 standard; protein; 86 AA.
 DE Human prokineticin 1 (PK1) protein, SEQ ID NO: 9.
 PN US2006172335-A1.
 PD 03-AUG-2006.
 PA (ZHOU/) ZHOU Q.
 PA (BULL/) BULLOCK C M.
 PA (STEG/) STEGEL J.
 Query Match 84.6%; Score 498; DB 10; Length 86;
 Best Local Similarity 100.0%; Pred. No. 1.3e-44;
 RESULT 481
 ID AER60512 standard; protein; 86 AA.
 DE Human prokineticin 1.
 PN WO2006102112-A2.
 PD 28-SEP-2006.
 PA (JANC) JANSSEN PHARM NV.
 Query Match 84.6%; Score 498; DB 10; Length 86;
 Best Local Similarity 100.0%; Pred. No. 1.3e-44;
 RESULT 482
 ID AEL00449 standard; protein; 86 AA.
 DE Human human prokineticin-1 ligand #1.
 PN WO2006104713-A1.
 PD 05-OCT-2006.
 PA (JANC) JANSSEN PHARM NV.
 PA (MISK/) MISKOWSKI T A.
 Query Match 84.6%; Score 498; DB 10; Length 86;
 Best Local Similarity 100.0%; Pred. No. 1.3e-44;
 RESULT 483
 ID AAE24395 standard; protein; 87 AA.
 DE Human prokineticin 1 mutant protein #4.
 PN WO200236625-A2.
 PD 10-MAY-2002.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 84.6%; Score 498; DB 5; Length 87;
 Best Local Similarity 100.0%; Pred. No. 1.4e-44;
 RESULT 484
 ID ADS75509 standard; protein; 87 AA.
 DE Prokineticin receptor antagonist Met PK1.
 PN WO2004087054-A2.
 PD 14-OCT-2004.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 84.6%; Score 498; DB 8; Length 87;
 Best Local Similarity 100.0%; Pred. No. 1.4e-44;
 RESULT 485
 ID AAE24392 standard; protein; 89 AA.
 DE Human prokineticin 1 mutant protein #1.
 PN WO200236625-A2.
 PD 10-MAY-2002.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 84.6%; Score 498; DB 5; Length 89;
 Best Local Similarity 100.0%; Pred. No. 1.4e-44;
 RESULT 486
 ID ADS75506 standard; protein; 89 AA.
 DE Prokineticin receptor related synthetic construct protein, SEQ ID 15.
 PN WO2004087054-A2.
 PD 14-OCT-2004.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 84.6%; Score 498; DB 8; Length 89;
 Best Local Similarity 100.0%; Pred. No. 1.4e-44;
 RESULT 487
 ID AAB70145 standard; protein; 86 AA.
 DE Human G protein-coupled receptor protein-related sequence #1.
 PN WO200116309-A1.

PD 08-MAR-2001.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 84.4%; Score 497; DB 4; Length 86;
Best Local Similarity 98.8%; Pred. No. 1.7e-44;
RESULT 488
ID AAO15528 standard; protein; 86 AA.
DE Human physiologically-active ZAQ ligand-related protein 3.
PN WO200257443-A1.
PD 25-JUL-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 84.4%; Score 497; DB 5; Length 86;
Best Local Similarity 98.8%; Pred. No. 1.7e-44;
RESULT 489
ID ABB06305 standard; protein; 86 AA.
DE Human G protein-coupled receptor ZAQ ligand protein SEQ ID NO:20.
PN WO200206483-A1.
PD 24-JAN-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 84.4%; Score 497; DB 5; Length 86;
Best Local Similarity 98.8%; Pred. No. 1.7e-44;
RESULT 490
ID ADD69103 standard; protein; 86 AA.
DE Human ZAQ-related protein - SEQ ID 81.
PN WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 84.4%; Score 497; DB 7; Length 86;
Best Local Similarity 98.8%; Pred. No. 1.7e-44;
RESULT 491
ID ADR24004 standard; protein; 86 AA.
DE Human ZAQ-1 ligand protein #2.
PN WO2004065419-A1.
PD 05-AUG-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 84.4%; Score 497; DB 8; Length 86;
Best Local Similarity 98.8%; Pred. No. 1.7e-44;
RESULT 492
ID ADS86469 standard; protein; 86 AA.
DE Human ZAQ ligand protein related to eating disorders & obesity Seq 1.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 84.4%; Score 497; DB 8; Length 86;
Best Local Similarity 98.8%; Pred. No. 1.7e-44;
RESULT 493
ID ADZ58576 standard; protein; 86 AA.
DE Human ZAQ-1 amino acid sequence - SEQ ID 3.
PN WO2005037870-A1.
PD 28-APR-2005.
PA (TAKE) TAKEDA PHARM CO LTD.
Query Match 84.4%; Score 497; DB 9; Length 86;
Best Local Similarity 98.8%; Pred. No. 1.7e-44;
RESULT 494
ID AAE24393 standard; protein; 85 AA.
DE Human prokineticin 1 mutant protein #2.
PN WO200236625-A2.
PD 10-MAY-2002.
PA (REGC) UNIV CALIFORNIA.
Query Match 83.9%; Score 494; DB 5; Length 85;
Best Local Similarity 100.0%; Pred. No. 3.5e-44;
RESULT 495
ID ADS7507 standard; protein; 85 AA.
DE Prokineticin receptor antagonist dela-PK1.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 83.9%; Score 494; DB 8; Length 85;
Best Local Similarity 100.0%; Pred. No. 3.5e-44;
RESULT 496
ID ADS75511 standard; protein; 86 AA.
DE Prokineticin receptor antagonist MV PK1.
PN WO2004087054-A2.
PD 14-OCT-2004.

PA (REGC) UNIV CALIFORNIA.
Query Match 83.9%; Score 494; DB 8; Length 86;
Best Local Similarity 100.0%; Pred. No. 3.5e-44;
RESULT 497
ID AAE24394 standard; protein; 86 AA.
DE Human prokineticin 1 mutant protein #3.
PN WO200236625-A2.
PD 10-MAY-2002.
PA (REGC) UNIV CALIFORNIA.
Query Match 81.2%; Score 478; DB 5; Length 86;
Best Local Similarity 95.3%; Pred. No. 1.7e-42;
RESULT 498
ID ADS75508 standard; protein; 86 AA.
DE Prokineticin receptor related synthetic construct protein, SEQ ID 17.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 81.2%; Score 478; DB 8; Length 86;
Best Local Similarity 95.3%; Pred. No. 1.7e-42;
RESULT 499
ID ADZ88902 standard; protein; 82 AA.
DE Human prokineticin 1.
PN WO2005042717-A2.
PD 12-MAY-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 80.8%; Score 476; DB 9; Length 82;
Best Local Similarity 100.0%; Pred. No. 2.7e-42;
RESULT 500
ID AEX60513 standard; protein; 82 AA.
DE Human prokineticin 1 (C-terminal truncation).
PN WO2006102112-A2.
PD 28-SEP-2006.
PA (JANC) JANSSEN PHARM NV.
Query Match 80.8%; Score 476; DB 10; Length 82;
Best Local Similarity 100.0%; Pred. No. 2.7e-42;
RESULT 501
ID AEL00450 standard; protein; 82 AA.
DE Human prokineticin-1 ligand #2.
PN WO2006104713-A1.
PD 05-OCT-2006.
PA (JANC) JANSSEN PHARM NV.
Query Match 80.8%; Score 476; DB 10; Length 82;
Best Local Similarity 100.0%; Pred. No. 2.7e-42;
RESULT 502
ID ABB99154 standard; protein; 86 AA.
DE Rat ZAQ protein.
PN WO200262996-A1.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 80.3%; Score 473; DB 5; Length 86;
Best Local Similarity 91.9%; Pred. No. 5.8e-42;
RESULT 503
ID ABB06959 standard; protein; 86 AA.
DE Rat G protein-coupled receptor ZAQ ligand protein SEQ ID NO:49.
PN WO200216607-A1.
PD 28-FEB-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 80.3%; Score 473; DB 5; Length 86;
Best Local Similarity 91.9%; Pred. No. 5.8e-42;
RESULT 504
ID ADD69160 standard; protein; 86 AA.
DE Rat ZAQ-related protein - SEQ ID 138.
PN WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 80.3%; Score 473; DB 7; Length 86;
Best Local Similarity 91.9%; Pred. No. 5.8e-42;
RESULT 505
ID ADN43261 standard; protein; 86 AA.
DE Amino acid sequence of rat prokineticin 1 (PK1).
PN WO2004032851-A2.
PD 22-APR-2004.

PA (REGC) UNIV CALIFORNIA.
Query Match 80.3%; Score 473; DB 8; Length 86;
Best Local Similarity 91.9%; Pred. No. 5.8e-42;
RESULT 506
ID ADS86481 standard; protein; 86 AA.
DE Rat ZAQ ligand protein related to eating disorders & obesity Seq 13.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 80.3%; Score 473; DB 8; Length 86;
Best Local Similarity 91.9%; Pred. No. 5.8e-42;
RESULT 507
ID ADS75521 standard; protein; 86 AA.
DE Modified rat prokineticin 1 receptor, SEQ ID 30.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 80.3%; Score 473; DB 8; Length 86;
Best Local Similarity 91.9%; Pred. No. 5.8e-42;
RESULT 508
ID ABB99156 standard; protein; 86 AA.
DE Rat ZAQ protein.
PN WO200262996-A1.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 79.6%; Score 469; DB 5; Length 86;
Best Local Similarity 90.7%; Pred. No. 1.5e-41;
RESULT 509
ID ABB06961 standard; protein; 86 AA.
DE Rat G protein-coupled receptor ZAQ ligand protein SEQ ID NO:53.
PN WO200216607-A1.
PD 28-FEB-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 79.6%; Score 469; DB 5; Length 86;
Best Local Similarity 90.7%; Pred. No. 1.5e-41;
RESULT 510
ID ADD69164 standard; protein; 86 AA.
DE Rat ZAQ-related protein - SEQ ID 142.
PN WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 79.6%; Score 469; DB 7; Length 86;
Best Local Similarity 90.7%; Pred. No. 1.5e-41;
RESULT 511
ID ADS86485 standard; protein; 86 AA.
DE Rat ZAQ ligand protein related to eating disorders & obesity Seq 17.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 79.6%; Score 469; DB 8; Length 86;
Best Local Similarity 90.7%; Pred. No. 1.5e-41;
RESULT 512
ID ABB99155 standard; protein; 86 AA.
DE Rat ZAQ protein.
PN WO200262996-A1.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 79.3%; Score 467; DB 5; Length 86;
Best Local Similarity 90.7%; Pred. No. 2.5e-41;
RESULT 513
ID ABB06960 standard; protein; 86 AA.
DE Rat G protein-coupled receptor ZAQ ligand protein SEQ ID NO:51.
PN WO200216607-A1.
PD 28-FEB-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 79.3%; Score 467; DB 5; Length 86;
Best Local Similarity 90.7%; Pred. No. 2.5e-41;
RESULT 514
ID ADD69162 standard; protein; 86 AA.
DE Rat ZAQ-related protein - SEQ ID 140.
PN WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.

Query Match 79.3%; Score 467; DB 7; Length 86;
Best Local Similarity 90.7%; Pred. No. 2.5e-41;
RESULT 515
ID ADS86483 standard; protein; 86 AA.
DE Rat ZAQ ligand protein related to eating disorders & obesity Seq 15.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 79.3%; Score 467; DB 8; Length 86;
Best Local Similarity 90.7%; Pred. No. 2.5e-41;
RESULT 516
ID ABB99149 standard; protein; 86 AA.
DE Mouse ZAQ protein.
PN WO200262996-A1.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 77.2%; Score 455; DB 5; Length 86;
Best Local Similarity 88.4%; Pred. No. 4.6e-40;
RESULT 517
ID ADD69131 standard; protein; 86 AA.
DE Murine ZAQ-related protein - SEQ ID 109.
PN WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 77.2%; Score 455; DB 7; Length 86;
Best Local Similarity 88.4%; Pred. No. 4.6e-40;
RESULT 518
ID ADO05361 standard; protein; 86 AA.
DE Mouse prokineticin 1 (PK1), SEQ ID NO:10.
PN WO2003088904-A2.
PD 30-OCT-2003.
PA (REGC) UNIV CALIFORNIA.
Query Match 77.2%; Score 455; DB 7; Length 86;
Best Local Similarity 88.4%; Pred. No. 4.6e-40;
RESULT 519
ID ADM43259 standard; protein; 86 AA.
DE Amino acid sequence of murine prokineticin 1 (PK1).
PN WO2004032851-A2.
PD 22-APR-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 77.2%; Score 455; DB 8; Length 86;
Best Local Similarity 88.4%; Pred. No. 4.6e-40;
RESULT 520
ID ADS86477 standard; protein; 86 AA.
DE Murine ZAQ ligand protein related to eating disorders & obesity Seq 9.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 77.2%; Score 455; DB 8; Length 86;
Best Local Similarity 88.4%; Pred. No. 4.6e-40;
RESULT 521
ID ADS75519 standard; protein; 86 AA.
DE Modified mouse prokineticin 1 receptor, SEQ ID 28.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 77.2%; Score 455; DB 8; Length 86;
Best Local Similarity 88.4%; Pred. No. 4.6e-40;
RESULT 522
ID ADM00760 standard; protein; 86 AA.
DE Amino acid sequence of murine prokineticin 1 (PK1).
PN WO2004113361-A2.
PD 29-DEC-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 77.2%; Score 455; DB 9; Length 86;
Best Local Similarity 88.4%; Pred. No. 4.6e-40;
RESULT 523
ID ADZ88903 standard; protein; 86 AA.
DE Mouse prokineticin 1.
PN WO2005042717-A2.
PD 12-MAY-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 77.2%; Score 455; DB 9; Length 86;

Best Local Similarity 88.4%; Pred. No. 4.6e-40;
RESULT 524
ID AED0600 standard; protein; 86 AA.
DE Mouse prokineticin 1 (PK1) SEQ ID NO 12.
PN WO2005091925-A2.
PD 06-OCT-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 77.2%; Score 455; DB 9; Length 86;
Best Local Similarity 88.4%; Pred. No. 4.6e-40;
RESULT 525
ID AEJ43368 standard; protein; 86 AA.
DE Mouse prokineticin 1 (PK1) protein, SEQ ID NO: 10.
PN US2006172935-A1.
PD 03-AUG-2006.
PA (ZHOU/) ZHOU Q.
PA (BULL/) BULLOCK C M.
PA (SIEG/) SIEGEL J.
Query Match 77.2%; Score 455; DB 10; Length 86;
Best Local Similarity 88.4%; Pred. No. 4.6e-40;
RESULT 526
ID AAY1745 standard; protein; 81 AA.
DE Human 5' EST secreted protein SEQ ID NO: 345.
PN WO9906550-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 76.7%; Score 452; DB 2; Length 81;
Best Local Similarity 98.8%; Pred. No. 8.9e-40;
RESULT 527
ID AAG00617 standard; protein; 80 AA.
DE Human secreted protein, SEQ ID NO: 4698.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 76.1%; Score 448; DB 3; Length 80;
Best Local Similarity 98.8%; Pred. No. 2.3e-39;
RESULT 528
ID AAE24391 standard; protein; 86 AA.
DE Human prokineticin chimera 21 protein.
PN WO200236625-A2.
PD 10-MAY-2002.
PA (REGC) UNIV CALIFORNIA.
Query Match 70.1%; Score 413; DB 5; Length 86;
Best Local Similarity 76.7%; Pred. No. 1.2e-35;
RESULT 529
ID AD005372 standard; protein; 86 AA.
DE PK2/PK1 chimeric protein, SEQ ID NO:21.
PN WO200308904-A2.
PD 30-OCT-2003.
PA (REGC) UNIV CALIFORNIA.
Query Match 70.1%; Score 413; DB 7; Length 86;
Best Local Similarity 76.7%; Pred. No. 1.2e-35;
RESULT 530
ID ADN43267 standard; protein; 86 AA.
DE Amino acid sequence of human prokineticin 2 (PK2)/PK1 chimera.
PN WO2004032851-A2.
PD 22-APR-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 70.1%; Score 413; DB 8; Length 86;
Best Local Similarity 76.7%; Pred. No. 1.2e-35;
RESULT 531
ID ADS75505 standard; protein; 86 AA.
DE Modified human prokineticin chimeric receptor, PK2-PK1.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 70.1%; Score 413; DB 8; Length 86;
Best Local Similarity 76.7%; Pred. No. 1.2e-35;
RESULT 532
ID ADW00765 standard; protein; 86 AA.
DE Amino acid sequence of a PK2/PK1 chimera.
PN WO2004113361-A2.
PD 29-DEC-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 70.1%; Score 413; DB 8; Length 86;
Best Local Similarity 76.7%; Pred. No. 1.2e-35;
RESULT 533
ID AED0600 standard; protein; 86 AA.
DE Mouse prokineticin 1 (PK1) SEQ ID NO 12.
PN WO2005091925-A2.
PD 06-OCT-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 77.2%; Score 455; DB 9; Length 86;
Best Local Similarity 88.4%; Pred. No. 4.6e-40;
RESULT 524
ID AED0600 standard; protein; 86 AA.
DE Mouse prokineticin 1 (PK1) SEQ ID NO 12.
PN WO2005091925-A2.
PD 06-OCT-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 77.2%; Score 455; DB 9; Length 86;
Best Local Similarity 88.4%; Pred. No. 4.6e-40;
RESULT 525
ID AEJ43368 standard; protein; 86 AA.
DE Mouse prokineticin 1 (PK1) protein, SEQ ID NO: 10.
PN US2006172935-A1.
PD 03-AUG-2006.
PA (ZHOU/) ZHOU Q.
PA (BULL/) BULLOCK C M.
PA (SIEG/) SIEGEL J.
Query Match 77.2%; Score 455; DB 10; Length 86;
Best Local Similarity 88.4%; Pred. No. 4.6e-40;
RESULT 526
ID AAY1745 standard; protein; 81 AA.
DE Human 5' EST secreted protein SEQ ID NO: 345.
PN WO9906550-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 76.7%; Score 452; DB 2; Length 81;
Best Local Similarity 98.8%; Pred. No. 8.9e-40;
RESULT 527
ID AAG00617 standard; protein; 80 AA.
DE Human secreted protein, SEQ ID NO: 4698.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 76.1%; Score 448; DB 3; Length 80;
Best Local Similarity 98.8%; Pred. No. 2.3e-39;
RESULT 528
ID AAE24391 standard; protein; 86 AA.
DE Human prokineticin chimera 21 protein.
PN WO200236625-A2.
PD 10-MAY-2002.
PA (REGC) UNIV CALIFORNIA.
Query Match 70.1%; Score 413; DB 5; Length 86;
Best Local Similarity 76.7%; Pred. No. 1.2e-35;
RESULT 529
ID AD005372 standard; protein; 86 AA.
DE PK2/PK1 chimeric protein, SEQ ID NO:21.
PN WO200308904-A2.
PD 30-OCT-2003.
PA (REGC) UNIV CALIFORNIA.
Query Match 70.1%; Score 413; DB 7; Length 86;
Best Local Similarity 76.7%; Pred. No. 1.2e-35;
RESULT 530
ID ADN43267 standard; protein; 86 AA.
DE Amino acid sequence of human prokineticin 2 (PK2)/PK1 chimera.
PN WO2004032851-A2.
PD 22-APR-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 70.1%; Score 413; DB 8; Length 86;
Best Local Similarity 76.7%; Pred. No. 1.2e-35;
RESULT 531
ID ADS75505 standard; protein; 86 AA.
DE Modified human prokineticin chimeric receptor, PK2-PK1.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 70.1%; Score 413; DB 8; Length 86;
Best Local Similarity 76.7%; Pred. No. 1.2e-35;
RESULT 532
ID ADW00765 standard; protein; 86 AA.
DE Amino acid sequence of a PK2/PK1 chimera.
PN WO2004113361-A2.
PD 29-DEC-2004.
PA (REGC) UNIV CALIFORNIA.

Query Match 70.1%; Score 413; DB 9; Length 86;
Best Local Similarity 76.7%; Pred. No. 1.2e-35;
RESULT 533
ID ADZ88908 standard; protein; 86 AA.
DE Human prokineticin 2/prokineticin 1 chimera.
PN WO2005042717-A2.
PD 12-MAY-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 70.1%; Score 413; DB 9; Length 86;
Best Local Similarity 76.7%; Pred. No. 1.2e-35;
RESULT 534
ID AED06005 standard; protein; 86 AA.
DE Human PK2-PK1 chimera SEQ ID NO 17.
PN WO2005091925-A2.
PD 06-OCT-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 70.1%; Score 413; DB 9; Length 86;
Best Local Similarity 76.7%; Pred. No. 1.2e-35;
RESULT 535
ID AEJ43379 standard; protein; 86 AA.
DE Human PK1 exons 1 and 2 - PK2 exon 3 fusion protein.
PN US2006172935-A1.
PD 03-AUG-2006.
PA (ZHOU/) ZHOU Q.
PA (BULL/) BULLOCK C M.
PA (SIEG/) SIEGEL J.
Query Match 70.1%; Score 413; DB 10; Length 86;
Best Local Similarity 76.7%; Pred. No. 1.2e-35;
RESULT 536
ID AAE24390 standard; protein; 81 AA.
DE Human prokineticin chimera 12 protein.
PN WO200236625-A2.
PD 10-MAY-2002.
PA (REGC) UNIV CALIFORNIA.
Query Match 63.8%; Score 376; DB 5; Length 81;
Best Local Similarity 84.4%; Pred. No. 9e-32;
RESULT 537
ID AD005371 standard; protein; 81 AA.
DE PK1/PK2 chimeric protein, SEQ ID NO:20.
PN WO200308904-A2.
PD 30-OCT-2003.
PA (REGC) UNIV CALIFORNIA.
Query Match 63.8%; Score 376; DB 7; Length 81;
Best Local Similarity 84.4%; Pred. No. 9e-32;
RESULT 538
ID ADN43266 standard; protein; 81 AA.
DE Amino acid sequence of human prokineticin 1 (PK1)/PK2 chimera.
PN WO2004032851-A2.
PD 22-APR-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 63.8%; Score 376; DB 8; Length 81;
Best Local Similarity 84.4%; Pred. No. 9e-32;
RESULT 539
ID ADS75504 standard; protein; 81 AA.
DE Modified human prokineticin chimeric receptor, PK1-PK2.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 63.8%; Score 376; DB 8; Length 81;
Best Local Similarity 84.4%; Pred. No. 9e-32;
RESULT 540
ID ADW00764 standard; protein; 81 AA.
DE Amino acid sequence of a PK1/PK2 chimera.
PN WO2004113361-A2.
PD 29-DEC-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 63.8%; Score 376; DB 9; Length 81;
Best Local Similarity 84.4%; Pred. No. 9e-32;
RESULT 541
ID ADZ88907 standard; protein; 81 AA.
DE Human prokineticin 1/prokineticin 2 chimera.
PN WO2005042717-A2.
PD 12-MAY-2005.

PA (REGC) UNIV CALIFORNIA.
Query Match 63.8%; Score 376; DB 9; Length 81;
Best Local Similarity 84.4%; Pred. No. 9e-32;
RESULT 542
ID AED00604 standard; protein; 81 AA.
DE Human PK1-PK2 chimera SEQ ID NO 16.
PN WO2005091925-A2.
PD 06-OCT-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 63.8%; Score 376; DB 9; Length 81;
Best Local Similarity 84.4%; Pred. No. 9e-32;
RESULT 543
ID ASB43378 standard; protein; 81 AA.
DE Human PK1 exons 1 and 2 - PK2 exon 3 fusion protein.
PN US2006172935-A1.
PD 03-AUG-2006.
PA (ZHOU/) ZHOU Q.
PA (BULL/) BULLOCK C M.
PA (SIEG/) SIEGEL J.
Query Match 63.8%; Score 376; DB 10; Length 81;
Best Local Similarity 84.4%; Pred. No. 9e-32;
RESULT 544
ID ABG94399 standard; protein; 80 AA.
DE Dendroaspis polylepsis MITI protein.
PN WO200262344-A2.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 53.5%; Score 315; DB 5; Length 80;
Best Local Similarity 62.3%; Pred. No. 2.4e-25;
RESULT 545
ID ABH99160 standard; protein; 80 AA.
DE PolyIlepis MITI.
PN WO200262996-A1.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 53.5%; Score 315; DB 5; Length 80;
Best Local Similarity 62.3%; Pred. No. 2.4e-25;
RESULT 546
ID ABB06310 standard; protein; 80 AA.
DE Dendroaspis polylepsis MITI protein sequence SEQ ID NO:34.
PN WO200206483-A1.
PD 24-JAN-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 53.5%; Score 315; DB 5; Length 80;
Best Local Similarity 62.3%; Pred. No. 2.4e-25;
RESULT 547
ID ADD69043 standard; protein; 80 AA.
DE Dendroaspis polylepsis MITI-related protein.
PN WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 53.5%; Score 315; DB 7; Length 80;
Best Local Similarity 62.3%; Pred. No. 2.4e-25;
RESULT 548
ID ADJ71812 standard; protein; 80 AA.
DE Black mamba intestinal toxin protein.
PN WO2003040326-A2.
PD 15-MAY-2003.
PA (HYSE-) HYSEQ INC.
Query Match 53.5%; Score 315; DB 7; Length 80;
Best Local Similarity 62.3%; Pred. No. 2.4e-25;
RESULT 549
ID ADO05364 standard; protein; 80 AA.
DE Snake prokineticin orthologue MITI, SEQ ID NO:13.
PN WO2003088904-A2.
PD 30-OCT-2003.
PA (REGC) UNIV CALIFORNIA.
Query Match 53.5%; Score 315; DB 7; Length 80;
Best Local Similarity 62.3%; Pred. No. 2.4e-25;
RESULT 550
ID ADS86504 standard; protein; 80 AA.
DE D.polyIlepis MITI protein related to eating disorders & obesity Seq 36.
PN WO2004084945-A1.

PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 53.5%; Score 315; DB 8; Length 80;
Best Local Similarity 62.3%; Pred. No. 2.4e-25;
RESULT 551
ID ADW00763 standard; protein; 80 AA.
DE Amino acid sequence of snake MITI.
PN WO2004113361-A2.
PD 29-DEC-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 53.5%; Score 315; DB 9; Length 80;
Best Local Similarity 62.3%; Pred. No. 2.4e-25;
RESULT 552
ID ADZ88906 standard; protein; 80 AA.
DE Snake prokineticin 1 homologue, MITI.
PN WO2005042717-A2.
PD 12-MAY-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 53.5%; Score 315; DB 9; Length 80;
Best Local Similarity 62.3%; Pred. No. 2.4e-25;
RESULT 553
ID AED00603 standard; protein; 80 AA.
DE Snake MITI SEQ ID NO 15.
PN WO2005091925-A2.
PD 06-OCT-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 53.5%; Score 315; DB 9; Length 80;
Best Local Similarity 62.3%; Pred. No. 2.4e-25;
RESULT 554
ID AEJ43371 standard; protein; 80 AA.
DE Snake MITI protein, SEQ ID NO: 13.
PN US2006172935-A1.
PD 03-AUG-2006.
PA (ZHOU/) ZHOU Q.
PA (BULL/) BULLOCK C M.
PA (SIEG/) SIEGEL J.
Query Match 53.5%; Score 315; DB 10; Length 80;
Best Local Similarity 62.3%; Pred. No. 2.4e-25;
RESULT 555
ID ADY86167 standard; protein; 79 AA.
DE Black mamba venom protein A (VPRA), SEQ ID NO:5.
PN US2005064522-A1.
PD 24-MAR-2005.
PA (GETH) GENENTECH INC.
Query Match 52.9%; Score 311.5; DB 9; Length 79;
Best Local Similarity 63.6%; Pred. No. 5.5e-25;
RESULT 556
ID ADN43263 standard; protein; 81 AA.
DE Amino acid sequence of MITI.
PN WO2004032851-A2.
PD 22-APR-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 52.7%; Score 310.5; DB 8; Length 81;
Best Local Similarity 62.8%; Pred. No. 7.2e-25;
RESULT 557
ID ADS75503 standard; protein; 81 AA.
DE Modified black mamba prokineticin receptor, MITI.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 52.7%; Score 310.5; DB 8; Length 81;
Best Local Similarity 62.8%; Pred. No. 7.2e-25;
RESULT 558
ID ADY86166 standard; protein; 100 AA.
DE Human Bv8 homolog protein, SEQ ID NO:4.
PN US2005064522-A1.
PD 24-MAR-2005.
PA (GETH) GENENTECH INC.
Query Match 52.0%; Score 306; DB 9; Length 100;
Best Local Similarity 57.0%; Pred. No. 2.7e-24;
RESULT 559
ID AAB68426 standard; protein; 108 AA.
DE Amino acid sequence of a human Zven1 polypeptide.

PN WO200136465-A2.
 PD 25-MAY-2001.
 PA (ZYMO) ZYMOGENETICS INC.
 Query Match 51.4%; Score 303; DB 4; Length 108;
 Best Local Similarity 55.2%; Pred. No. 6e-24;
 RESULT 560
 ID ABG94397 standard; protein; 108 AA.
 DE Human GPCR ligand Bv8 protein sequence #1.
 PN WO200262944-A2.
 PD 15-AUG-2002.
 PA (TAKE) TAKEDA CHEM IND LTD.
 Query Match 51.4%; Score 303; DB 5; Length 108;
 Best Local Similarity 55.2%; Pred. No. 6e-24;
 RESULT 561
 ID AAO15531 standard; protein; 108 AA.
 DE Human physiologically-active ZAQ ligand-related protein 6.
 PN WO200257443-A1.
 PD 25-JUL-2002.
 PA (TAKE) TAKEDA CHEM IND LTD.
 Query Match 51.4%; Score 303; DB 5; Length 108;
 Best Local Similarity 55.2%; Pred. No. 6e-24;
 RESULT 562
 ID AAE24384 standard; protein; 108 AA.
 DE Human prokineticin 2 precursor protein.
 PN WO200236625-A2.
 PD 10-MAY-2002.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 51.4%; Score 303; DB 5; Length 108;
 Best Local Similarity 55.2%; Pred. No. 6e-24;
 RESULT 563
 ID ASU07602 standard; protein; 108 AA.
 DE Human ZVEN1.
 PN US6485938-B1.
 PD 26-NOV-2002.
 PA (ZYMO) ZYMOGENETICS INC.
 Query Match 51.4%; Score 303; DB 6; Length 108;
 Best Local Similarity 55.2%; Pred. No. 6e-24;
 RESULT 564
 ID AAE36789 standard; protein; 108 AA.
 DE Human Bv8 homologue splice variant protein.
 PN WO2003020892-A2.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 51.4%; Score 303; DB 6; Length 108;
 Best Local Similarity 55.2%; Pred. No. 6e-24;
 RESULT 565
 ID ADD69039 standard; protein; 108 AA.
 DE Human Bv8-related protein - SEQ ID 17.
 PN WO2003066860-A1.
 PD 14-AUG-2003.
 PA (TAKE) TAKEDA CHEM IND LTD.
 Query Match 51.4%; Score 303; DB 7; Length 108;
 Best Local Similarity 55.2%; Pred. No. 6e-24;
 RESULT 566
 ID ADF28067 standard; protein; 108 AA.
 DE Human Zven 1.
 PN US2003148317-A1.
 PD 07-AUG-2003.
 PA (ZYMO) ZYMOGENETICS INC.
 Query Match 51.4%; Score 303; DB 7; Length 108;
 Best Local Similarity 55.2%; Pred. No. 6e-24;
 RESULT 567
 ID ABG75087 standard; protein; 108 AA.
 DE Human prokineticin 2 (PROK2).
 PN WO2003083073-A2.
 PD 09-OCT-2003.
 PA (FARB) BAYER PHARM CORP.
 Query Match 51.4%; Score 303; DB 7; Length 108;
 Best Local Similarity 55.2%; Pred. No. 6e-24;
 RESULT 568
 ID ADJ71811 standard; protein; 108 AA.
 DE Human prokineticin 2 protein.
 PN WO2003040326-A2.

PD 15-MAY-2003.
 PA (HYSE-) HYSEQ INC.
 Query Match 51.4%; Score 303; DB 7; Length 108;
 Best Local Similarity 55.2%; Pred. No. 6e-24;
 RESULT 569
 ID ADN41839 standard; protein; 108 AA.
 DE Amino acid sequence of a human Zven1 polypeptide.
 PN WO2004032850-A2.
 PD 22-APR-2004.
 PA (ZYMO) ZYMOGENETICS INC.
 Query Match 51.4%; Score 303; DB 8; Length 108;
 Best Local Similarity 55.2%; Pred. No. 6e-24;
 RESULT 570
 ID ADO24421 standard; protein; 108 AA.
 DE Human PRO28691 protein SEQ ID NO:60.
 PN WO2004043397-A2.
 PD 27-MAY-2004.
 PA (GETH) GENENTECH INC.
 Query Match 51.4%; Score 303; DB 8; Length 108;
 Best Local Similarity 55.2%; Pred. No. 6e-24;
 RESULT 571
 ID ADS86957 standard; protein; 108 AA.
 DE Human Zven1 protein.
 PN WO2004031367-A2.
 PD 15-APR-2004.
 PA (ZYMO) ZYMOGENETICS INC.
 Query Match 51.4%; Score 303; DB 8; Length 108;
 Best Local Similarity 55.2%; Pred. No. 6e-24;
 RESULT 572
 ID ADS00460 standard; protein; 108 AA.
 DE Human Bv8 homologue variant #2, SEQ ID 4.
 PN WO2004081229-A2.
 PD 23-SEP-2004.
 PA (GETH) GENENTECH INC.
 Query Match 51.4%; Score 303; DB 8; Length 108;
 Best Local Similarity 55.2%; Pred. No. 6e-24;
 RESULT 573
 ID ADS86495 standard; protein; 108 AA.
 DE Human Bv8 protein related to eating disorders & obesity Seq 27.
 PN WO2004084945-A1.
 PD 07-OCT-2004.
 PA (TAKE) TAKEDA CHEM IND LTD.
 Query Match 51.4%; Score 303; DB 8; Length 108;
 Best Local Similarity 55.2%; Pred. No. 6e-24;
 RESULT 574
 ID ADS75496 standard; protein; 108 AA.
 DE Human prokineticin 1 receptor protein isoform 2.
 PN WO2004087054-A2.
 PD 14-OCT-2004.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 51.4%; Score 303; DB 8; Length 108;
 Best Local Similarity 55.2%; Pred. No. 6e-24;
 RESULT 575
 ID AEA23706 standard; protein; 108 AA.
 DE Human PRO polypeptide SEQ ID NO 248.
 PN WO2005051988-A2.
 PD 09-JUN-2005.
 PA (GETH) GENENTECH INC.
 Query Match 51.4%; Score 303; DB 9; Length 108;
 Best Local Similarity 55.2%; Pred. No. 6e-24;
 RESULT 576
 ID AEA45585 standard; protein; 108 AA.
 DE Human Zven1 protein, SEQ ID NO: 2.
 PN US2005153322-A1.
 PD 14-JUL-2005.
 PA (ZYMO) ZYMOGENETICS INC.
 Query Match 51.4%; Score 303; DB 9; Length 108;
 Best Local Similarity 55.2%; Pred. No. 6e-24;
 RESULT 577
 ID AED08085 standard; protein; 108 AA.
 DE Human Zven1 protein.
 PN US2005214800-A1.
 PD 29-SEP-2005.

PA (ZYMO) ZYMOGENETICS INC.
Query Match 51.4%; Score 303; DB 9; Length 108;
Best Local Similarity 55.2%; Pred. No. 6e-24;
RESULT 578
ID ADN41861 standard; protein; 116 AA.
DE Amino acid sequence of a human Zven1 with Glu-Glu tag and Gly linker.
PN WO2004032850-A2.
PD 22-APR-2004.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 51.4%; Score 303; DB 8; Length 116;
Best Local Similarity 55.2%; Pred. No. 6.5e-24;
RESULT 579
ID ADS86981 standard; protein; 116 AA.
DE Human Zven1 protein expressed in baculovirus cell expression system.
PN WO2004031367-A2.
PD 15-APR-2004.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 51.4%; Score 303; DB 8; Length 116;
Best Local Similarity 55.2%; Pred. No. 6.5e-24;
RESULT 580
ID ADZ88897 standard; protein; 108 AA.
DE Rhesus monkey prokineticin receptor 2.
PN WO2005042717-A2.
PD 12-MAY-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 50.9%; Score 300; DB 9; Length 108;
Best Local Similarity 55.2%; Pred. No. 1.2e-23;
RESULT 581
ID AED00594 standard; protein; 108 AA.
DE Rhesus monkey prokineticin receptor 2 (PKR2) SEQ ID NO 6.
PN WO2005091925-A2.
PD 06-OCT-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 50.9%; Score 300; DB 9; Length 108;
Best Local Similarity 55.2%; Pred. No. 1.2e-23;
RESULT 582
ID ABG94408 standard; protein; 107 AA.
DE Mouse GPCR ligand Bv8 protein.
PN WO200262944-A2.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 50.6%; Score 298; DB 5; Length 107;
Best Local Similarity 49.0%; Pred. No. 2e-23;
RESULT 583
ID ABG94401 standard; protein; 107 AA.
DE Rat GPCR ligand Bv8 protein sequence #1.
PN WO200262944-A2.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 50.6%; Score 298; DB 5; Length 107;
Best Local Similarity 54.0%; Pred. No. 2e-23;
RESULT 584
ID ABB06962 standard; protein; 107 AA.
DE Rat G protein-coupled receptor protein sequence SEQ ID NO:69.
PN WO200216607-A1.
PD 28-FEB-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 50.6%; Score 298; DB 5; Length 107;
Best Local Similarity 54.0%; Pred. No. 2e-23;
RESULT 585
ID AAE36790 standard; protein; 107 AA.
DE Mouse Bv8 homologue protein.
PN WO2003020892-A2.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 50.6%; Score 298; DB 6; Length 107;
Best Local Similarity 49.0%; Pred. No. 2e-23;
RESULT 586
ID ADD69059 standard; protein; 107 AA.
DE Rat Bv8-related protein - SEQ ID 37.
PN WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.

Query Match 50.6%; Score 298; DB 7; Length 107;
Best Local Similarity 54.0%; Pred. No. 2e-23;
RESULT 587
ID ADD69077 standard; protein; 107 AA.
DE Murine Bv8-related protein - SEQ ID 55.
PN WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 50.6%; Score 298; DB 7; Length 107;
Best Local Similarity 49.0%; Pred. No. 2e-23;
RESULT 588
ID ADS00462 standard; protein; 107 AA.
DE Murine Bv8 homologue, SEQ ID 6.
PN WO2004081229-A2.
PD 23-SEP-2004.
PA (GETH) GENENTECH INC.
Query Match 50.6%; Score 298; DB 8; Length 107;
Best Local Similarity 49.0%; Pred. No. 2e-23;
RESULT 589
ID ADS86500 standard; protein; 107 AA.
DE Rat Bv8 protein related to eating disorders & obesity Seq 32.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 50.6%; Score 298; DB 8; Length 107;
Best Local Similarity 54.0%; Pred. No. 2e-23;
RESULT 590
ID ADS86502 standard; protein; 107 AA.
DE Murine Bv8 peptide DNA related to eating disorders & obesity Seq 34.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 50.6%; Score 298; DB 8; Length 107;
Best Local Similarity 49.0%; Pred. No. 2e-23;
RESULT 591
ID AEL00451 standard; protein; 116 AA.
DE Recombinant N-terminal FLAG-tagged human prokineticin-2.
PN WO2006104713-A1.
PD 05-OCT-2006.
PA (JANC) JANSSEN PHARM NV.
PA (MISK) MISKOWSKI T A.
Query Match 49.9%; Score 294; DB 10; Length 116;
Best Local Similarity 58.2%; Pred. No. 5.8e-23;
RESULT 592
ID ABG94400 standard; protein; 80 AA.
DE C-terminal Lys truncated human GPCR ligand Bv8 protein.
PN WO200262944-A2.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 49.4%; Score 291; DB 5; Length 80;
Best Local Similarity 58.4%; Pred. No. 8.1e-23;
RESULT 593
ID ADB69044 standard; protein; 80 AA.
DE Human Bv8-related protein - SEQ ID 22.
PN WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 49.4%; Score 291; DB 7; Length 80;
Best Local Similarity 58.4%; Pred. No. 8.1e-23;
RESULT 594
ID ABG94398 standard; protein; 81 AA.
DE Human GPCR ligand Bv8 protein sequence #2.
PN WO200262944-A2.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 49.4%; Score 291; DB 5; Length 81;
Best Local Similarity 58.4%; Pred. No. 8.2e-23;
RESULT 595
ID AA015530 standard; protein; 81 AA.
DE Human physiologically-active ZAQ ligand-related protein 5.
PN WO200257443-A1.
PD 25-JUL-2002.
PA (TAKE) TAKEDA CHEM IND LTD.

Query Match 49.4%; Score 291; DB 5; Length 81;
 Best Local Similarity 58.4%; Pred. No. 8.2e-23;
 RESULT 596
 ID AAE24385 standard; protein; 81 AA.
 DE Human prokineticin 2 mature protein.
 PN WO200236625-A2.
 PD 10-MAY-2002.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 49.4%; Score 291; DB 5; Length 81;
 Best Local Similarity 58.4%; Pred. No. 8.2e-23;
 RESULT 597
 ID ADD69041 standard; protein; 81 AA.
 DE Human Bv8-related protein - SEQ ID 19.
 PN WO2003066860-A1.
 PD 14-AUG-2003.
 PA (TAKE) TAKEDA CHEM IND LTD.
 Query Match 49.4%; Score 291; DB 7; Length 81;
 Best Local Similarity 58.4%; Pred. No. 8.2e-23;
 RESULT 598
 ID ADO05356 standard; protein; 81 AA.
 DE Human major prokineticin 2 (PK2), SEQ ID NO:5.
 PN WO2003088904-A2.
 PD 30-OCT-2003.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 49.4%; Score 291; DB 7; Length 81;
 Best Local Similarity 58.4%; Pred. No. 8.2e-23;
 RESULT 599
 ID ADN43258 standard; protein; 81 AA.
 DE Amino acid sequence of human prokineticin 2 (PK2) isoform 2.
 PN WO2004032851-A2.
 PD 22-APR-2004.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 49.4%; Score 291; DB 8; Length 81;
 Best Local Similarity 58.4%; Pred. No. 8.2e-23;
 RESULT 600
 ID ADR24005 standard; protein; 81 AA.
 DE Human ZAO-1 ligand-associated protein.
 PN WO2004065419-A1.
 PD 05-AUG-2004.
 PA (TAKE) TAKEDA CHEM IND LTD.
 Query Match 49.4%; Score 291; DB 8; Length 81;
 Best Local Similarity 58.4%; Pred. No. 8.2e-23;
 RESULT 601
 ID ADS86493 standard; protein; 81 AA.
 DE Human Bv8 protein related to eating disorders & obesity Seq 25.
 PN WO2004084945-A1.
 PD 07-OCT-2004.
 PA (TAKE) TAKEDA CHEM IND LTD.
 Query Match 49.4%; Score 291; DB 8; Length 81;
 Best Local Similarity 58.4%; Pred. No. 8.2e-23;
 RESULT 602
 ID ADS75497 standard; protein; 81 AA.
 DE Human prokineticin 1 receptor protein isoform 1.
 PN WO2004087054-A2.
 PD 14-OCT-2004.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 49.4%; Score 291; DB 8; Length 81;
 Best Local Similarity 58.4%; Pred. No. 8.2e-23;
 RESULT 603
 ID ADW00755 standard; protein; 81 AA.
 DE Amino acid sequence of human prokineticin 2 (PK2).
 PN WO2004113361-A2.
 PD 29-DEC-2004.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 49.4%; Score 291; DB 9; Length 81;
 Best Local Similarity 58.4%; Pred. No. 8.2e-23;
 RESULT 604
 ID ADZ88900 standard; protein; 81 AA.
 DE Human prokineticin 2.
 PN WO2005042717-A2.
 PD 12-MAY-2005.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 49.4%; Score 291; DB 9; Length 81;

Best Local Similarity 58.4%; Pred. No. 8.2e-23;
 RESULT 605
 ID ADZ58574 standard; protein; 81 AA.
 DE Human ZAO1-2 amino acid sequence - SEQ ID 1.
 PN WO2005037870-A1.
 PD 28-APR-2005.
 PA (TAKE) TAKEDA PHARM CO LTD.
 Query Match 49.4%; Score 291; DB 9; Length 81;
 Best Local Similarity 58.4%; Pred. No. 8.2e-23;
 RESULT 606
 ID AEB45593 standard; protein; 81 AA.
 DE Human zveni protein fragment.
 PN US2005153322-A1.
 PD 14-JUL-2005.
 PA (ZYMO) ZYMOGENETICS INC.
 Query Match 49.4%; Score 291; DB 9; Length 81;
 Best Local Similarity 58.4%; Pred. No. 8.2e-23;
 RESULT 607
 ID AED00597 standard; protein; 81 AA.
 DE Human prokineticin receptor 2 (PKR2) SEQ ID NO 9.
 PN WO2005091925-A2.
 PD 06-OCT-2005.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 49.4%; Score 291; DB 9; Length 81;
 Best Local Similarity 58.4%; Pred. No. 8.2e-23;
 RESULT 608
 ID AEJ43363 standard; protein; 81 AA.
 DE Human prokineticin 2 (PK2) protein, SEQ ID NO: 5.
 PN US2006172935-A1.
 PD 03-AUG-2006.
 PA (ZHOU/) ZHOU Q.
 PA (BULL/) BULLOCK C M.
 PA (STEG/) SIEGEL J.
 Query Match 49.4%; Score 291; DB 10; Length 81;
 Best Local Similarity 58.4%; Pred. No. 8.2e-23;
 RESULT 609
 ID ADJ71813 standard; protein; 96 AA.
 DE Toad Bv8 protein.
 PN WO2003040326-A2.
 PD 15-MAY-2003.
 PA (HYSE-) HYSEQ INC.
 Query Match 48.8%; Score 287.5; DB 7; Length 96;
 Best Local Similarity 50.5%; Pred. No. 2.3e-22;
 RESULT 610
 ID ADS75502 standard; protein; 96 AA.
 DE Modified frog prokineticin receptor, Bv8.
 PN WO2004087054-A2.
 PD 14-OCT-2004.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 48.8%; Score 287.5; DB 8; Length 96;
 Best Local Similarity 50.5%; Pred. No. 2.3e-22;
 RESULT 611
 ID ADZ88901 standard; protein; 80 AA.
 DE Mouse prokineticin 2.
 PN WO2005042717-A2.
 PD 12-MAY-2005.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 48.6%; Score 286; DB 9; Length 80;
 Best Local Similarity 57.1%; Pred. No. 2.7e-22;
 RESULT 612
 ID AED00598 standard; protein; 80 AA.
 DE Mouse/rat prokineticin receptor 2 (PKR2) SEQ ID NO 10.
 PN WO2005091925-A2.
 PD 06-OCT-2005.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 48.6%; Score 286; DB 9; Length 80;
 Best Local Similarity 57.1%; Pred. No. 2.7e-22;
 RESULT 613
 ID ABG94402 standard; protein; 81 AA.
 DE Rat GPCR ligand Bv8 protein sequence #2.
 PN WO200262944-A2.
 PD 15-AUG-2002.
 PA (TAKE) TAKEDA CHEM IND LTD.

Query Match
Best Local Similarity 48.6%; Score 286; DB 5; Length 81;
RESULT 614
ID ABE06963 standard; protein; 81 AA.
DE Rat G protein-coupled receptor protein sequence SEQ ID NO:71.
PN WO200216607-A1.
PD 28-FEB-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match
Best Local Similarity 48.6%; Score 286; DB 5; Length 81;
RESULT 615
ID ADD69061 standard; protein; 81 AA.
DE Rat Bv8-related protein - SEQ ID 39.
PN WO200306860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match
Best Local Similarity 48.6%; Score 286; DB 7; Length 81;
RESULT 616
ID ADO05358 standard; protein; 81 AA.
DE Mouse major prokineticin 2 (PK2), SEQ ID NO:7.
PN WO2003088904-A2.
PD 30-OCT-2003.
PA (REGC) UNIV CALIFORNIA.
Query Match
Best Local Similarity 48.6%; Score 286; DB 7; Length 81;
RESULT 617
ID ADN43260 standard; protein; 81 AA.
DE Amino acid sequence of murine prokineticin 2 (PK2).
PN WO2004032851-A2.
PD 22-APR-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match
Best Local Similarity 48.6%; Score 286; DB 8; Length 81;
RESULT 618
ID ADN43262 standard; protein; 81 AA.
DE Amino acid sequence of rat prokineticin 2 (PK2).
PN WO2004032851-A2.
PD 22-APR-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match
Best Local Similarity 48.6%; Score 286; DB 8; Length 81;
RESULT 619
ID ADS86497 standard; protein; 81 AA.
DE Rat/ murine Bv8 protein related to eating disorders & obesity Seq 29.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match
Best Local Similarity 48.6%; Score 286; DB 8; Length 81;
RESULT 620
ID ADS75520 standard; protein; 81 AA.
DE Modified mouse prokineticin 2 receptor, SEQ ID 29.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match
Best Local Similarity 48.6%; Score 286; DB 8; Length 81;
RESULT 621
ID ADS75522 standard; protein; 81 AA.
DE Modified rat prokineticin 2 receptor, SEQ ID 31.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match
Best Local Similarity 48.6%; Score 286; DB 8; Length 81;
RESULT 622
ID ADW00757 standard; protein; 81 AA.
DE Amino acid sequence of murine prokineticin 2 (PK2).
PN WO2004113361-A2.
PD 29-DEC-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match
Best Local Similarity 48.6%; Score 286; DB 9; Length 81;
RESULT 623
ID AEU43365 standard; protein; 81 AA.
DE Mouse prokineticin 2 (PK2) protein, SEQ ID NO: 7.
PN US2006172935-A1.
PD 03-AUG-2006.
PA (ZHOU/) ZHOU Q.
PA (BULL/) BULLOCK C M.
PA (SIEG/) SIEGEL J.
Query Match
Best Local Similarity 48.6%; Score 286; DB 10; Length 81;
RESULT 624
ID ADJ71808 standard; protein; 124 AA.
DE Human Bv8 protein.
PN WO2003040326-A2.
PD 15-MAY-2003.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 48.0%; Score 282.5; DB 7; Length 124;
RESULT 625
ID AAE36788 standard; protein; 129 AA.
DE Human Bv8 homologue protein.
PN WO2003020892-A2.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 48.0%; Score 282.5; DB 6; Length 129;
RESULT 626
ID ADJ71815 standard; protein; 129 AA.
DE Human prokineticin 2 precursor protein.
PN WO2003040326-A2.
PD 15-MAY-2003.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 48.0%; Score 282.5; DB 7; Length 129;
RESULT 627
ID ADN41864 standard; protein; 129 AA.
DE Amino acid sequence of a longer human Zven1 polypeptide.
PN WO2004032850-A2.
PD 22-APR-2004.
PA (ZYMO) ZYMOGENETICS INC.
Query Match
Best Local Similarity 48.0%; Score 282.5; DB 8; Length 129;
RESULT 628
ID ADS86984 standard; protein; 129 AA.
DE Human Zven1 protein longer form.
PN WO2004031367-A2.
PD 15-APR-2004.
PA (ZYMO) ZYMOGENETICS INC.
Query Match
Best Local Similarity 48.0%; Score 282.5; DB 8; Length 129;
RESULT 629
ID ADS00458 standard; protein; 129 AA.
DE Human Bv8 homologue variant #1, SEQ ID 2.
PN WO2004081229-A2.
PD 23-SEP-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 48.0%; Score 282.5; DB 8; Length 129;
RESULT 630
ID ADN43265 standard; protein; 77 AA.
DE Amino acid sequence of a Bv8 homologue.
PN WO2004032851-A2.
PD 22-APR-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match
Best Local Similarity 47.3%; Score 278.5; DB 8; Length 77;
RESULT 631
ID ADS75523 standard; protein; 77 AA.
DE Modified toad prokineticin receptor.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.

Best Local Similarity 57.1%; Pred. No. 2.7e-22;
RESULT 623
ID AEU43365 standard; protein; 81 AA.
DE Mouse prokineticin 2 (PK2) protein, SEQ ID NO: 7.
PN US2006172935-A1.
PD 03-AUG-2006.
PA (ZHOU/) ZHOU Q.
PA (BULL/) BULLOCK C M.
PA (SIEG/) SIEGEL J.
Query Match
Best Local Similarity 48.6%; Score 286; DB 10; Length 81;
RESULT 624
ID ADJ71808 standard; protein; 124 AA.
DE Human Bv8 protein.
PN WO2003040326-A2.
PD 15-MAY-2003.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 48.0%; Score 282.5; DB 7; Length 124;
RESULT 625
ID AAE36788 standard; protein; 129 AA.
DE Human Bv8 homologue protein.
PN WO2003020892-A2.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 48.0%; Score 282.5; DB 6; Length 129;
RESULT 626
ID ADJ71815 standard; protein; 129 AA.
DE Human prokineticin 2 precursor protein.
PN WO2003040326-A2.
PD 15-MAY-2003.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 48.0%; Score 282.5; DB 7; Length 129;
RESULT 627
ID ADN41864 standard; protein; 129 AA.
DE Amino acid sequence of a longer human Zven1 polypeptide.
PN WO2004032850-A2.
PD 22-APR-2004.
PA (ZYMO) ZYMOGENETICS INC.
Query Match
Best Local Similarity 48.0%; Score 282.5; DB 8; Length 129;
RESULT 628
ID ADS86984 standard; protein; 129 AA.
DE Human Zven1 protein longer form.
PN WO2004031367-A2.
PD 15-APR-2004.
PA (ZYMO) ZYMOGENETICS INC.
Query Match
Best Local Similarity 48.0%; Score 282.5; DB 8; Length 129;
RESULT 629
ID ADS00458 standard; protein; 129 AA.
DE Human Bv8 homologue variant #1, SEQ ID 2.
PN WO2004081229-A2.
PD 23-SEP-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 48.0%; Score 282.5; DB 8; Length 129;
RESULT 630
ID ADN43265 standard; protein; 77 AA.
DE Amino acid sequence of a Bv8 homologue.
PN WO2004032851-A2.
PD 22-APR-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match
Best Local Similarity 47.3%; Score 278.5; DB 8; Length 77;
RESULT 631
ID ADS75523 standard; protein; 77 AA.
DE Modified toad prokineticin receptor.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.

Query Match 47.3%; Score 278.5; DB 8; Length 77;
Best Local Similarity 61.5%; Pred. No. 1.6e-21;
RESULT 632
ID ADJ71809 standard; protein; 128 AA.
DE Mouse Bv8 variant 1 protein.
PN WO2003040326-A2.
PD 15-MAY-2003.
PA (HYSE-) HYSEQ INC.
Query Match 47.1%; Score 277.5; DB 7; Length 128;
Best Local Similarity 40.7%; Pred. No. 3.5e-21;
RESULT 633
ID ADN43257 standard; protein; 102 AA.
DE Amino acid sequence of human prokineticin 2 (PK2) isoform 1.
PN WO2004032851-A2.
PD 22-APR-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 45.9%; Score 270.5; DB 8; Length 102;
Best Local Similarity 45.9%; Pred. No. 1.5e-20;
RESULT 634
ID ADN43264 standard; protein; 77 AA.
DE Amino acid sequence of Bv8.
PN WO2004032851-A2.
PD 22-APR-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 45.4%; Score 267.5; DB 7; Length 77;
Best Local Similarity 57.7%; Pred. No. 2.3e-20;
RESULT 635
ID ADN43264 standard; protein; 77 AA.
DE Amino acid sequence of Bv8.
PN WO2004032851-A2.
PD 22-APR-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 45.4%; Score 267.5; DB 8; Length 77;
Best Local Similarity 57.7%; Pred. No. 2.3e-20;
RESULT 636
ID ADW00761 standard; protein; 77 AA.
DE Amino acid sequence of frog Bv8.
PN WO2004113361-A2.
PD 29-DEC-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 45.4%; Score 267.5; DB 9; Length 77;
Best Local Similarity 57.7%; Pred. No. 2.3e-20;
RESULT 637
ID AD288905 standard; protein; 77 AA.
DE Frog prokineticin 1 homologue, Bv8.
PN WO2005042717-A2.
PD 12-MAY-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 45.4%; Score 267.5; DB 9; Length 77;
Best Local Similarity 57.7%; Pred. No. 2.3e-20;
RESULT 638
ID AED00602 standard; protein; 77 AA.
DE Frog Bv8 SEQ ID NO 14.
PN WO2005091925-A2.
PD 06-OCT-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 45.4%; Score 267.5; DB 9; Length 77;
Best Local Similarity 57.7%; Pred. No. 2.3e-20;
RESULT 639
ID AEJ43369 standard; protein; 77 AA.
DE Frog Bv8 protein, SEQ ID NO: 11.
PN US2006172935-A1.
PD 03-AUG-2006.
PA (ZHOU//) ZHOU Q.
PA (BULL//) BULLOCK C M.
PA (SIEG//) SIEGEL J.
Query Match 45.4%; Score 267.5; DB 10; Length 77;
Best Local Similarity 57.7%; Pred. No. 2.3e-20;
RESULT 640
ID ADO05359 standard; protein; 102 AA.
DE Mouse minor prokineticin 2 (PK2), SEQ ID NO:8.
PN WO2003088904-A2.
PD 30-OCT-2003.

PA (REGC) UNIV CALIFORNIA.
Query Match 45.1%; Score 265.5; DB 7; Length 102;
Best Local Similarity 44.9%; Pred. No. 5.1e-20;
RESULT 641
ID ADW00758 standard; protein; 102 AA.
DE Amino acid sequence of murine prokineticin 2 (PK2).
PN WO2004113361-A2.
PD 29-DEC-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 45.1%; Score 265.5; DB 9; Length 102;
Best Local Similarity 44.9%; Pred. No. 5.1e-20;
RESULT 642
ID AEJ43366 standard; protein; 102 AA.
DE Mouse prokineticin 2 (PK2) protein, SEQ ID NO: 8.
PN US2006172935-A1.
PD 03-AUG-2006.
PA (ZHOU//) ZHOU Q.
PA (BULL//) BULLOCK C M.
PA (SIEG//) SIEGEL J.
Query Match 45.1%; Score 265.5; DB 10; Length 102;
Best Local Similarity 44.9%; Pred. No. 5.1e-20;
RESULT 643
ID ADF17105 standard; peptide; 77 AA.
DE Bombina maxima neurotrophic peptide.
PN CN1390849-A.
PD 15-JAN-2003.
PA (KUNM-) KUNMING ZOOLOGY INST CHINESE ACAD SCI.
Query Match 43.2%; Score 254.5; DB 7; Length 77;
Best Local Similarity 56.4%; Pred. No. 5.4e-19;
RESULT 644
ID ADO05357 standard; protein; 100 AA.
DE Human tissue specific (testis) prokineticin 2 (PK2), SEQ ID NO:6.
PN WO2003088904-A2.
PD 30-OCT-2003.
PA (REGC) UNIV CALIFORNIA.
Query Match 42.7%; Score 251.5; DB 7; Length 100;
Best Local Similarity 44.9%; Pred. No. 1.5e-18;
RESULT 645
ID ADW00756 standard; protein; 100 AA.
DE Amino acid sequence of human prokineticin 2 (PK2).
PN WO2004113361-A2.
PD 29-DEC-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 42.7%; Score 251.5; DB 9; Length 100;
Best Local Similarity 44.9%; Pred. No. 1.5e-18;
RESULT 646
ID AEJ43364 standard; protein; 100 AA.
DE Human prokineticin 2 (PK2) protein, SEQ ID NO: 6.
PN US2006172935-A1.
PD 03-AUG-2006.
PA (ZHOU//) ZHOU Q.
PA (BULL//) BULLOCK C M.
PA (SIEG//) SIEGEL J.
Query Match 42.7%; Score 251.5; DB 10; Length 100;
Best Local Similarity 44.9%; Pred. No. 1.5e-18;
RESULT 647
ID ADO05363 standard; protein; 75 AA.
DE Toad prokineticin orthologue Bv8, SEQ ID NO:12.
PN WO2003088904-A2.
PD 30-OCT-2003.
PA (REGC) UNIV CALIFORNIA.
Query Match 42.5%; Score 250.5; DB 7; Length 75;
Best Local Similarity 56.4%; Pred. No. 1.4e-18;
RESULT 648
ID ADW00762 standard; protein; 75 AA.
DE Amino acid sequence of toad Bv8.
PN WO2004113361-A2.
PD 29-DEC-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 42.5%; Score 250.5; DB 9; Length 75;
Best Local Similarity 56.4%; Pred. No. 1.4e-18;
RESULT 649
ID AD288904 standard; protein; 75 AA.

DE Toad prokineticin 1 homologue, BV8.
 PN WO2005042717-A2.
 PD 12-MAY-2005.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 42.5%; Score 250.5; DB 9; Length 75;
 Best Local Similarity 56.4%; Pred. No. 1.4e-18;
 RESULT 650
 ID AED00601 standard; protein; 75 AA.
 DE Toad bv8 SEQ ID NO 13.
 PN WO2005091925-A2.
 PD 06-OCT-2005.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 42.5%; Score 250.5; DB 9; Length 75;
 Best Local Similarity 56.4%; Pred. No. 1.4e-18;
 RESULT 651
 ID AE43370 standard; protein; 75 AA.
 DE Toad BV8 protein, SEQ ID NO: 12.
 PN US2006172935-A1.
 PD 03-AUG-2006.
 PA (BULL/) ZHOU Q.
 PA (BULL/) BULLOCK C M.
 PA (SIEG/) SIEGEL J.
 Query Match 42.5%; Score 250.5; DB 10; Length 75;
 Best Local Similarity 56.4%; Pred. No. 1.4e-18;
 RESULT 652
 ID AD160152 standard; protein; 126 AA.
 DE Secreted polypeptide #36.
 PN WO2003025142-A2.
 PD 27-MAR-2003.
 PA (HYSE-) HYSEQ INC.
 Query Match 40.2%; Score 237; DB 7; Length 126;
 Best Local Similarity 42.6%; Pred. No. 6.4e-17;
 RESULT 653
 ID ADJ71800 standard; protein; 126 AA.
 DE Human prokineticin-like protein.
 PN WO2003040326-A2.
 PD 15-MAY-2003.
 PA (HYSE-) HYSEQ INC.
 Query Match 40.2%; Score 237; DB 7; Length 126;
 Best Local Similarity 42.6%; Pred. No. 6.4e-17;
 RESULT 654
 ID AED53711 standard; peptide; 56 AA.
 DE Amino acid sequence of human PK2beta peptide.
 PN WO2005097826-A2.
 PD 20-OCT-2005.
 PA (JANC) JANSSEN PHARM NV.
 Query Match 31.6%; Score 186; DB 9; Length 56;
 Best Local Similarity 52.7%; Pred. No. 6.4e-12;
 RESULT 655
 ID AED53712 standard; peptide; 56 AA.
 DE Amino acid sequence of human PK2beta peptide #2.
 PN WO2005097826-A2.
 PD 20-OCT-2005.
 PA (JANC) JANSSEN PHARM NV.
 Query Match 31.2%; Score 184; DB 9; Length 56;
 Best Local Similarity 57.4%; Pred. No. 1e-11;
 RESULT 656
 ID AA027072 standard; peptide; 30 AA.
 DE Monkey AXOR8 receptor N-terminal peptide, SEQ ID NO 20.
 PN GB2378183-A.
 PD 05-FEB-2003.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 Query Match 26.5%; Score 156; DB 6; Length 30;
 Best Local Similarity 90.0%; Pred. No. 4.8e-09;
 RESULT 657
 ID AE18405 standard; peptide; 24 AA.
 DE R. saharaica insulin releasing peptide #1.
 PN WO2005047316-A2.
 PD 26-MAY-2005.
 PA (UYUL-) UNIV ULSTER.
 Query Match 20.4%; Score 120; DB 9; Length 24;
 Best Local Similarity 91.3%; Pred. No. 2.4e-05;
 RESULT 658
 ID AAY44934 standard; protein; 271 AA.
 DE Human dickkopf-1 homolog 3 protein.
 PN WO200006714-A1.
 PD 10-FEB-2000.
 PA (ELIL) LILLY & CO ELI.
 Query Match 19.0%; Score 112; DB 3; Length 271;
 Best Local Similarity 32.9%; Pred. No. 0.0021;
 RESULT 659
 ID ADF28074 standard; peptide; 23 AA.
 DE Human Zven polypeptide motif #2.
 PN US2003148317-A1.
 PD 07-AUG-2003.
 PA (ZYMO) ZYMOGENETICS INC.
 Query Match 18.5%; Score 109; DB 7; Length 23;
 Best Local Similarity 73.9%; Pred. No. 0.00033;
 RESULT 660
 ID ADN41845 standard; peptide; 23 AA.
 DE Motif found in Zven1 and Zven1 polypeptides.
 PN WO2004032850-A2.
 PD 22-APR-2004.
 PA (ZYMO) ZYMOGENETICS INC.
 Query Match 18.5%; Score 109; DB 8; Length 23;
 Best Local Similarity 73.9%; Pred. No. 0.00033;
 RESULT 661
 ID ADS86964 standard; peptide; 23 AA.
 DE Human Zven protein motif #2.
 PN WO2004031367-A2.
 PD 15-APR-2004.
 PA (ZYMO) ZYMOGENETICS INC.
 Query Match 18.5%; Score 109; DB 8; Length 23;
 Best Local Similarity 73.9%; Pred. No. 0.00033;
 RESULT 662
 ID AEB45592 standard; peptide; 23 AA.
 DE Human Zven1 and Zven2 motif peptide, SEQ ID NO: 9.
 PN US2005153322-A1.
 PD 14-JUL-2005.
 PA (ZYMO) ZYMOGENETICS INC.
 Query Match 18.5%; Score 109; DB 9; Length 23;
 Best Local Similarity 73.9%; Pred. No. 0.00033;
 RESULT 663
 ID AED08092 standard; peptide; 23 AA.
 DE Human Zven1/Zven2 motif peptide - SEQ ID 9.
 PN US2005214800-A1.
 PD 29-SEP-2005.
 PA (ZYMO) ZYMOGENETICS INC.
 Query Match 18.5%; Score 109; DB 9; Length 23;
 Best Local Similarity 73.9%; Pred. No. 0.00033;
 RESULT 664
 ID AEA16257 standard; protein; 221 AA.
 DE Mouse Dickkopf-4 (Dkk-4) protein.
 PN WO2005049797-A2.
 PD 02-JUN-2005.
 PA (MERI) MERCK & CO INC.
 Query Match 18.4%; Score 108.5; DB 9; Length 221;
 Best Local Similarity 35.5%; Pred. No. 0.004;
 RESULT 665
 ID AEC06122 standard; peptide; 18 AA.
 DE Human EG-VEGF peptide (amino acids 50-67).
 PN WO2005076972-A2.
 PD 25-AUG-2005.
 PA (OHIS) UNIV OHIO STATE RES FOUND.
 Query Match 18.3%; Score 108; DB 9; Length 18;
 Best Local Similarity 100.0%; Pred. No. 0.00032;
 RESULT 666
 ID AD160388 standard; protein; 40 AA.
 DE Secreted polypeptide encoded by gene splice variant #24.
 PN WO2003025142-A2.
 PD 27-MAR-2003.
 PA (HYSE-) HYSEQ INC.
 Query Match 18.3%; Score 108; DB 7; Length 40;
 Best Local Similarity 58.1%; Pred. No. 0.00075;
 RESULT 667

ID ADJ71801 standard; protein; 40 AA.
DE Human prokineticin-like protein.
PN WO2003040326-A2.
PD 15-MAY-2003.
PA (HYSE-) HYSQ INC.

Query Match 18.3%; Score 108; DB 7; Length 40;
Best Local Similarity 58.1%; Pred. No. 0.00075;

RESULT 668
ID ADE28655 standard; protein; 161 AA.
DE Human NOV9c protein - SEQ ID 32.
PN WO2003040330-A2.
PD 15-MAY-2003.
PA (CURA-) CURAGEN CORP.

Query Match 18.3%; Score 107.5; DB 7; Length 161;
Best Local Similarity 35.5%; Pred. No. 0.0037;

RESULT 669
ID ADM93400 standard; protein; 161 AA.
DE Human NOVX polypeptide #16.
PN US2004067882-A1.

PD 08-APR-2004.
PA (ALSO/) ALSOBROOK J P.
PA (ALVA/) ALVAREZ E.
PA (ANDE/) ANDERSON D W.
PA (BARO/) BARON M.
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (CASM/) CASMAN S J.
PA (CHAP/) CHAPOVAL A.
PA (DHAN/) DHANABAL M.
PA (EDIN/) EDINGER S R.
PA (EISE/) EISEN A.
PA (ELLE/) ELLERMAN K.
PA (ETTE/) ETENBERG S.
PA (GANG/) GANGOLLI E A.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (GROS/) GROSSE W M.
PA (GUOX/) GUO X.
PA (HACK/) HACKETT C.
PA (JIWV/) JI W.

PA (KEKU/) KEKUDA R.
PA (KHRA/) KHRAMTSOV N V.
PA (LEPL/) LEPLEY D M.
PA (LILL/) LI L.
PA (MACD/) MACDOUGALL J R.
PA (MALY/) MALYANKAR U M.
PA (MAZU/) MAZUR A.
PA (MCQU/) MCQUEENEY K.
PA (MEZE/) MEZES P S.
PA (MILL/) MILLER C E.
PA (MILL/) MILLET I.
PA (MISH/) MISHRA V.
PA (PADI/) PADIGARU M.
PA (PATI/) PATTURAJAN M.
PA (PENA/) PENNA C E A.
PA (PEYM/) PEYMAN J A.
PA (RAST/) RASTELLI L.
PA (RIEG/) RIEGER D K.
PA (ROTH/) ROTHENBERG M E.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (SMIT/) SMITHSON G.
PA (SPAD/) SPADERNA S K.
PA (STAR/) STARLING G.
PA (SPYT/) SPYTEK K A.
PA (STON/) STONE D J.
PA (TCHE/) TCHERNEV V T.
PA (TWOM/) TWOMLOW N.
PA (VERN/) VERNET C A M.
PA (ZERR/) ZERRHUSEN B D.
PA (VOSS/) VOSS E Z.
PA (ZHON/) ZHONG M.

Query Match 18.3%; Score 107.5; DB 8; Length 161;

Best Local Similarity 35.5%; Pred. No. 0.0037;
RESULT 670
ID ADE28653 standard; protein; 173 AA.
DE Human NOV9b protein - SEQ ID 30.
PN WO2003040330-A2.
PD 15-MAY-2003.
PA (CURA-) CURAGEN CORP.

Query Match 18.3%; Score 107.5; DB 7; Length 173;
Best Local Similarity 35.5%; Pred. No. 0.004;

RESULT 671
ID ADM93398 standard; protein; 173 AA.
DE Human NOVX polypeptide #15.
PN US2004067882-A1.

PD 08-APR-2004.
PA (ALSO/) ALSOBROOK J P.
PA (ALVA/) ALVAREZ E.
PA (ANDE/) ANDERSON D W.
PA (BARO/) BARON M.
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (CASM/) CASMAN S J.
PA (CHAP/) CHAPOVAL A.
PA (DHAN/) DHANABAL M.
PA (EDIN/) EDINGER S R.
PA (EISE/) EISEN A.
PA (ELLE/) ELLERMAN K.
PA (ETTE/) ETENBERG S.
PA (GANG/) GANGOLLI E A.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (GROS/) GROSSE W M.
PA (GUOX/) GUO X.
PA (HACK/) HACKETT C.
PA (JIWV/) JI W.

PA (KEKU/) KEKUDA R.
PA (KHRA/) KHRAMTSOV N V.
PA (LEPL/) LEPLEY D M.
PA (LILL/) LI L.
PA (MACD/) MACDOUGALL J R.
PA (MALY/) MALYANKAR U M.
PA (MAZU/) MAZUR A.
PA (MCQU/) MCQUEENEY K.
PA (MEZE/) MEZES P S.
PA (MILL/) MILLER C E.
PA (MILL/) MILLET I.
PA (MISH/) MISHRA V.
PA (PADI/) PADIGARU M.
PA (PATI/) PATTURAJAN M.
PA (PENA/) PENNA C E A.
PA (PEYM/) PEYMAN J A.
PA (RAST/) RASTELLI L.
PA (RIEG/) RIEGER D K.
PA (ROTH/) ROTHENBERG M E.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (SMIT/) SMITHSON G.
PA (SPAD/) SPADERNA S K.
PA (STAR/) STARLING G.
PA (SPYT/) SPYTEK K A.
PA (STON/) STONE D J.
PA (TCHE/) TCHERNEV V T.
PA (TWOM/) TWOMLOW N.
PA (VERN/) VERNET C A M.
PA (ZERR/) ZERRHUSEN B D.
PA (VOSS/) VOSS E Z.
PA (ZHON/) ZHONG M.

Query Match 18.3%; Score 107.5; DB 8; Length 173;
Best Local Similarity 35.5%; Pred. No. 0.004;

RESULT 672
ID ADE28657 standard; protein; 180 AA.
DE Human NOV9d protein - SEQ ID 34.
PN WO2003040330-A2.
PD 15-MAY-2003.

PA (CURA-) CURAGEN CORP. 18.3%; Score 107.5; DB 7; Length 180;
Query Match Best Local Similarity 35.5%; Pred. No. 0.0041;
RESULT 673
ID ADM93402 standard; protein; 180 AA.
DE Human NOVX polypeptide #17.
PN US2004067882-A1.
PD 08-APR-2004.
PA (ALSO/) ALSOBROOK J P.
PA (ALVA/) ALVAREZ E.
PA (ANDE/) ANDERSON D W.
PA (BARO/) BARON M.
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (CASM/) CASMAN S J.
PA (CHAP/) CHAPOVAL A.
PA (DHAN/) DHANABAL M.
PA (EDIN/) EDINGER S R.
PA (EISE/) EISEN A.
PA (ELLE/) ELLERMAN K.
PA (ETTE/) ETENBERG S.
PA (GANG/) GANGOLLI E A.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (GROS/) GROSSE W M.
PA (GUOX/) GUO X.
PA (HACK/) HACKETT C.
PA (JIMW/) JI W.
PA (KEKU/) KEKUDA R.
PA (KHRA/) KHRAMTSOV N V.
PA (LEPL/) LEPLEY D M.
PA (LILL/) LI L.
PA (MACD/) MACDOUGALL J R.
PA (MALY/) MALYANKAR U M.
PA (MAZU/) MAZUR A.
PA (MCQU/) MCQUEENEY K.
PA (MEZE/) MEZES P S.
PA (MILL/) MILLER C E.
PA (MILLET/) MILLET I.
PA (MISH/) MISHRA V.
PA (PADI/) PADIGARU M.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENA C E A.
PA (PEYM/) PEYMAN J A.
PA (RAST/) RASTELLI L.
PA (RIEG/) RIEGER D K.
PA (ROTH/) ROTHENBERG M E.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (SMIT/) SMITHSON G.
PA (SPAD/) SPADERNA S K.
PA (STAR/) STARLING G.
PA (SPYT/) SPYTEK K A.
PA (STON/) STONE D J.
PA (TCHE/) TCHERNEV V T.
PA (TWOI/) TWOMLOW N.
PA (VERN/) VERNET C A M.
PA (ZERH/) ZERHUSEN B D.
PA (VOSS/) VOSS E Z.
PA (ZHON/) ZHONG M.
Query Match 18.3%; Score 107.5; DB 8; Length 180;
Best Local Similarity 35.5%; Pred. No. 0.0041;
RESULT 674
ID AAW73017 standard; protein; 224 AA.
DE Human cysteine-rich secreted protein CRSP-2.
PN WO9846755-A1.
PD 22-OCT-1998.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Query Match 18.3%; Score 107.5; DB 2; Length 224;
Best Local Similarity 35.5%; Pred. No. 0.0052;
RESULT 675
ID AAY92075 standard; protein; 224 AA.
DE Human DKR-4.

PN WO200018914-A2.
PD 06-APR-2000.
PA (ANGE-) AMGEN INC.
Query Match 18.3%; Score 107.5; DB 3; Length 224;
Best Local Similarity 35.5%; Pred. No. 0.0052;
RESULT 676
ID AAB08875 standard; protein; 224 AA.
DE Amino acid sequence of a human Dickkopf (Dkk)-4 protein.
PN WO200052047-A2.
PD 08-SEP-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 18.3%; Score 107.5; DB 3; Length 224;
Best Local Similarity 35.5%; Pred. No. 0.0052;
RESULT 677
ID ABU55916 standard; protein; 224 AA.
DE Human protein DKK4.
PN WO200277204-A2.
PD 03-OCT-2002.
PA (AXOR-) AXORDIA LTD.
Query Match 18.3%; Score 107.5; DB 6; Length 224;
Best Local Similarity 35.5%; Pred. No. 0.0052;
RESULT 678
ID AAE34070 standard; protein; 224 AA.
DE DKK 4 protein.
PN WO200290992-A2.
PD 14-NOV-2002.
PA (AXOR-) AXORDIA LTD.
Query Match 18.3%; Score 107.5; DB 6; Length 224;
Best Local Similarity 35.5%; Pred. No. 0.0052;
RESULT 679
ID ADE28651 standard; protein; 224 AA.
DE Human NOV9a protein - SEQ ID 28.
PN WO2003040330-A2.
PD 15-MAY-2003.
PA (CURA-) CURAGEN CORP.
Query Match 18.3%; Score 107.5; DB 7; Length 224;
Best Local Similarity 35.5%; Pred. No. 0.0052;
RESULT 680
ID ADJ68529 standard; protein; 224 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID335.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 18.3%; Score 107.5; DB 7; Length 224;
Best Local Similarity 35.5%; Pred. No. 0.0052;
RESULT 681
ID ADN39310 standard; protein; 224 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:628.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 18.3%; Score 107.5; DB 7; Length 224;
Best Local Similarity 35.5%; Pred. No. 0.0052;
RESULT 682
ID ADM93396 standard; protein; 224 AA.
DE Human NOVX polypeptide #14.
PN US2004067882-A1.
PD 08-APR-2004.
PA (ALSO/) ALSOBROOK J P.
PA (ALVA/) ALVAREZ E.
PA (ANDE/) ANDERSON D W.
PA (BARO/) BARON M.
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (CASM/) CASMAN S J.
PA (CHAP/) CHAPOVAL A.
PA (DHAN/) DHANABAL M.
PA (EDIN/) EDINGER S R.
PA (EISE/) EISEN A.
PA (ELLE/) ELLERMAN K.
PA (ETTE/) ETENBERG S.
PA (GANG/) GANGOLLI E A.

PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (GROS/) GROSSE W M.
PA (GUOX/) GUO X.
PA (HACK/) HACKETT C.
PA (JIWJ/) JI W.
PA (KEKU/) KHRAMTSOV N V.
PA (LEPL/) LEPLLEY D M.
PA (LILL/) LI L.
PA (MACD/) MACDOUGALL J R.
PA (MAZY/) MALYANKAR U M.
PA (MAZU/) MAZUR A.
PA (MCOU/) MCQUEENEY K.
PA (MEZE/) MEZES P S.
PA (MILL/) MILLER C E.
PA (MILL/) MILLET I.
PA (MISH/) MISHRA V.
PA (PADI/) PADIGARU M.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENA C E A.
PA (PEYM/) PEYMAN J A.
PA (RAST/) RASTELLI L.
PA (RIEG/) RIEGER D K.
PA (ROTH/) ROTHENBERG M E.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (SMIT/) SMITHSON G.
PA (SPAD/) SPADERNA S K.
PA (STAR/) STARLING G.
PA (SPYT/) SPYTEK K A.
PA (STON/) STONE D J.
PA (TCHE/) TCHERNEV V T.
PA (TWOM/) TWOMLOW N.
PA (VERN/) VERNET C A M.
PA (ZERH/) ZERHUSEN B D.
PA (VOSS/) VOSS E Z.
PA (ZHON/) ZHONG M.
Query Match
Best Local Similarity 18.3%; Score 107.5; DB 8; Length 224;
RESULT 683
ID AEAl6256 standard; protein; 224 AA.
DE Human Dickkopf-4 (Dkk-4) protein.
PD 02-JUN-2005.
PA (MERI) MERCK & CO INC.
Query Match
Best Local Similarity 18.3%; Score 107.5; DB 9; Length 224;
RESULT 684
ID AEAl6254 standard; protein; 224 AA.
DE Cynomolgus monkey Dickkopf-4 (cdkk-4) protein.
PD 02-JUN-2005.
PA (MERI) MERCK & CO INC.
Query Match
Best Local Similarity 18.3%; Score 107.5; DB 9; Length 224;
RESULT 685
ID AEI44169 standard; protein; 224 AA.
DE Dickkopf homolog 4, DKK4, SEQ ID 2.
PD 29-JUN-2006.
PA (UYHI-) UNIV HIROSHIMA.
Query Match
Best Local Similarity 18.3%; Score 107.5; DB 10; Length 224;
RESULT 686
ID AAW73019 standard; protein; 179 AA.
DE Human cysteine-rich secreted protein CRSP-4.
PD 22-OCT-1998.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Query Match
Best Local Similarity 17.3%; Score 102; DB 2; Length 179;
RESULT 687
ID AAB08877 standard; protein; 179 AA.
DE A partial human Dickkopf (Dkk)-2 protein.
PD 08-SEP-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 17.3%; Score 102; DB 3; Length 179;
RESULT 688
ID ADO35297 standard; protein; 179 AA.
DE Human Dkk2 carboxy terminal cysteine rich region.
PD 22-JAN-2004.
PA (LASS/) LASSAR A B.
PA (MERC/) MERCOLA M.
PA (GUPT/) GUPTA R.
PA (MARV/) MARVIN M.
PA (SCHN/) SCHNEIDER V.
PA (TZA/) TZAHOOR E.
PA (BROT/) BROTT B.
PA (SOKO/) SOKOL S.
Query Match
Best Local Similarity 17.3%; Score 102; DB 8; Length 179;
RESULT 689
ID AAY92074 standard; protein; 207 AA.
DE Human DKK-2 splice variant, DKR-2a.
PD 06-APR-2000.
PA (AMGE-) AMGEN INC.
Query Match
Best Local Similarity 17.3%; Score 102; DB 3; Length 207;
RESULT 690
ID AAY92073 standard; protein; 259 AA.
DE Human DKK-2.
PD 06-APR-2000.
PA (AMGE-) AMGEN INC.
Query Match
Best Local Similarity 17.3%; Score 102; DB 3; Length 259;
RESULT 691
ID AAY9360 standard; protein; 259 AA.
DE Human PRO1316 (UNQ682) amino acid sequence SEQ ID NO:70.
PD 09-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 17.3%; Score 102; DB 3; Length 259;
RESULT 692
ID AAB66109 standard; protein; 259 AA.
DE Protein of the invention #21.
PD 28-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 17.3%; Score 102; DB 4; Length 259;
RESULT 693
ID AAY29148 standard; protein; 259 AA.
DE Human PRO polypeptide sequence #125.
PD 20-SEP-2001.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 17.3%; Score 102; DB 4; Length 259;
RESULT 694
ID ABUS8524 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 17.3%; Score 102; DB 4; Length 259;
RESULT 695
ID ABUS8072 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PD 02-SEP-2001.

PD 13-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 696
ID AB084387 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003032112-A1.
PD 13-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 697
ID ABR66261 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003027278-A1.
PD 06-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 698
ID ABR65651 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 699
ID AB095951 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 700
ID AB082830 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 701
ID AB089951 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 702
ID ABR68200 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 703
ID AB096253 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 704
ID AB092684 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 705
ID AB008761 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;

RESULT 706
ID AB002813 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 707
ID ABR74967 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 708
ID ABR94729 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 709
ID AB085702 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 710
ID AB098862 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 711
ID AB098077 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 712
ID AB091783 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 713
ID AB089476 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 714
ID AB086317 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 715
ID AB067530 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;

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RESULT 716
ID AB080558 standard; protein; 259 AA.
DE Human PRO protein #125.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 717
ID ABR99476 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040063-A1.
PD 27-FEB-2003.
PA (AXOR-) AXORDIA LTD.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 718
ID ABR98866 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040064-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 719
ID AB016389 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003027267-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 720
ID ABR92289 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003036160-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 721
ID AB018930 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003044925-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 722
ID ABR78351 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 723
ID AB085087 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003032114-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 724
ID AB000226 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003032101-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 725
ID AB011558 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036124-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 726
ID AB016084 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036133-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 727
ID AB022203 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003040054-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 728
ID AB08777 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003036133-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 729
ID AB083472 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036134-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 730
ID AB06273 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003022294-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 731
ID ABR59309 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003027275-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 732
ID AB009371 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003027324-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 733
ID AB019235 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 734
ID AB011253 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036123-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 735
ID ABR66871 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003036148-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 736
ID AB016084 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036124-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
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DE Human secreted/transmembrane protein (PRO) #125.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 737
ID AB013790 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 738
ID AB065693 standard; protein; 259 AA.
DE Human secreted/transmembrane protein, SEQ ID 250.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 739
ID AB007541 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 740
ID AB003728 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 741
ID ABR67176 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 742
ID AB015779 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 743
ID AAE34068 standard; protein; 259 AA.
DE DKK 2 protein.
PN WO200290992-A2.
PD 14-NOV-2002.
PA (AXOR-) AXORDIA LTD.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 744
ID AB056060 standard; protein; 259 AA.
DE Human secreted/transmembrane protein, PRO1316.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 745
ID AB065388 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 746
ID AB095333 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.

PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 747
ID AB071236 standard; protein; 259 AA.
DE Human PRO1316 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 748
ID AB007846 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 749
ID ABR70087 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 750
ID ABR69420 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 751
ID AB001561 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 752
ID AB081363 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 753
ID ABR60160 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 754
ID ABR67895 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 755
ID ABR65283 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 756
ID ABR68505 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003027274-A1.

PD 06-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 757
ID ABR71917 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 758
ID ASU85397 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 759
ID ABU89087 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 760
ID ABU83167 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 761
ID ABU95023 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 762
ID ABU90571 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 763
ID ABU84082 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 764
ID ABU93733 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 765
ID ABR64978 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 766
ID ABR68810 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US20030327271-A1.
PD 06-FEB-2003.

Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 767
ID ABO06626 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 768
ID ABR99171 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 769
ID ABU57055 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 770
ID ABU86007 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 771
ID ABU82294 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 772
ID ABU87305 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 773
ID ABU83777 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 774
ID ABO08151 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 775
ID ABU81862 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 776
ID ABU66026 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 777

ID ABR59855 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 778
ID ABU94043 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 779
ID ABU99896 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003032296-A1.
PD 30-JAN-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 780
ID ABR6566 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 781
ID ABR90984 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 782
ID ABU94411 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 783
ID ABU79293 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 784
ID ABU86622 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 785
ID ABU86927 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 786
ID ABU94716 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 787
ID ABO04643 standard; protein; 259 AA.
DE Human PRO polypeptide #125.

PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 788
ID ABR70392 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 789
ID ABU98557 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003032301-A1.
PD 30-JAN-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 790
ID ABR65956 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 791
ID ABR64673 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 792
ID ABU79598 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 793
ID ABU92989 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 794
ID ABU95948 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 795
ID ABU91168 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 796
ID ABU90261 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 797
ID ABO09676 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003044931-A1.
PD 06-MAR-2003.

Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 798
 ID ABO10948 standard; protein; 259 AA.
 DE Human secreted/transmembrane protein (PRO) #125.
 PN US2003036150-A1.
 PD 20-FEB-2003.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 799
 ID ABR71002 standard; protein; 259 AA.
 DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
 PN US2003040069-A1.
 PD 27-FEB-2003.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 800
 ID ABR71002 standard; protein; 259 AA.
 DE Human secreted polypeptide #125.
 PN US2003022293-A1.
 PD 30-JAN-2003.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 801
 ID ABR71002 standard; protein; 259 AA.
 DE Human secreted polypeptide #125.
 PN US2003032128-A1.
 PD 13-FEB-2003.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 802
 ID ABR71002 standard; protein; 259 AA.
 DE Human secreted/transmembrane protein (PRO) #125.
 PN US2003032116-A1.
 PD 13-FEB-2003.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 803
 ID ABR69782 standard; protein; 259 AA.
 DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
 PN US2003032122-A1.
 PD 13-FEB-2003.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 804
 ID ABR69782 standard; protein; 259 AA.
 DE Human secreted/transmembrane protein (PRO) #125.
 PN US2003036139-A1.
 PD 20-FEB-2003.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 805
 ID ABR69782 standard; protein; 259 AA.
 DE Human secreted polypeptide #125.
 PN US2003036139-A1.
 PD 20-FEB-2003.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 806
 ID ABR69782 standard; protein; 259 AA.
 DE Human secreted/transmembrane protein (PRO) #125.
 PN US2003036139-A1.
 PD 20-FEB-2003.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 807
 ID ABR69782 standard; protein; 259 AA.
 DE Human secreted/transmembrane protein (PRO) #125.
 PN US2003036152-A1.
 PD 20-FEB-2003.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 808

ID ABU10634 standard; protein; 259 AA.
 DE Human secreted/transmembrane protein #125.
 PN US2002127584-A1.
 PD 12-SEP-2002.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 809
 ID ABU95643 standard; protein; 259 AA.
 DE Human PRO polypeptide #125.
 PN US2003032115-A1.
 PD 13-FEB-2003.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 810
 ID ABU95643 standard; protein; 259 AA.
 DE Novel human secreted and transmembrane protein PRO1316.
 PN US2003032140-A1.
 PD 13-FEB-2003.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 811
 ID ABR70697 standard; protein; 259 AA.
 DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
 PN US2003040076-A1.
 PD 27-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 812
 ID ABO05048 standard; protein; 259 AA.
 DE Novel human secreted and transmembrane protein PRO1316.
 PN US2003008352-A1.
 PD 09-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 813
 ID ABO08456 standard; protein; 259 AA.
 DE Human secreted/transmembrane protein (PRO) #125.
 PN US2003044922-A1.
 PD 06-MAR-2003.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 814
 ID ABO05663 standard; protein; 259 AA.
 DE Human secreted/transmembrane protein (PRO) #125.
 PN US2003032118-A1.
 PD 13-FEB-2003.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 815
 ID ABR74052 standard; protein; 259 AA.
 DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
 PN US2003036135-A1.
 PD 20-FEB-2003.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 816
 ID ABR95644 standard; protein; 259 AA.
 DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
 PN US2003054455-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 817
 ID ABR80941 standard; protein; 259 AA.
 DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
 PN US2003049741-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;

Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 818
ID ABR81246 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 819
ID ABM00942 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 820
ID ABR88544 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 821
ID ABM77365 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 822
ID ABO28849 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 823
ID ABO31594 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 824
ID ABM08011 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 825
ID ABO40491 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 826
ID ABO35916 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 827
ID ABO44055 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 828
ID ADA78002 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 829
ID ABM24850 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104539-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 830
ID ABO31118 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036131-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 831
ID ABR90374 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040075-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 832
ID ABM17288 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 833
ID ABR95034 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003044930-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 834
ID ABR95339 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 835
ID ABO21577 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 836
ID ABR97841 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064452-A1.
PD 03-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 837
ID ABR87629 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 838
ID ABR7670 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 839
ID ABR27900 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064440-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 840
ID ABR06181 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 841
ID ABR03687 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 842
ID ABR35138 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 843
ID ABR26375 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 844
ID ABR48157 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 845
ID ABR32899 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;

Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 846
ID ABO24660 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 847
ID ABR1671 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 848
ID ABR02772 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 849
ID ABR16068 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 850
ID ABO27629 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 851
ID ABR29120 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 852
ID ABR07096 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 853
ID ABR21190 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 854
ID ABR09536 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;

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RESULT 855
ID ABO41406 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 17.3%; Score 102; DB 6; Length 259;
  Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 856
ID ABO36221 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 17.3%; Score 102; DB 6; Length 259;
  Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 857
ID ABO43750 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 17.3%; Score 102; DB 6; Length 259;
  Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 858
ID ABO43750 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 17.3%; Score 102; DB 6; Length 259;
  Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 859
ID ABO43750 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003082717-A1.
PD 01-MAY-2003.
  Query Match 17.3%; Score 102; DB 6; Length 259;
  Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 860
ID ABO43750 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
  Query Match 17.3%; Score 102; DB 6; Length 259;
  Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 861
ID ABO43750 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104542-A1.
PD 05-JUN-2003.
  Query Match 17.3%; Score 102; DB 6; Length 259;
  Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 862
ID ABO43750 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104543-A1.
PD 05-JUN-2003.
  Query Match 17.3%; Score 102; DB 6; Length 259;
  Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 863
ID ABO43750 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036127-A1.
PD 20-FEB-2003.
  Query Match 17.3%; Score 102; DB 6; Length 259;
  Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 864
ID ABO43750 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003036130-A1.
PD 20-FEB-2003.
  Query Match 17.3%; Score 102; DB 6; Length 259;
  Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 865
ID ABO43750 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 17.3%; Score 102; DB 6; Length 259;
  Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 866
ID ABO16999 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 17.3%; Score 102; DB 6; Length 259;
  Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 867
ID ABR94424 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003044917-A1.
PD 06-MAR-2003.
  Query Match 17.3%; Score 102; DB 6; Length 259;
  Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 868
ID ABR75931 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003044929-A1.
PD 06-MAR-2003.
  Query Match 17.3%; Score 102; DB 6; Length 259;
  Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 869
ID ABR71307 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 17.3%; Score 102; DB 6; Length 259;
  Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 870
ID ABR93204 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 17.3%; Score 102; DB 6; Length 259;
  Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 871
ID ABR93509 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 17.3%; Score 102; DB 6; Length 259;
  Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 872
ID ABR87934 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 17.3%; Score 102; DB 6; Length 259;
  Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 873
ID ABO33602 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003073130-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 17.3%; Score 102; DB 6; Length 259;
  Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 874
ID ABO27934 standard; protein; 259 AA.
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DE Human secreted/transmembrane protein (PRO) #125.
 PN US2003064454-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 875
 ID ABO30069 standard; protein; 259 AA.
 DE Human secreted/transmembrane protein (PRO) #125.
 PN US2003064461-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 876
 ID ABO33278 standard; protein; 259 AA.
 DE Human PRO polypeptide #125.
 PN US2003068724-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 877
 ID ABO4966 standard; protein; 259 AA.
 DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
 PN US2003068727-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 878
 ID ABO8926 standard; protein; 259 AA.
 DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
 PN US2003068772-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 879
 ID ABO36526 standard; protein; 259 AA.
 DE Human secreted/transmembrane protein (PRO) #125.
 PN US2003068714-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 880
 ID ABO35611 standard; protein; 259 AA.
 DE Human PRO polypeptide #125.
 PN US2003068758-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 881
 ID ABO39576 standard; protein; 259 AA.
 DE Human secreted/transmembrane protein (PRO) #125.
 PN US2003068776-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 882
 ID ABO10451 standard; protein; 259 AA.
 DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
 PN US2003069407-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 883
 ID ABO11976 standard; protein; 259 AA.
 DE Human secreted polypeptide PRO1316, SEQ ID NO:250.

PN US2003104555-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 884
 ID ABO52122 standard; protein; 259 AA.
 DE Human PRO polypeptide #125.
 PN US2003049768-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 885
 ID ABO52427 standard; protein; 259 AA.
 DE Human PRO polypeptide #125.
 PN US2003049771-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 886
 ID ABO23745 standard; protein; 259 AA.
 DE Human secreted/transmembrane protein (PRO) #125.
 PN US2003032134-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 887
 ID ABR97231 standard; protein; 259 AA.
 DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
 PN US2003054481-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 888
 ID ABR87019 standard; protein; 259 AA.
 DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
 PN US2003049778-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 889
 ID ABM11061 standard; protein; 259 AA.
 DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
 PN US2003049782-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 890
 ID ABM28205 standard; protein; 259 AA.
 DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
 PN US2003054476-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 891
 ID ABO32204 standard; protein; 259 AA.
 DE Human secreted/transmembrane protein (PRO) #125.
 PN US2003068733-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 892
 ID ABM15331 standard; protein; 259 AA.
 DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
 PN US2003068692-A1.
 PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 893
ID ABM06486 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 894
ID ABM04297 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 895
ID ABM22410 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 896
ID ABM07706 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 897
ID ABO40796 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 898
ID ABM35443 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 899
ID ABM33206 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003087374-A1.
PD 08-MAY-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 900
ID ABO52732 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 901
ID ABO50292 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 902
ID ABU9286 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003040055-A1.
PD 27-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 903
ID ABO04338 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036164-A1.
PD 20-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 904
ID ABO05968 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003040074-A1.
PD 27-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 905
ID ABM18508 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 906
ID ABR97536 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 907
ID ABR80636 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 908
ID ABM01247 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 909
ID ABR88849 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003073169-A1.
PD 17-APR-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 910
ID ABM13501 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 911
ID ABM20885 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068711-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 912
ID ABO42016 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 913
ID ABO42626 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 914
ID ABR86714 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 915
ID ABO38661 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 916
ID ABO32901 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 917
ID ABO22715 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003087373-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 918
ID ABO74926 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003096353-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 919
ID ADA79794 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003073173-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 920
ID ABR96316 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054458-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 921
ID ABO37746 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 922
ID ABR86409 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 923
ID ABR86714 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 924
ID ABR16678 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 925
ID ABO29730 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 926
ID ABO29154 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 927
ID ABO23935 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 928
ID ABO23325 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 929
ID ABO22105 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 930
ID ABO37746 standard; protein; 259 AA.

DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 931
ID ABM28510 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003082715-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 932
ID ABM28815 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003082716-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 933
ID ABM6459 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 934
ID ABM75841 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 935
ID ABM34121 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 936
ID ABM34426 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 937
ID ABO20357 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003032125-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 938
ID ABO21272 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003054454-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 939
ID ABO22187 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 940
ID ABR9621 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 941
ID ABR85799 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 942
ID ABR99781 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 943
ID ABM00332 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 944
ID ABM00637 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 945
ID ABO29764 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 946
ID ABM23630 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 947
ID ABM29425 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 948
ID ABO38356 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 949
ID ABO45656 standard; protein; 259 AA.

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DE Human PRO polypeptide #125.
 PN US2003073182-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 950
 ID ABR89764 standard; protein; 259 AA.
 DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
 PN US2003073171-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 951
 ID ADAB1521 standard; protein; 259 AA.
 DE Human secreted/transmembrane protein (PRO) #125.
 PN US2003092121-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 952
 ID ABO16694 standard; protein; 259 AA.
 DE Human secreted/transmembrane protein (PRO) #125.
 PN US2003027276-A1.
 PD 06-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 953
 ID ABO18320 standard; protein; 259 AA.
 DE Human secreted/transmembrane protein (PRO) #125.
 PN US2003044920-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 954
 ID ABO22747 standard; protein; 259 AA.
 DE Human PRO polypeptide #125.
 PN US2003027265-A1.
 PD 06-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 955
 ID ABO23052 standard; protein; 259 AA.
 DE Human PRO polypeptide #125.
 PN US2003054461-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 956
 ID ABR92594 standard; protein; 259 AA.
 DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
 PN US2003064446-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 957
 ID ABR81551 standard; protein; 259 AA.
 DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
 PN US2003049744-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 958
 ID ABR77975 standard; protein; 259 AA.
 DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
 PN US2003049783-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 959
 ID ABR89764 standard; protein; 259 AA.
 DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
 PN US2003073171-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 960
 ID ABR26680 standard; protein; 259 AA.
 DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
 PN US2003032121-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 961
 ID ABR13806 standard; protein; 259 AA.
 DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
 PN US2003064458-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 962
 ID ABO28544 standard; protein; 259 AA.
 DE Human secreted/transmembrane protein (PRO) #125.
 PN US2003064460-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 963
 ID ABO30374 standard; protein; 259 AA.
 DE Human secreted/transmembrane protein (PRO) #125.
 PN US2003064464-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 964
 ID ABO7401 standard; protein; 259 AA.
 DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
 PN US2003068702-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 965
 ID ABO3992 standard; protein; 259 AA.
 DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
 PN US2003068734-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 966
 ID ABO37136 standard; protein; 259 AA.
 DE Human secreted/transmembrane protein (PRO) #125.
 PN US2003068719-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 967
 ID ABO41711 standard; protein; 259 AA.
 DE Human secreted/transmembrane protein (PRO) #125.
 PN US2003068729-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 968
 ID ABR77975 standard; protein; 259 AA.
 DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
 PN US2003049783-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.

ID	ABO35306 standard; protein; 259 AA.
DE	Human PRO polypeptide #125.
PN	US2003068738-A1.
PD	10-APR-2003.
PA	(GETH) GENENTECH INC.
Query Match	17.3%; Score 102; DB 6; Length 259;
Best Local Similarity	31.5%; Pred. No. 0.023;
RESULT 969	
ID	ABM25155 standard; protein; 259 AA.
DE	Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN	US2003104540-A1.
PD	05-JUN-2003.
PA	(GETH) GENENTECH INC.
Query Match	17.3%; Score 102; DB 6; Length 259;
Best Local Similarity	31.5%; Pred. No. 0.023;
RESULT 970	
ID	ABO47547 standard; protein; 259 AA.
DE	Human secreted/transmembrane protein (PRO) #125.
PN	US2003049742-A1.
PD	13-MAR-2003.
PA	(GETH) GENENTECH INC.
Query Match	17.3%; Score 102; DB 6; Length 259;
Best Local Similarity	31.5%; Pred. No. 0.023;
RESULT 971	
ID	ABO47852 standard; protein; 259 AA.
DE	Human secreted/transmembrane protein (PRO) #125.
PN	US2003049747-A1.
PD	13-MAR-2003.
PA	(GETH) GENENTECH INC.
Query Match	17.3%; Score 102; DB 6; Length 259;
Best Local Similarity	31.5%; Pred. No. 0.023;
RESULT 972	
ID	ABO48462 standard; protein; 259 AA.
DE	Human secreted/transmembrane protein (PRO) #125.
PN	US2003049750-A1.
PD	13-MAR-2003.
PA	(GETH) GENENTECH INC.
Query Match	17.3%; Score 102; DB 6; Length 259;
Best Local Similarity	31.5%; Pred. No. 0.023;
RESULT 973	
ID	ABO51512 standard; protein; 259 AA.
DE	Human PRO polypeptide #125.
PN	US2003049766-A1.
PD	13-MAR-2003.
PA	(GETH) GENENTECH INC.
Query Match	17.3%; Score 102; DB 6; Length 259;
Best Local Similarity	31.5%; Pred. No. 0.023;
RESULT 974	
ID	ABO51817 standard; protein; 259 AA.
DE	Human PRO polypeptide #125.
PN	US2003049767-A1.
PD	13-MAR-2003.
PA	(GETH) GENENTECH INC.
Query Match	17.3%; Score 102; DB 6; Length 259;
Best Local Similarity	31.5%; Pred. No. 0.023;
RESULT 975	
ID	ABO50597 standard; protein; 259 AA.
DE	Human secreted/transmembrane protein (PRO) #125.
PN	US2003049779-A1.
PD	13-MAR-2003.
PA	(GETH) GENENTECH INC.
Query Match	17.3%; Score 102; DB 6; Length 259;
Best Local Similarity	31.5%; Pred. No. 0.023;
RESULT 976	
ID	ABR79721 standard; protein; 259 AA.
DE	Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN	US2003040059-A1.
PD	27-FEB-2003.
PA	(GETH) GENENTECH INC.
Query Match	17.3%; Score 102; DB 6; Length 259;
Best Local Similarity	31.5%; Pred. No. 0.023;
RESULT 977	
ID	ABM16983 standard; protein; 259 AA.
DE	Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN	US2003040078-A1.
PD	

PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 978
ID ABO18015 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003044918-A1.
PD 06-MAR-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 979
ID ABO20967 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 980
ID ABR96926 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 981
ID ABM12281 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 982
ID ABM16373 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 983
ID ABM24240 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064441-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 984
ID ABM14721 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 985
ID ABM04602 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 986
ID ABM06791 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;

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RESULT 987
ID ABM09231 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003073174-A1.
PD 17-APR-2003.
  Query Match
  Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
  Pred. No. 0.023;
RESULT 988
ID ABO39271 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
  Pred. No. 0.023;
RESULT 989
ID ABM75536 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
  Pred. No. 0.023;
RESULT 990
ID ABM25460 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104541-A1.
PD 05-JUN-2003.
  Query Match
  Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
  Pred. No. 0.023;
RESULT 991
ID ABM19970 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
  Pred. No. 0.023;
RESULT 992
ID ABO46876 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
  Pred. No. 0.023;
RESULT 993
ID ABO47181 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
  Pred. No. 0.023;
RESULT 994
ID ADA83319 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
  Pred. No. 0.023;
RESULT 995
ID ABR71612 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003032133-A1.
PD 13-FEB-2003.
  Query Match
  Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
  Pred. No. 0.023;
RESULT 996
ID ABR72222 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003032136-A1.
  Query Match
  Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
  Pred. No. 0.023;
RESULT 997
ID ABR98561 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003036129-A1.
PD 20-FEB-2003.
  Query Match
  Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
  Pred. No. 0.023;
RESULT 998
ID ABO6931 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003040053-A1.
PD 27-FEB-2003.
  Query Match
  Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
  Pred. No. 0.023;
RESULT 999
ID ABR84884 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040057-A1.
PD 27-FEB-2003.
  Query Match
  Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
  Pred. No. 0.023;
RESULT 1000
ID ABR73442 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
  Pred. No. 0.023;
RESULT 1001
ID ABR76536 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003044932-A1.
PD 06-MAR-2003.
  Query Match
  Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
  Pred. No. 0.023;
RESULT 1002
ID ABR73137 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003027270-A1.
PD 06-FEB-2003.
  Query Match
  Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
  Pred. No. 0.023;
RESULT 1003
ID ABM18203 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
  Pred. No. 0.023;
RESULT 1004
ID ABO20662 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003032126-A1.
PD 13-FEB-2003.
  Query Match
  Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
  Pred. No. 0.023;
RESULT 1005
ID ABO25405 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 17.3%; Score 102; DB 6; Length 259;
  Pred. No. 0.023;
RESULT 1006
ID ABO25710 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003054466-A1.

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PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1007
ID ABR94119 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1008
ID ABR80026 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049738-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1009
ID ABM11366 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1010
ID ABO32973 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1011
ID ABO30679 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1012
ID ABO30984 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1013
ID ABM27290 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1014
ID ABM30035 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1015
ID ABM05571 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1016
ID ABM15636 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1017
ID ABM08621 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1018
ID ABO42321 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1019
ID ABO38051 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1020
ID ABO45961 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1021
ID ABM66764 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1022
ID ADB20362 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003082767-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1023
ID ABM19665 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1024
ID ABO49377 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1025
ID ABO49377 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;

RESULT 1025
ID ABO49682 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1026
ID ADA78614 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1027
ID ABR8239 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1028
ID ABM26985 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1029
ID ABM03382 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1030
ID ABO39881 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1031
ID ABO49987 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1032
ID ABO50902 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1033
ID ABO05358 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036126-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1034
ID ABR74662 standard; protein; 259 AA.

DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003044924-A1.
PD 06-MAR-2003.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1035
ID ABO44455 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003044841-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1036
ID ABR77141 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003044927-A1.
PD 06-MAR-2003.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1037
ID ABM17898 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040072-A1.
PD 27-FEB-2003.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1038
ID ABR95949 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1039
ID ABO21882 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1040
ID ABO20052 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003032124-A1.
PD 13-FEB-2003.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1041
ID ABO24355 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1042
ID ABR86104 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1043
ID ABM10756 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;

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RESULT 1044
ID ABM76755 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 17.3%; Score 102; DB 7; Length 259;
RESULT 1045
ID ABR89459 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003073170-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 17.3%; Score 102; DB 7; Length 259;
RESULT 1046
ID ABM12586 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 17.3%; Score 102; DB 7; Length 259;
RESULT 1047
ID ABM05876 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 17.3%; Score 102; DB 7; Length 259;
RESULT 1048
ID ABO35001 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 17.3%; Score 102; DB 7; Length 259;
RESULT 1049
ID ABM03077 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 17.3%; Score 102; DB 7; Length 259;
RESULT 1050
ID ABM19055 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 17.3%; Score 102; DB 7; Length 259;
RESULT 1051
ID ABM19360 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 17.3%; Score 102; DB 7; Length 259;
RESULT 1052
ID ABO46571 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 17.3%; Score 102; DB 7; Length 259;
RESULT 1053
ID ABO49072 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 17.3%; Score 102; DB 7; Length 259;
RESULT 1054
ID ABR69115 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003027273-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 17.3%; Score 102; DB 7; Length 259;
RESULT 1055
ID ABR89154 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003036119-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 17.3%; Score 102; DB 7; Length 259;
RESULT 1056
ID ABR72527 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003036120-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 17.3%; Score 102; DB 7; Length 259;
RESULT 1057
ID ABR74357 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 17.3%; Score 102; DB 7; Length 259;
RESULT 1058
ID ABO18625 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003044921-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 17.3%; Score 102; DB 7; Length 259;
RESULT 1059
ID ABR80331 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 17.3%; Score 102; DB 7; Length 259;
RESULT 1060
ID ABM01552 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 17.3%; Score 102; DB 7; Length 259;
RESULT 1061
ID ABM02162 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 17.3%; Score 102; DB 7; Length 259;
RESULT 1062
ID ABR87324 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 17.3%; Score 102; DB 7; Length 259;
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Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 1063
 ID ABO1207 standard; protein; 259 AA.
 DE Human secreted/transmembrane protein (PRO) #125.
 PN US2003049781-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 7; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 1064
 ID ABO4033 standard; protein; 259 AA.
 DE Human secreted/transmembrane protein (PRO) #125.
 PN US2003036158-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 7; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 1065
 ID ABO10503 standard; protein; 259 AA.
 DE Human PRO polypeptide #125.
 PN US2003036151-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 7; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 1066
 ID ABR77746 standard; protein; 259 AA.
 DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
 PN US2003040067-A1.
 PD 27-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 7; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 1067
 ID ABR78956 standard; protein; 259 AA.
 DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
 PN US2003054456-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 7; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 1068
 ID ABR93814 standard; protein; 259 AA.
 DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
 PN US2003054457-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 7; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 1069
 ID ABO1857 standard; protein; 259 AA.
 DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
 PN US2003059883-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 7; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 1070
 ID ABO38966 standard; protein; 259 AA.
 DE Human secreted/transmembrane protein (PRO) #125.
 PN US2003068774-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 7; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 1071
 ID ABO33479 standard; protein; 259 AA.
 DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
 PN US2003104538-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 7; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 1072
 ID ABO33479 standard; protein; 259 AA.
 DE Novel human secreted and transmembrane protein PRO1316.
 PN US2003073129-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.

Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 1073
 ID ABO1207 standard; protein; 259 AA.
 DE Human secreted/transmembrane protein (PRO) #125.
 PN US2003049781-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 7; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 1074
 ID ABO4033 standard; protein; 259 AA.
 DE Human secreted/transmembrane protein (PRO) #125.
 PN US2003036158-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 7; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 1075
 ID ABO10503 standard; protein; 259 AA.
 DE Human PRO polypeptide #125.
 PN US2003036151-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 7; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 1076
 ID ABR77746 standard; protein; 259 AA.
 DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
 PN US2003040067-A1.
 PD 27-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 7; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 1077
 ID ABR78956 standard; protein; 259 AA.
 DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
 PN US2003054456-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 7; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 1078
 ID ABR93814 standard; protein; 259 AA.
 DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
 PN US2003054457-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 7; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 1079
 ID ABO1857 standard; protein; 259 AA.
 DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
 PN US2003059883-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 7; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 1080
 ID ABO38966 standard; protein; 259 AA.
 DE Human secreted/transmembrane protein (PRO) #125.
 PN US2003068774-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.3%; Score 102; DB 7; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.023;
 RESULT 1081
 ID ABO33479 standard; protein; 259 AA.
 DE Novel human secreted and transmembrane protein PRO1316.
 PN US2003073129-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.

Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1082
ID ABR90069 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1083
ID ABR27595 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1084
ID ASM13196 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1085
ID ABO31899 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1086
ID ASM14111 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068683-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1087
ID AEM08316 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1088
ID ABO40186 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068681-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1089
ID ASM74621 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1090
ID ASM33816 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1091

ID ABM20275 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1092
ID ABO48767 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1093
ID ABR72832 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003036122-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1094
ID ABO15474 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1095
ID ABR85189 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040065-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1096
ID ABO15169 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003044919-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1097
ID ABO17304 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003040077-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1098
ID ABM17593 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003044928-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1099
ID ABR85494 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1100
ID ABM77060 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;

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Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1101
ID ABO28239 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1102
ID ABO23020 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1103
ID ABO30340 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1104
ID ABO21800 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1105
ID ABO21495 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1106
ID ABO15026 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1107
ID ABO41101 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1108
ID ABO36831 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1109
ID ABO37441 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1110
ID ABO75231 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1111
ID ABO33511 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1112
ID ABO46266 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1113
ID ADA82685 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1114
ID ABO31865 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068680-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1115
ID ABO31255 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1116
ID ADB85993 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1117
ID ABO32170 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1118
ID ABO32475 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1119
ID ABO31560 standard; protein; 259 AA.
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DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1120
ID ADM30950 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1121
ID ADC17939 standard; protein; 259 AA.
DE Human PRO polypeptide #21.
PN US2003064925-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1122
ID ADD05723 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1123
ID ADD70585 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003099625-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1124
ID ADD39662 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003083462-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1125
ID ADD70108 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003054406-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1126
ID ADD38229 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003096955-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1127
ID ADD39185 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003096954-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1128
ID ADD38708 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.

PN US2003092061-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1129
ID ADD40139 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003082627-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1130
ID ADE50360 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003069179-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1131
ID ADE19972 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003092883-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1132
ID ADE49883 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003082626-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1133
ID ADE21441 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003082628-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1134
ID ADF29866 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003204053-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1135
ID ADF55759 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003204054-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1136
ID ADG02718 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1137
ID ADG01425 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003207399-A1.

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PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1138
ID ADF95600 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1139
ID ADG12415 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003207392-A1.
PD 06-NOV-2003.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1140
ID ADH09075 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1141
ID ADH99263 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003065142-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1142
ID ADL32856 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1143
ID ADM30390 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1144
ID ADN39361 standard; protein; 259 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:B45.
PN WO2003042861-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 17.3%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1145
ID ADE74387 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003211572-A1.
PD 13-NOV-2003.
Query Match 17.3%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1146
ID ADE74999 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003211574-A1.
PD 13-NOV-2003.
Query Match 17.3%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1147
ID ADE96443 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003195347-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1148
ID ADF25754 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003199675-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1149
ID ADF24653 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003198993-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1150
ID ADF29389 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003203401-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1151
ID ADE96920 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003195334-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1152
ID ADF96212 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003215909-A1.
PD 20-NOV-2003.
Query Match 17.3%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1153
ID ADG04483 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1154
ID ADG00643 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1155
ID ADG82899 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1156
ID ADH02958 standard; protein; 259 AA.

DE Human secreted/transmembrane protein PRO1316.
PN US2003216562-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1157
ID ADH03912 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003220471-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1158
ID ADH03435 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003224478-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1159
ID ADH26180 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1160
ID ADH33149 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1161
ID ADH04389 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2004005626-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1162
ID ADH61390 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US200401130-A1.
PD 22-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1163
ID ADJ54888 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1164
ID ADJ64659 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1165
ID ADM31555 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.

PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1166
ID ADM36602 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1167
ID ADM40407 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1168
ID ADL94589 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2004073015-A1.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1169
ID ADO35295 standard; protein; 259 AA.
DE Human Dkk family protein Dkk2.
PN US2004014209-A1.
PD 22-JAN-2004.
PA (LASS/) LASSAR A. B.
PA (MERC/) MERCOLA M.
PA (GUPT/) GUPTA R.
PA (MARV/) MARVIN M.
PA (SCHN/) SCHNEIDER V.
PA (TZA/) TZAHOOR E.
PA (BROT/) BROTT B.
PA (SOKO/) SOKOL S.
Query Match 17.3%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1170
ID ADN38015 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1171
ID ABD44976 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316, SEQ:70.
PN US2005181478-A1.
PD 18-AUG-2005.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
Query Match 17.3%; Score 102; DB 9; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1172
ID ABD50245 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2005163766-A1.

PD 28-JUL-2005.
Query Match 17.3%; Score 102; DB 9; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1173
ID AEG62937 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2006073544-A1.
PD 06-APR-2006.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 10; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1174
ID AEG72760 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2006074226-A1.
PD 06-APR-2006.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 10; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1175
ID AEG62325 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2006073545-A1.
PD 06-APR-2006.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 10; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1176
ID AEG88242 standard; protein; 259 AA.
DE Human PRO protein amino acid sequence - SEQ ID 250.
PN US2006074227-A1.
PD 06-APR-2006.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 10; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1177
ID AEGH1758 standard; protein; 259 AA.
DE Human tumor overexpressed cDNA protein product PRO1316 SEQ ID NO: 250.
PN US2006094864-A1.
PD 04-MAY-2006.
PA (GETH) GENENTECH INC.
Query Match 17.3%; Score 102; DB 10; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1178
ID AEG140730 standard; protein; 259 AA.
DE Human dickkopf ligand Dkk-2.
PN WO2006061717-A2.
PD 15-JUN-2006.
PA (NEUR-) NEURO THERAPEUTICS AB.
Query Match 17.3%; Score 102; DB 10; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1179
ID AEL56587 standard; protein; 259 AA.
DE Human dickkopf related protein-2 precursor, SEQ ID NO: 1050.
PN US2006216722-A1.
PD 28-SEP-2006.
PA (BETS/) BETSHOLTZ C.
PA (TRYG/) TRYGGVASON K.
PA (TAKE/) TAKEMOTO M.
PA (HELL/) HE L.
PA (PATR/) PATRAKKAS J.
Query Match 17.3%; Score 102; DB 10; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1180
ID AAO88880 standard; protein; 263 AA.
DE Amino acid sequence of a human Dickkopf (Dkk)-2 protein.
PN WO20052047-A2.
PD 08-SEP-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 17.3%; Score 102; DB 3; Length 263;
Best Local Similarity 31.5%; Pred. No. 0.023;
RESULT 1181
ID AAY92072 standard; protein; 259 AA.

DE Murine DKR-2.
PN WO200018914-A2.
PD 06-APR-2000.
PA (AMGE-) AMGEN INC.
Query Match 17.1%; Score 101; DB 3; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.029;
RESULT 1182
ID AEL55689 standard; protein; 259 AA.
DE Mouse dickkopf related protein-2 precursor, SEQ ID NO: 150.
PN US2006216722-A1.
PD 28-SEP-2006.
PA (BETS/) BETSHOLTZ C.
PA (TRYG/) TRYGGVASON K.
PA (TAKE/) TAKEMOTO M.
PA (HELL/) HE L.
PA (PATR/) PATRAKKAS J.
Query Match 17.1%; Score 101; DB 10; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.029;
RESULT 1183
ID AEI40729 standard; protein; 260 AA.
DE Mouse dickkopf ligand Dkk-2.
PN WO2006061717-A2.
PD 15-JUN-2006.
PA (NEUR-) NEURO THERAPEUTICS AB.
Query Match 17.1%; Score 101; DB 10; Length 260;
Best Local Similarity 31.5%; Pred. No. 0.029;
RESULT 1184
ID AEA38732 standard; protein; 272 AA.
DE Mouse dickkopf-1 (Dkk-1) protein, SEQ ID NO: 22.
PN WO2005049640-A2.
PD 02-JUN-2005.
PA (MERI) MERCK & CO INC.
Query Match 17.1%; Score 101; DB 9; Length 272;
Best Local Similarity 33.8%; Pred. No. 0.031;
RESULT 1185
ID AEF80274 standard; protein; 272 AA.
DE Mouse dickkopf-1 (Dkk-1) protein sequence.
PN WO2006015373-A2.
PD 09-FEB-2006.
PA (AMGE-) AMGEN INC.
Query Match 17.1%; Score 101; DB 10; Length 272;
Best Local Similarity 33.8%; Pred. No. 0.031;
RESULT 1186
ID AEI40727 standard; protein; 272 AA.
DE Mouse dickkopf ligand Dkk-1.
PN WO2006061717-A2.
PD 15-JUN-2006.
PA (NEUR-) NEURO THERAPEUTICS AB.
Query Match 17.1%; Score 101; DB 10; Length 272;
Best Local Similarity 33.8%; Pred. No. 0.031;
RESULT 1187
ID ADY86168 standard; protein; 83 AA.
DE Human dickkopf-3 protein, SEQ ID NO:6.
PN US2005064522-A1.
PD 24-MAR-2005.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 9; Length 83;
Best Local Similarity 37.7%; Pred. No. 0.0099;
RESULT 1188
ID ADB64042 standard; protein; 215 AA.
DE Human protein encoded by clone BRAWY20227860.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 17.1%; Score 100.5; DB 7; Length 215;
Best Local Similarity 37.7%; Pred. No. 0.027;
RESULT 1189
ID AAW73016 standard; protein; 350 AA.
DE Human cysteine-rich secreted protein CRSP-1.
PN WO9846755-A1.
PD 22-OCT-1998.
PA (MILL-) MILLENNIUM BIOTHEAPEUTICS INC.

Query Match 17.1%; Score 100.5; DB 2; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1190
ID AAM62595 standard; protein; 350 AA.
DE Homo sapiens cerebellum and embryo specific protein.
PN W09827932-A2.
PD 02-JUL-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 17.1%; Score 100.5; DB 2; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1191
ID AAY13384 standard; protein; 350 AA.
DE Amino acid sequence of protein PRO295.
PN W09914328-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 2; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1192
ID AAY92070 standard; protein; 350 AA.
DE Human DKR-3.
PN W0200018914-A2.
PD 06-APR-2000.
PA (AMGE-) AMGEN INC.
Query Match 17.1%; Score 100.5; DB 3; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1193
ID AAB08874 standard; protein; 350 AA.
DE Amino acid sequence of a human Dickkopf (Dkk)-3 protein.
PN W0200052047-A2.
PD 08-SEP-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 17.1%; Score 100.5; DB 3; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1194
ID ADC78556 standard; protein; 350 AA.
DE Human PRO295 protein.
PN W0200015796-A2.
PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 3; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1195
ID AAB80252 standard; protein; 350 AA.
DE Human PRO295 protein.
PN W0200104311-A1.
PD 18-JAN-2001.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 4; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1196
ID AAG80271 standard; protein; 350 AA.
DE Human DKK-3 protein.
PN W0200163295-A2.
PD 30-AUG-2001.
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
Query Match 17.1%; Score 100.5; DB 4; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1197
ID AAB87529 standard; protein; 350 AA.
DE Human PRO295.
PN W0200116318-A2.
PD 08-MAR-2001.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 4; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1198
ID AAG62468 standard; protein; 350 AA.
DE Human reduced expression in immortalised cells protein.
PN W0200138528-A1.
PD 31-MAY-2001.
PA (HISM) HISAMITSU PHARM CO LTD.
Query Match 17.1%; Score 100.5; DB 4; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1199
ID ABB90735 standard; protein; 350 AA.
DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 202.
PN W0200210217-A2.
PD 07-FEB-2002.
PA (UYJO-) UNIV JOHNS HOPKINS.
Query Match 17.1%; Score 100.5; DB 5; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1200
ID ABG95854 standard; protein; 350 AA.
DE Human secreted/transmembrane protein PRO295.
PN US2002119130-A1.
PD 29-AUG-2002.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 5; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1201
ID ABB84841 standard; protein; 350 AA.
DE Human PRO295 protein sequence SEQ ID NO:50.
PN W0200200690-A2.
PD 03-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 5; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1202
ID ABB95447 standard; protein; 350 AA.
DE Human angiogenesis related protein PRO295 SEQ ID NO: 50.
PN W0200208284-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 5; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1203
ID ABU71630 standard; protein; 350 AA.
DE Human PRO polypeptide #41.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1204
ID ABU71485 standard; protein; 350 AA.
DE Human PRO polypeptide #41.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1205
ID ABU54442 standard; protein; 350 AA.
DE Human tumour endothelial marker TEM 4.
PN W0200283874-A2.
PD 24-OCT-2002.
PA (UYJO-) UNIV JOHNS HOPKINS.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1206

ID ABU71931 standard; protein; 350 AA.
DE Human secreted/transmembrane protein PRO295.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1207
ID ABO01814 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1208
ID ABU90879 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1209
ID ABO33938 standard; protein; 350 AA.
DE Human secreted/transmembrane protein PRO295.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1210
ID ABU71955 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1211
ID ABU55915 standard; protein; 350 AA.
DE Human protein DKK3.
PN WO200277204-A2.
PD 03-OCT-2002.
PA (AXOR-) AXORDIA LTD.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1212
ID ABU54387 standard; protein; 350 AA.
DE Human secreted/transmembrane protein PRO295.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1213
ID ABO47402 standard; protein; 350 AA.
DE Human secreted/transmembrane polypeptide PRO295.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1214
ID ABU71509 standard; protein; 350 AA.
DE Human secreted polypeptide PRO295.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1215
ID AAE34069 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1216
ID ABU72290 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1217
ID ABU90963 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1218
ID ABO27284 standard; protein; 350 AA.
DE Human secreted/transmembrane polypeptide PRO295.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1219
ID ABU64539 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #43.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1220
ID ABU67385 standard; protein; 350 AA.
DE Human secreted protein PRO295.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1221
ID ABU92479 standard; protein; 350 AA.
DE Human secreted/transmembrane protein PRO295.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1222
ID ABO14905 standard; protein; 350 AA.
DE Human secreted / transmembrane polypeptide PRO295.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1223
ID ABU81149 standard; protein; 350 AA.
DE Human secreted polypeptide PRO295.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1224
ID ABO53264 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.

PD US2003027986-A1.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1225
ID ABU98266 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1226
ID ABU89271 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1227
ID ABU82478 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1228
ID ABU69662 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1229
ID ABU96442 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1230
ID ABU72112 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1231
ID ABO14844 standard; protein; 350 AA.
DE Human secreted / transmembrane polypeptide PRO295.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1232
ID ADB29441 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1233
ID ADB17065 standard; protein; 350 AA.
DE Human transmembrane PRO polypeptide (SeqID 8).
PN US2003050462-A1.

PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1234
ID ABO44242 standard; protein; 350 AA.
DE Human secreted/transmembrane polypeptide PRO 295.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1235
ID ADA18297 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1236
ID ABO32796 standard; protein; 350 AA.
DE Human secreted/transmembrane protein PRO295.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1237
ID ADA19870 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1238
ID ADB17253 standard; protein; 350 AA.
DE Human transmembrane PRO polypeptide (SeqID 8).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1239
ID ABO34856 standard; protein; 350 AA.
DE Human PRO polypeptide #41.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1240
ID ADA16272 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1241
ID ADA20042 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1242
ID ABO34170 standard; protein; 350 AA.
DE Human secreted/transmembrane polypeptide PRO 295.
PN US2003060601-A1.
PD 27-MAR-2003.

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PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1243
ID ADA42417 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1244
ID ABO17534 standard; protein; 350 AA.
DE Human PRO polypeptide #41.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1245
ID ADA00339 standard; protein; 350 AA.
DE Human secreted/transmembrane polypeptide PRO 295.
PN US2003027992-A1.
PD 08-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1246
ID ADA16696 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1247
ID ADA13125 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1248
ID ADA41993 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1249
ID ADA17340 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1250
ID ADA42843 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1251
ID ABO17595 standard; protein; 350 AA.
DE Human PRO polypeptide #41.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1252
ID ADB95581 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1253
ID ADB77762 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1254
ID ADB74898 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1255
ID ADB68260 standard; protein; 350 AA.
DE Human PRO295 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1256
ID ADB68067 standard; protein; 350 AA.
DE Human PRO295 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1257
ID ADB90884 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1258
ID ADC28544 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1259
ID ADC39744 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1260
ID ADC40258 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;

Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1261
ID ADC19082 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1262
ID ADC34382 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1263
ID ADC29437 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1264
ID ADC28968 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1265
ID ADC40853 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1266
ID ADC19510 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1267
ID ADC06964 standard; protein; 350 AA.
DE Human PRO295 protein.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1268
ID ADC17143 standard; protein; 350 AA.
DE Mammalian PRO polypeptide (Seqid 8).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1269
ID ADC33958 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1270
ID ADC13028 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1271
ID ADC14841 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1272
ID ADC52336 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1273
ID ADC12480 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1274
ID ADD10339 standard; protein; 350 AA.
DE Human secreted/transmembrane PRO polypeptide #25.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1275
ID ADD05035 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1276
ID ADD11299 standard; protein; 350 AA.
DE Human secreted/transmembrane PRO polypeptide #25.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1277
ID ADD04041 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1278
ID ADD03617 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1279

ID ADD37092 standard; protein; 350 AA.
DE Human secreted/transmembrane PRO polypeptide #25.
PD US2003105012-A1.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1280
ID ADD36012 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PD US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1281
ID ADB34869 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PD US2003077583-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1282
ID AG01013 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PD US2003078387-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1283
ID ADG08566 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PD US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1284
ID ADP95187 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PD US2003180795-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1285
ID ADH24040 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PD US2003180918-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1286
ID ADH34066 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PD US2003180858-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1287
ID ADH29899 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PD US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
ID ADH23870 standard; protein; 350 AA.

DE Novel human secreted and transmembrane protein PRO295.
PD US2003180919-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1289
ID ADG85274 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PD US2003180904-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1290
ID ADH24550 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PD US2003180907-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1291
ID ADH37406 standard; protein; 350 AA.
DE Human secreted and transmembrane protein PRO295.
PD US2003181646-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1292
ID ADH01995 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PD US2003180837-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1293
ID ADH37576 standard; protein; 350 AA.
DE Human secreted and transmembrane protein PRO295.
PD US2003181648-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1294
ID ADG85614 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PD US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1295
ID ADH24210 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PD US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1296
ID ADH38504 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PD US2003181643-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
ID ADG83625 standard; protein; 350 AA.
DE Human PRO polypeptide #4.

PN US2003180794-A1.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1298
ID ADH29433 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1299
ID ADH27549 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1300
ID ADH37746 standard; protein; 350 AA.
DE Human secreted and transmembrane protein PRO295.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1301
ID ADH37923 standard; protein; 350 AA.
DE Human secreted and transmembrane protein PRO295.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1302
ID ADH57343 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1303
ID ADH59352 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1304
ID ADH53485 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1305
ID ADH53655 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1306
ID ADH51991 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181638-A1.

PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1307
ID ADH49846 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1308
ID ADI25356 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1309
ID ADH90149 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1310
ID ADI25526 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1311
ID ADH97700 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1312
ID ADI38131 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1313
ID ADI03548 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1314
ID ADI11905 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1315
ID ADH89979 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181697-A1.
PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1316
ID ADH98380 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1317
ID ADI11055 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1318
ID ADI11565 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1319
ID ADH98210 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1320
ID ADH98550 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1321
ID ADH98040 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1322
ID ADI05028 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1323
ID ADI03378 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1324
ID ADI04773 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1325
ID ADH78227 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1326
ID ADI19571 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1327
ID ADH90319 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1328
ID ADI03038 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1329
ID ADH77887 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1330
ID ADH97870 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1331
ID ADI01255 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1332
ID ADI01950 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1333
ID ADI03208 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;

Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1334
ID AD11395 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
FN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1335
ID AD102297 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
FN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1336
ID AD111735 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
FN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1337
ID AD105372 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
FN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1338
ID ADH79444 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
FN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1339
ID AD119401 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
FN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1340
ID AD105202 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
FN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1341
ID ADH79614 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
FN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1342
ID AD101440 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
FN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1343
ID AD101610 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
FN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1344
ID AD101780 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
FN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1345
ID ADH79784 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
FN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1346
ID AD104602 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
FN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1347
ID AD102738 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
FN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1348
ID ADH78057 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
FN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1349
ID AD125696 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
FN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1350
ID AD125866 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
FN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1351
ID ADK65378 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
FN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1352

ID ADH98720 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1353
ID ADH79961 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1354
ID ADJ26399 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1355
ID ADL93692 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1356
ID ADP65205 standard; protein; 350 AA.
DE Human dickkopf homologue 3, RIG-like 7-1, RIG-like 5-6.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 17.1%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1357
ID ADC52146 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1358
ID ADE79314 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1359
ID ADE79738 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1360
ID ADE73414 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1361
ID ADE41300 standard; protein; 350 AA.

DE Human secreted/transmembrane PRO polypeptide #25.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1362
ID ADE73949 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1363
ID ADE99503 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1364
ID ADE98622 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1365
ID ADE99049 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1366
ID ADG40519 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOVERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1367
ID ADP73913 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1368
ID ADF73489 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1369
ID ADH06578 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180852-A1.
PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
 Query Match 17.1%; Score 100.5; DB 8; Length 350;
 Best Local Similarity 37.7%; Pred. No. 0.045;
 RESULT 1370
 ID ADH06408 standard; protein; 350 AA.
 DE Novel human secreted and transmembrane protein PRO295.
 PN US2003180853-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.1%; Score 100.5; DB 8; Length 350;
 Best Local Similarity 37.7%; Pred. No. 0.045;
 RESULT 1371
 ID ADG68829 standard; protein; 350 AA.
 DE Novel human secreted and transmembrane protein PRO295.
 PN US2003180855-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.1%; Score 100.5; DB 8; Length 350;
 Best Local Similarity 37.7%; Pred. No. 0.045;
 RESULT 1372
 ID ADH27719 standard; protein; 350 AA.
 DE Novel human secreted and transmembrane protein PRO295.
 PN US2003180912-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.1%; Score 100.5; DB 8; Length 350;
 Best Local Similarity 37.7%; Pred. No. 0.045;
 RESULT 1373
 ID ADH25060 standard; protein; 350 AA.
 DE Novel human secreted and transmembrane protein PRO295.
 PN US2003180913-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.1%; Score 100.5; DB 8; Length 350;
 Best Local Similarity 37.7%; Pred. No. 0.045;
 RESULT 1374
 ID ADH33692 standard; protein; 350 AA.
 DE Human PRO polypeptide #4.
 PN US2003181645-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.1%; Score 100.5; DB 8; Length 350;
 Best Local Similarity 37.7%; Pred. No. 0.045;
 RESULT 1375
 ID ADG92332 standard; protein; 350 AA.
 DE Human secreted/transmembrane protein, #45.
 PN US2003027145-A1.
 PD 06-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.1%; Score 100.5; DB 8; Length 350;
 Best Local Similarity 37.7%; Pred. No. 0.045;
 RESULT 1376
 ID ADH02335 standard; protein; 350 AA.
 DE Human PRO polypeptide #4.
 PN US2003180839-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.1%; Score 100.5; DB 8; Length 350;
 Best Local Similarity 37.7%; Pred. No. 0.045;
 RESULT 1377
 ID ADH07942 standard; protein; 350 AA.
 DE Novel human secreted and transmembrane protein PRO295.
 PN US2003180845-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.1%; Score 100.5; DB 8; Length 350;
 Best Local Similarity 37.7%; Pred. No. 0.045;
 RESULT 1378
 ID ADG69339 standard; protein; 350 AA.
 DE Novel human secreted and transmembrane protein PRO295.
 PN US2003180846-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.

Query Match 17.1%; Score 100.5; DB 8; Length 350;
 Best Local Similarity 37.7%; Pred. No. 0.045;
 RESULT 1379
 ID ADH39160 standard; protein; 350 AA.
 DE Novel human secreted and transmembrane protein PRO295.
 PN US2003180917-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.1%; Score 100.5; DB 8; Length 350;
 Best Local Similarity 37.7%; Pred. No. 0.045;
 RESULT 1380
 ID ADG92759 standard; protein; 350 AA.
 DE Human secreted/transmembrane protein, #45.
 PN US2003027146-A1.
 PD 06-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.1%; Score 100.5; DB 8; Length 350;
 Best Local Similarity 37.7%; Pred. No. 0.045;
 RESULT 1381
 ID ADG83900 standard; protein; 350 AA.
 DE Human PRO polypeptide #4.
 PN US2003180842-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.1%; Score 100.5; DB 8; Length 350;
 Best Local Similarity 37.7%; Pred. No. 0.045;
 RESULT 1382
 ID ADG85444 standard; protein; 350 AA.
 DE Novel human secreted and transmembrane protein PRO295.
 PN US2003166848-A1.
 PD 04-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.1%; Score 100.5; DB 8; Length 350;
 Best Local Similarity 37.7%; Pred. No. 0.045;
 RESULT 1383
 ID ADH06238 standard; protein; 350 AA.
 DE Novel human secreted and transmembrane protein PRO295.
 PN US2003180854-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.1%; Score 100.5; DB 8; Length 350;
 Best Local Similarity 37.7%; Pred. No. 0.045;
 RESULT 1384
 ID ADH30068 standard; protein; 350 AA.
 DE Novel human secreted and transmembrane protein PRO295.
 PN US2003180856-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.1%; Score 100.5; DB 8; Length 350;
 Best Local Similarity 37.7%; Pred. No. 0.045;
 RESULT 1385
 ID ADH24380 standard; protein; 350 AA.
 DE Novel human secreted and transmembrane protein PRO295.
 PN US2003180910-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.1%; Score 100.5; DB 8; Length 350;
 Best Local Similarity 37.7%; Pred. No. 0.045;
 RESULT 1386
 ID ADG69509 standard; protein; 350 AA.
 DE Novel human secreted and transmembrane protein PRO295.
 PN US2003180844-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.1%; Score 100.5; DB 8; Length 350;
 Best Local Similarity 37.7%; Pred. No. 0.045;
 RESULT 1387
 ID ADH07772 standard; protein; 350 AA.
 DE Novel human secreted and transmembrane protein PRO295.
 PN US2003180851-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.1%; Score 100.5; DB 8; Length 350;
 Best Local Similarity 37.7%; Pred. No. 0.045;
 RESULT 1388

Best Local Similarity 37.7%; Pred. No. 0.045;
 RESULT 1388
 ID ADH24890 standard; protein; 350 AA.
 DE Novel human secreted and transmembrane protein PRO295.
 PN US2003180909-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.1%; Score 100.5; DB 8; Length 350;
 Best Local Similarity 37.7%; Pred. No. 0.045;
 RESULT 1389
 ID ADH39507 standard; protein; 350 AA.
 DE Novel human secreted and transmembrane protein PRO295.
 PN US2003180915-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.1%; Score 100.5; DB 8; Length 350;
 Best Local Similarity 37.7%; Pred. No. 0.045;
 RESULT 1390
 ID ADH33522 standard; protein; 350 AA.
 DE Human PRO polypeptide #4.
 PN US2003181637-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.1%; Score 100.5; DB 8; Length 350;
 Best Local Similarity 37.7%; Pred. No. 0.045;
 RESULT 1391
 ID ADH33862 standard; protein; 350 AA.
 DE Human PRO polypeptide #4.
 PN US2003181644-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.1%; Score 100.5; DB 8; Length 350;
 Best Local Similarity 37.7%; Pred. No. 0.045;
 RESULT 1392
 ID ADH01072 standard; protein; 350 AA.
 DE Human PRO polypeptide #4.
 PN US2003180838-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.1%; Score 100.5; DB 8; Length 350;
 Best Local Similarity 37.7%; Pred. No. 0.045;
 RESULT 1393
 ID ADG69679 standard; protein; 350 AA.
 DE Novel human secreted and transmembrane protein PRO295.
 PN US2003180843-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.1%; Score 100.5; DB 8; Length 350;
 Best Local Similarity 37.7%; Pred. No. 0.045;
 RESULT 1394
 ID ADH02165 standard; protein; 350 AA.
 DE Human PRO polypeptide #4.
 PN US2003180841-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.1%; Score 100.5; DB 8; Length 350;
 Best Local Similarity 37.7%; Pred. No. 0.045;
 RESULT 1395
 ID ADG69169 standard; protein; 350 AA.
 DE Novel human secreted and transmembrane protein PRO295.
 PN US2003180847-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.1%; Score 100.5; DB 8; Length 350;
 Best Local Similarity 37.7%; Pred. No. 0.045;
 RESULT 1396
 ID ADG85954 standard; protein; 350 AA.
 DE Novel human secreted and transmembrane protein PRO295.
 PN US2003180862-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.1%; Score 100.5; DB 8; Length 350;
 Best Local Similarity 37.7%; Pred. No. 0.045;
 RESULT 1397
 ID ADH24890 standard; protein; 350 AA.
 DE Novel human secreted and transmembrane protein PRO295.
 PN US2003180909-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.1%; Score 100.5; DB 8; Length 350;
 Best Local Similarity 37.7%; Pred. No. 0.045;
 RESULT 1398
 ID ADH39507 standard; protein; 350 AA.
 DE Novel human secreted and transmembrane protein PRO295.
 PN US2003180915-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.1%; Score 100.5; DB 8; Length 350;
 Best Local Similarity 37.7%; Pred. No. 0.045;
 RESULT 1399
 ID ADH02505 standard; protein; 350 AA.
 DE Human PRO polypeptide #4.
 PN US2003180840-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.1%; Score 100.5; DB 8; Length 350;
 Best Local Similarity 37.7%; Pred. No. 0.045;
 RESULT 1400
 ID ADG69999 standard; protein; 350 AA.
 DE Novel human secreted and transmembrane protein PRO295.
 PN US2003180849-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.1%; Score 100.5; DB 8; Length 350;
 Best Local Similarity 37.7%; Pred. No. 0.045;
 RESULT 1401
 ID ADH07602 standard; protein; 350 AA.
 DE Novel human secreted and transmembrane protein PRO295.
 PN US2003180850-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.1%; Score 100.5; DB 8; Length 350;
 Best Local Similarity 37.7%; Pred. No. 0.045;
 RESULT 1402
 ID ADG86124 standard; protein; 350 AA.
 DE Novel human secreted and transmembrane protein PRO295.
 PN US2003180863-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.1%; Score 100.5; DB 8; Length 350;
 Best Local Similarity 37.7%; Pred. No. 0.045;
 RESULT 1403
 ID ADH24720 standard; protein; 350 AA.
 DE Novel human secreted and transmembrane protein PRO295.
 PN US2003180908-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.1%; Score 100.5; DB 8; Length 350;
 Best Local Similarity 37.7%; Pred. No. 0.045;
 RESULT 1404
 ID ADH25768 standard; protein; 350 AA.
 DE Novel human secreted and transmembrane protein PRO295.
 PN US2003180911-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.1%; Score 100.5; DB 8; Length 350;
 Best Local Similarity 37.7%; Pred. No. 0.045;
 RESULT 1405
 ID ADH38334 standard; protein; 350 AA.
 DE Novel human secreted and transmembrane protein PRO295.
 PN US2003180922-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.1%; Score 100.5; DB 8; Length 350;
 Best Local Similarity 37.7%; Pred. No. 0.045;
 RESULT 1406

ID ADH20548 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
US2004000553-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1407
ID ADH57173 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
US2003181642-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1408
ID ADH43483 standard; protein; 350 AA.
DE Human PRO polypeptide #25.
US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1409
ID ADH07403 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
US2004006211-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1410
ID ADH52161 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
US2003180921-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1411
ID ADH59948 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
US2003215904-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1412
ID ADH49527 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
US2003180857-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1413
ID ADH06976 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
US2004005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1414
ID ADH90489 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
US2003181700-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1415
ID ADI11225 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
US2003181683-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1416
ID ADI18718 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
US2003152999-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1417
ID ADH98890 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
US2003190698-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1418
ID ADI65438 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
US2003148419-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1419
ID ADI02120 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
US2003190699-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1420
ID ADH90659 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
US2003181701-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1421
ID ADI37697 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
US2003096340-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1422
ID ADH97497 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
US2003190610-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;

Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1423
ID ADI5865 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003148371-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1424
ID ADH60608 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2004023331-A1.
PD 05-FEB-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A. J.
PA (GODO/) GODOWSKI P. J.
PA (GURN/) GURNEY A. L.
PA (MATH/) MATHER J. P.
PA (WILL/) WILLIAMS P. M.
PA (WOOD/) WOOD W. I.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1425
ID ADJ99665 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003187238-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1426
ID ADL08858 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003186358-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1427
ID ADJ98534 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1428
ID ADJ98704 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1429
ID ADH7863 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1430
ID ADJ99097 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1431
ID ADJ99267 standard; protein; 350 AA.

DE Novel human secreted and transmembrane protein PRO295.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1432
ID ADJ98885 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1433
ID ADH79033 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1434
ID ADK00893 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1435
ID ADK14414 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1436
ID ADM25199 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003096233-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1437
ID ADM29949 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1438
ID ADK82828 standard; protein; 350 AA.
DE Human PRO polypeptide #25.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1439
ID ADM60863 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1440
ID ADO06271 standard; protein; 350 AA.
DE Human PRO polypeptide #41.

PN	US6686451-B1.
PD	Q3-FEB-2004.
PA	(GETH) GENENTECH INC.
Query Match	17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity	37.7%; Pred. No. 0.045;
RESULT 1441	
ID	ADR11123 standard; protein; 350 AA.
DE	Human secreted/transmembrane protein, #45.
PN	US2004137561-A1.
PD	15-JUL-2004.
PA	(GETH) GENENTECH INC.
Query Match	17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity	37.7%; Pred. No. 0.045;
RESULT 1442	
ID	ADRI8032 standard; protein; 350 AA.
DE	Human secreted/transmembrane protein, #45.
PN	US2004147017-A1.
PD	29-JUL-2004.
PA	(ASHK/) ASHKENAZI A.
PA	(BOTS/) BOTSTEIN D.
PA	(DESN/) DESNOYERS L.
PA	(EATO/) EATON D L.
PA	(FERR/) FERRARA N.
PA	(FILV/) FILVAROFF E.
PA	(FONG/) FONG S.
PA	(GAOW/) GAO W.
PA	(GERB/) GERBER H.
PA	(GERR/) GERRITSEN M E.
PA	(GODD/) GODDARD A.
PA	(GODO/) GODOWSKI P J.
PA	(GRIM/) GRIMALDI C J.
PA	(GURN/) GURNEY A L.
PA	(HILL/) HILLAN K J.
PA	(KLJA/) KLJAVIN I J.
PA	(MATH/) MATHER J P.
PA	(PANJ/) PAN J.
PA	(PAONI) PAONI N F.
PA	(ROYM/) ROY M A.
PA	(STEW/) STEWART T A.
PA	(TUMA/) TUMAS D.
PA	(WILL/) WILLIAMS P M.
PA	(WOOD/) WOOD W I.
Query Match	17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity	37.7%; Pred. No. 0.045;
RESULT 1443	
ID	ADS74671 standard; protein; 350 AA.
DE	Human secreted/transmembrane protein #45.
PN	US2004185531-A1.
PD	23-SEP-2004.
PA	(ASHK/) ASHKENAZI A.
PA	(BOTS/) BOTSTEIN D.
PA	(DESN/) DESNOYERS L.
PA	(EATO/) EATON D L.
PA	(FERR/) FERRARA N.
PA	(FILV/) FILVAROFF E.
PA	(FONG/) FONG S.
PA	(GAOW/) GAO W.
PA	(GERB/) GERBER H.
PA	(GERR/) GERRITSEN M E.
PA	(GODD/) GODDARD A.
PA	(GODO/) GODOWSKI P J.
PA	(GRIM/) GRIMALDI C J.
PA	(GURN/) GURNEY A L.
PA	(HILL/) HILLAN K J.
PA	(KLJA/) KLJAVIN I J.
PA	(MATH/) MATHER J P.
PA	(PAONI) PAONI N F.
PA	(ROYM/) ROY M A.
PA	(STEW/) STEWART T A.
PA	(TUMA/) TUMAS D.
PA	(WILL/) WILLIAMS P M.
PA	(WOOD/) WOOD W I.
Query Match	17.1%; Score 100.5; DB 10; Length 350;
Best Local Similarity	37.7%; Pred. No. 0.045;
RESULT 1444	
ID	ADT03708 standard; protein; 350 AA.
DE	Human secreted/transmembrane protein, #45.
PN	US2003152922-A1.
PD	14-AUG-2003.
PA	(GETH) GENENTECH INC.
Query Match	17.1%; Score 100.5; DB 8; Length 350;
Best Local Similarity	37.7%; Pred. No. 0.045;
RESULT 1445	
ID	ADX77703 standard; protein; 350 AA.
DE	Neoplastic disease detection protein PRO295.
PN	US2005059102-A1.
PD	17-MAR-2005.
PA	(EATO/) EATON D L.
PA	(FILV/) FILVAROFF E.
PA	(GERR/) GERRITSEN M E.
PA	(GODD/) GODDARD A.
PA	(GODO/) GODOWSKI P J.
PA	(GRIM/) GRIMALDI J C.
PA	(GURN/) GURNEY A L.
PA	(WATA/) WATANABE C K.
PA	(WOOD/) WOOD W I.
Query Match	17.1%; Score 100.5; DB 9; Length 350;
Best Local Similarity	37.7%; Pred. No. 0.045;
RESULT 1446	
ID	AEA37946 standard; protein; 350 AA.
DE	Human secreted/transmembrane protein, #45.
PN	US2005112725-A1.
PD	26-MAY-2005.
PA	(GETH) GENENTECH INC.
Query Match	17.1%; Score 100.5; DB 9; Length 350;
Best Local Similarity	37.7%; Pred. No. 0.045;
RESULT 1447	
ID	AED23980 standard; protein; 350 AA.
DE	Human secreted protein PRO 295, SEQ ID 236.
PN	US2005214904-A1.
PD	29-SEP-2005.
PA	(GETH) GENENTECH INC.
Query Match	17.1%; Score 100.5; DB 9; Length 350;
Best Local Similarity	37.7%; Pred. No. 0.045;
RESULT 1448	
ID	AE669149 standard; protein; 350 AA.
DE	Integrin homologous PRO295 protein, SEQ ID 236.
PN	US6974689-B1.
PD	13-DEC-2005.
PA	(GETH) GENENTECH INC.
Query Match	17.1%; Score 100.5; DB 10; Length 350;
Best Local Similarity	37.7%; Pred. No. 0.045;
RESULT 1449	
ID	AEF12534 standard; protein; 350 AA.
DE	Human PRO295 protein SEQ ID NO:8.
PN	US200608901-A1.
PD	12-JAN-2006.
PA	(GETH) GENENTECH INC.
Query Match	17.1%; Score 100.5; DB 10; Length 350;
Best Local Similarity	37.7%; Pred. No. 0.045;
RESULT 1450	
ID	AEF74223 standard; protein; 350 AA.
DE	Human PRO295 protein SEQ ID NO:8.
PN	US2005260647-A1.
PD	24-NOV-2005.
PA	(EATO/) EATON D L.
PA	(FILV/) FILVAROFF E.
PA	(GERR/) GERRITSEN M E.
PA	(GODD/) GODDARD A.
PA	(GODO/) GODOWSKI P J.
PA	(GRIM/) GRIMALDI J C.
PA	(GURN/) GURNEY A L.
PA	(WATA/) WATANABE C K.
PA	(WOOD/) WOOD W I.
Query Match	17.1%; Score 100.5; DB 10; Length 350;
Best Local Similarity	37.7%; Pred. No. 0.045;
RESULT 1451	
ID	AEF74223 standard; protein; 350 AA.
DE	Human secreted/transmembrane protein, #45.
PN	US2004185531-A1.
PD	23-SEP-2004.
PA	(ASHK/) ASHKENAZI A.
PA	(BOTS/) BOTSTEIN D.
PA	(DESN/) DESNOYERS L.
PA	(EATO/) EATON

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Best Local Similarity 37.7%; Pred. No. 0.045;
RESULT 1451
ID AAF92069 standard; protein; 349 AA.
DE Murine DKR-3.
FN WO200018914-A2.
PD 06-APR-2000.
PA (AMGE-) AMGEN INC.
Query Match 16.7%; Score 98.5; DB 3; Length 349;
Best Local Similarity 37.7%; Pred. No. 0.074;
RESULT 1459
ID AAB08879 standard; protein; 349 AA.
DE A murine Dickkopf (Dkk)-3 protein.
FN WO200052047-A2.
PD 08-SEP-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 16.7%; Score 98.5; DB 3; Length 349;
Best Local Similarity 37.7%; Pred. No. 0.074;
RESULT 1460
ID AAF68233 standard; protein; 349 AA.
DE Murine Dickkopf homolog 3 (DKK-3) protein.
FN WO2006010534-A1.
PD 02-FEB-2006.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Query Match 16.7%; Score 98.5; DB 10; Length 349;
Best Local Similarity 37.7%; Pred. No. 0.074;
RESULT 1461
ID ADB82539 standard; protein; 84 AA.
DE Antibody that binds to DKK #6.
FN WO200292015-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 16.5%; Score 97; DB 7; Length 84;
Best Local Similarity 32.3%; Pred. No. 0.024;
RESULT 1462
ID ADE82541 standard; protein; 107 AA.
DE Antibody that binds to DKK #8.
FN WO200292015-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 16.5%; Score 97; DB 7; Length 107;
Best Local Similarity 32.3%; Pred. No. 0.03;
RESULT 1463
ID ADU66981 standard; protein; 108 AA.
DE Human DDK-1 LRP-6 binding domain.
FN US2004235166-A1.
PD 25-NOV-2004.
PA (PROC/) PROCKOP D.
PA (SEKI/) SEKIYA I.
PA (GREG/) GREGORY C.
PA (SPEE/) SPEES J.
PA (SMIT/) SMITH J.
PA (POCH/) POCHAMPALLY R.
Query Match 16.5%; Score 97; DB 8; Length 108;
Best Local Similarity 32.3%; Pred. No. 0.031;
RESULT 1464
ID ADZ51669 standard; protein; 108 AA.
DE Dickkopf-1 LDL receptor-related protein 6 binding site.
FN US2005084494-A1.
PD 21-APR-2005.
PA (PROC/) PROCKOP D.
PA (GREG/) GREGORY C.
PA (GUNN/) GUNN W.
Query Match 16.5%; Score 97; DB 9; Length 108;
Best Local Similarity 32.3%; Pred. No. 0.031;
RESULT 1465
ID ADE82538 standard; protein; 128 AA.
DE Antibody that binds to DKK #5.
FN WO200292015-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 16.5%; Score 97; DB 7; Length 128;
Best Local Similarity 32.3%; Pred. No. 0.074;

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Best Local Similarity 32.3%; Pred. No. 0.037;
 RESULT 1466
 ID ADE82540 standard; protein; 149 AA.
 DE Antibody that binds to DKK #7.
 PN WO200292015-A2.
 PD 21-NOV-2002.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 PA (AMHP) WYETH.
 Query Match 16.5%; Score 97; DB 7; Length 149;
 Best Local Similarity 32.3%; Pred. No. 0.043;
 RESULT 1467
 ID ADB99065 standard; protein; 151 AA.
 DE LRP5 constrained peptide OST264.
 PN WO200292000-A2.
 PD 21-NOV-2002.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 PA (AMHP) WYETH.
 Query Match 16.5%; Score 97; DB 7; Length 151;
 Best Local Similarity 32.3%; Pred. No. 0.044;
 RESULT 1468
 ID ADE82633 standard; protein; 151 AA.
 DE LRP5 peptide aptamer #10.
 PN WO200292015-A2.
 PD 21-NOV-2002.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 PA (AMHP) WYETH.
 Query Match 16.5%; Score 97; DB 7; Length 151;
 Best Local Similarity 32.3%; Pred. No. 0.044;
 RESULT 1469
 ID ADE82537 standard; protein; 170 AA.
 DE Antibody that binds to DKK #4.
 PN WO200292015-A2.
 PD 21-NOV-2002.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 PA (AMHP) WYETH.
 Query Match 16.5%; Score 97; DB 7; Length 170;
 Best Local Similarity 32.3%; Pred. No. 0.05;
 RESULT 1470
 ID ADB99066 standard; protein; 172 AA.
 DE LRP5 constrained peptide OST265.
 PN WO200292000-A2.
 PD 21-NOV-2002.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 PA (AMHP) WYETH.
 Query Match 16.5%; Score 97; DB 7; Length 172;
 Best Local Similarity 32.3%; Pred. No. 0.05;
 RESULT 1471
 ID ADE82634 standard; protein; 172 AA.
 DE LRP5 peptide aptamer #11.
 PN WO200292015-A2.
 PD 21-NOV-2002.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 PA (AMHP) WYETH.
 Query Match 16.5%; Score 97; DB 7; Length 172;
 Best Local Similarity 32.3%; Pred. No. 0.05;
 RESULT 1472
 ID ADO35296 standard; protein; 180 AA.
 DE Human Dkk1 carboxy terminal cysteine rich region.
 PN US2004014209-A1.
 PD 22-JAN-2004.
 PA (LASS) LASSAR A B.
 PA (MERC) MERCOLA M.
 PA (GUPT) GUPTA R.
 PA (WV) MARVIN M.
 PA (SCHN) SCHNEIDER V.
 PA (TZA) TZAHAOR B.
 PA (BROT) BROTT B.
 PA (SOKO) SOKOL S.
 Query Match 16.5%; Score 97; DB 8; Length 180;
 Best Local Similarity 32.3%; Pred. No. 0.053;
 RESULT 1473
 ID ADE82535 standard; protein; 212 AA.
 DE Antibody that binds to DKK #2.

PN WO200292015-A2.
 PD 21-NOV-2002.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 PA (AMHP) WYETH.
 Query Match 16.5%; Score 97; DB 7; Length 212;
 Best Local Similarity 32.3%; Pred. No. 0.063;
 RESULT 1474
 ID ADE82534 standard; protein; 233 AA.
 DE Antibody that binds to DKK #1.
 PN WO200292015-A2.
 PD 21-NOV-2002.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 PA (AMHP) WYETH.
 Query Match 16.5%; Score 97; DB 7; Length 233;
 Best Local Similarity 32.3%; Pred. No. 0.069;
 RESULT 1475
 ID AEA38731 standard; protein; 265 AA.
 DE Human dickkopf-1 (Dkk-1) protein, SEQ ID NO: 21 #1.
 PN WO2005049640-A2.
 PD 02-JUN-2005.
 PA (MERI) MERCK & CO INC.
 Query Match 16.5%; Score 97; DB 9; Length 265;
 Best Local Similarity 32.3%; Pred. No. 0.079;
 RESULT 1476
 ID AAW73018 standard; protein; 266 AA.
 DE Human cysteine-rich secreted protein CRSP-3.
 PN WO9846755-A1.
 PD 22-OCT-1998.
 PA (MILL) MILLENNIUM BIOTHERAPEUTICS INC.
 Query Match 16.5%; Score 97; DB 2; Length 266;
 Best Local Similarity 32.3%; Pred. No. 0.08;
 RESULT 1477
 ID AAY41757 standard; protein; 266 AA.
 DE Human PRO1008 protein sequence.
 PN WO9946281-A2.
 PD 16-SEP-1999.
 PA (GETH) GENENTECH INC.
 Query Match 16.5%; Score 97; DB 2; Length 266;
 Best Local Similarity 32.3%; Pred. No. 0.08;
 RESULT 1478
 ID AAY92071 standard; protein; 266 AA.
 DE Human DKR-1.
 PN WO200018914-A2.
 PD 06-APR-2000.
 PA (AMGE) AMGEN INC.
 Query Match 16.5%; Score 97; DB 3; Length 266;
 Best Local Similarity 32.3%; Pred. No. 0.08;
 RESULT 1479
 ID AAB44313 standard; protein; 266 AA.
 DE Human PRO1008 (UNQ492) protein sequence SEQ ID NO:456.
 PN WO200053756-A2.
 PD 14-SEP-2000.
 PA (GETH) GENENTECH INC.
 Query Match 16.5%; Score 97; DB 3; Length 266;
 Best Local Similarity 32.3%; Pred. No. 0.08;
 RESULT 1480
 ID AAB08876 standard; protein; 266 AA.
 DE Amino acid sequence of a human Dickkopf (Dkk)-1 protein.
 PN WO200052047-A2.
 PD 08-SEP-2000.
 PA (MILL) MILLENNIUM PHARM INC.
 Query Match 16.5%; Score 97; DB 3; Length 266;
 Best Local Similarity 32.3%; Pred. No. 0.08;
 RESULT 1481
 ID AAU12385 standard; protein; 266 AA.
 DE Human PRO1008 polypeptide sequence.
 PN WO200140466-A2.
 PD 07-JUN-2001.
 PA (GETH) GENENTECH INC.
 Query Match 16.5%; Score 97; DB 4; Length 266;
 Best Local Similarity 32.3%; Pred. No. 0.08;
 RESULT 1482
 ID AAW78517 standard; protein; 266 AA.

DE Human protein SEQ ID NO 1179.
 PN WO200157190-A2.
 PD 09-AUG-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 16.5%; Score 97; DB 4; Length 266;
 Best Local Similarity 32.3%; Pred. No. 0.08;
 RESULT 1483
 ID ABO17829 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO1008.
 PN US2003032156-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.5%; Score 97; DB 6; Length 266;
 Best Local Similarity 32.3%; Pred. No. 0.08;
 RESULT 1484
 ID ABO25259 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO1008.
 PN US2003050239-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.5%; Score 97; DB 6; Length 266;
 Best Local Similarity 32.3%; Pred. No. 0.08;
 RESULT 1485
 ID ABO81083 standard; protein; 266 AA.
 DE Human PRO polypeptide #214.
 PN US2003004311-A1.
 PD 02-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.5%; Score 97; DB 6; Length 266;
 Best Local Similarity 32.3%; Pred. No. 0.08;
 RESULT 1486
 ID ABO72265 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO1008.
 PN US2002192706-A1.
 PD 19-DEC-2002.
 PA (GETH) GENENTECH INC.
 Query Match 16.5%; Score 97; DB 6; Length 266;
 Best Local Similarity 32.3%; Pred. No. 0.08;
 RESULT 1487
 ID ASU66783 standard; protein; 266 AA.
 DE Human PRO polypeptide #214.
 PN US2003036180-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.5%; Score 97; DB 6; Length 266;
 Best Local Similarity 32.3%; Pred. No. 0.08;
 RESULT 1488
 ID ABUS5913 standard; protein; 266 AA.
 DE Human protein DKK1.
 PN WO200277204-A2.
 PD 03-OCT-2002.
 PA (AXOR-) AXORDIA LTD.
 Query Match 16.5%; Score 97; DB 6; Length 266;
 Best Local Similarity 32.3%; Pred. No. 0.08;
 RESULT 1489
 ID ABUS4945 standard; protein; 266 AA.
 DE Human secreted and transmembrane PRO polypeptide #21.
 PN US2002177553-A1.
 PD 28-NOV-2002.
 PA (GETH) GENENTECH INC.
 Query Match 16.5%; Score 97; DB 6; Length 266;
 Best Local Similarity 32.3%; Pred. No. 0.08;
 RESULT 1490
 ID AAE34067 standard; protein; 266 AA.
 DE DKK1 protein.
 PN WO200290992-A2.
 PD 14-NOV-2002.
 PA (AXOR-) AXORDIA LTD.
 Query Match 16.5%; Score 97; DB 6; Length 266;
 Best Local Similarity 32.3%; Pred. No. 0.08;
 RESULT 1491
 ID ABUS9864 standard; protein; 266 AA.
 DE Novel secreted and transmembrane protein PRO1008.

PN US2003017563-A1.
 PD 23-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.5%; Score 97; DB 6; Length 266;
 Best Local Similarity 32.3%; Pred. No. 0.08;
 RESULT 1492
 ID ABUG1143 standard; protein; 266 AA.
 DE Human PRO1008 polypeptide.
 PN US2002169284-A1.
 PD 14-NOV-2002.
 PA (GETH) GENENTECH INC.
 Query Match 16.5%; Score 97; DB 6; Length 266;
 Best Local Similarity 32.3%; Pred. No. 0.08;
 RESULT 1493
 ID ABUS7630 standard; protein; 266 AA.
 DE Differentially expressed breast cancer associated protein #17.
 PN US2002156263-A1.
 PD 24-OCT-2002.
 PA (CHEN/) CHEN H.
 Query Match 16.5%; Score 97; DB 6; Length 266;
 Best Local Similarity 32.3%; Pred. No. 0.08;
 RESULT 1494
 ID ABO25054 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #214.
 PN US2003036179-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.5%; Score 97; DB 6; Length 266;
 Best Local Similarity 32.3%; Pred. No. 0.08;
 RESULT 1495
 ID ABR01793 standard; protein; 266 AA.
 DE Human cancer-related protein, 151P1C7A.
 PN WO200283921-A2.
 PD 24-OCT-2002.
 PA (AGEN-) AGENSYS INC.
 Query Match 16.5%; Score 97; DB 6; Length 266;
 Best Local Similarity 32.3%; Pred. No. 0.08;
 RESULT 1496
 ID ABUS0412 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein PRO1008.
 PN US2003004102-A1.
 PD 02-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.5%; Score 97; DB 6; Length 266;
 Best Local Similarity 32.3%; Pred. No. 0.08;
 RESULT 1497
 ID ABUS7059 standard; protein; 266 AA.
 DE Human secreted/transmembrane, PRO, protein SEQ ID 428.
 PN US2003032155-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.5%; Score 97; DB 6; Length 266;
 Best Local Similarity 32.3%; Pred. No. 0.08;
 RESULT 1498
 ID ADA45947 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO1008.
 PN US2003022328-A1.
 PD 30-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.5%; Score 97; DB 6; Length 266;
 Best Local Similarity 32.3%; Pred. No. 0.08;
 RESULT 1499
 ID ADA76378 standard; protein; 266 AA.
 DE Human PRO polypeptide #214.
 PN US2003073212-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.5%; Score 97; DB 6; Length 266;
 Best Local Similarity 32.3%; Pred. No. 0.08;
 RESULT 1500
 ID ADA19028 standard; protein; 266 AA.
 DE Human PRO polypeptide #214.
 PN US2003054517-A1.

PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.08;

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OM protein - protein search, using sw model

Run on: November 29, 2007, 17:24:47 ; Search time 13 Seconds

(without alignments)

519.494 Million cell updates/sec

Title: US-10-692-299-2

Perfect score: 589

Sequence: 1 MRGATRVSIMLLLVTSVSDCA.....CSRPFDRGRCMDLKNINF 105

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Gapop 10.0 , Gapext 0.5

Searched: 284443 seqs, 65276767 residues

Total number of hits satisfying chosen parameters: 284443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : Published Applications AA_New:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
2	589	100.0	105	7	US-11-552-437-166
3	589	100.0	105	7	US-11-537-472-2
4	589	100.0	105	7	US-11-537-235-470
5	589	100.0	105	7	US-11-553-810-470
6	498	84.6	86	7	US-11-536-880-7
7	311.5	52.9	79	7	US-11-537-472-5
8	306	52.0	100	7	US-11-537-472-4
9	303	51.4	108	7	US-11-536-880-4
10	298	50.6	107	7	US-11-536-880-6
11	282.5	48.0	129	7	US-11-536-880-2
13	100.5	17.1	83	7	US-11-537-472-6
14	100.5	17.1	350	6	US-10-594-211-251
15	97	16.5	266	6	US-10-594-211-154
16	97	16.5	266	7	US-11-537-235-428
17	97	16.5	266	7	US-11-553-810-428
18	95.5	16.2	79	7	US-11-537-472-7
19	83.5	14.2	1814	7	US-11-257-477-162
20	78.5	13.3	1581	7	US-11-649-663A-906
21	76.5	13.0	2762	7	US-11-649-663A-2676
22	75	12.7	1563	7	US-11-649-663A-2514
23	75	12.6	1565	7	US-11-649-663A-2142
24	74.5	12.6	536	7	US-11-360-355-149216
25	74.5	12.6	593	7	US-11-528-927-483
26	74.5	12.6	593	7	US-11-528-950-483
27	74.5	12.6	3942	7	US-11-726-028-2

28	74.5	12.6	4125	7	US-11-726-028-1	Sequence 1, Appli
29	74	12.6	1248	7	US-11-649-663A-934	Sequence 934, App
30	73	12.4	435	7	US-11-799-117-10	Sequence 10, Appl
31	73	12.4	461	6	US-10-551-004-74	Sequence 74, Appl
32	73	12.4	461	7	US-11-714-841-462	Sequence 462, App
33	73	12.4	461	7	US-11-714-841-467	Sequence 467, App
34	73	12.4	461	7	US-11-799-117-4	Sequence 4, Appli
35	73	12.4	461	7	US-11-783-419-462	Sequence 462, App
36	73	12.4	461	7	US-11-783-419-467	Sequence 467, App
37	73	12.4	461	7	US-11-741-492-186	Sequence 186, App
38	73	12.4	467	7	US-11-502-761-618	Sequence 618, App
39	73	12.4	844	7	US-11-714-841-246	Sequence 246, App
40	73	12.4	844	7	US-11-714-841-251	Sequence 251, App
41	73	12.4	844	7	US-11-783-419-246	Sequence 246, App
42	73	12.4	844	7	US-11-783-419-251	Sequence 251, App
43	73	12.4	1170	7	US-11-649-663A-1988	Sequence 1988, Ap
44	73	12.4	3075	7	US-11-633-858-220	Sequence 220, App
45	73	12.4	3204	7	US-11-649-663A-2004	Sequence 2004, Ap
46	72.5	12.3	183	7	US-11-689-173-6573	Sequence 6573, Ap
47	72.5	12.3	183	7	US-11-689-173-9632	Sequence 9632, Ap
48	72.5	12.3	1391	7	US-11-649-663A-4782	Sequence 4782, Ap
49	72.5	12.3	2871	6	US-10-529-351A-4185	Sequence 4185, Ap
50	71.5	12.1	199	7	US-11-360-355-119444	Sequence 119444,
51	71.5	12.1	524	6	US-10-663-431-160	Sequence 160, App
52	71.5	12.1	559	6	US-10-663-431-152	Sequence 152, App
53	71.5	12.1	566	6	US-10-663-431-162	Sequence 162, App
54	71.5	12.1	581	6	US-10-663-431-154	Sequence 154, App
55	71.5	12.1	601	6	US-10-663-431-168	Sequence 168, App
56	71.5	12.1	639	6	US-10-663-431-158	Sequence 158, App
57	71.5	12.1	659	6	US-10-663-431-150	Sequence 150, App
58	71.5	12.1	681	6	US-10-663-431-166	Sequence 166, App
59	71.5	12.1	698	6	US-10-663-431-156	Sequence 156, App
60	71.5	12.1	701	6	US-10-663-431-164	Sequence 164, App
61	71.5	12.1	703	6	US-10-589-677-57	Sequence 57, Appl
62	71	12.1	593	6	US-10-529-351A-4846	Sequence 4846, Ap
63	71	12.1	789	7	US-11-649-663A-818	Sequence 818, App
64	71	12.1	789	7	US-11-649-663A-1730	Sequence 1730, Ap
65	71	12.1	1883	7	US-11-649-663A-708	Sequence 708, App
66	70.5	12.0	2380	7	US-11-649-663A-1698	Sequence 1698, Ap
67	70	11.9	682	6	US-10-438-246-33505	Sequence 33505, A
68	70	11.9	1255	7	US-11-649-663A-1594	Sequence 1594, Ap
69	70	11.9	1673	7	US-11-649-663A-1178	Sequence 1178, Ap
70	70	11.9	2658	7	US-11-649-663A-2464	Sequence 2464, Ap
71	70	11.9	3250	7	US-11-649-663A-2262	Sequence 2262, Ap
72	70	11.9	3682	7	US-11-649-663A-2486	Sequence 2486, Ap
73	69.5	11.8	1353	7	US-11-649-663A-66	Sequence 66, Appl
74	69	11.7	1131	7	US-11-649-663A-1604	Sequence 1604, Ap
75	69	11.7	1345	7	US-11-649-663A-2248	Sequence 2248, Ap
76	69	11.7	1568	7	US-11-649-663A-2546	Sequence 2546, Ap
77	69	11.7	1595	7	US-11-649-663A-2100	Sequence 2100, Ap
78	69	11.7	2910	7	US-11-403-116-1113	Sequence 1113, Ap
79	68.5	11.6	240	6	US-10-438-246-8761	Sequence 8761, Ap
80	68.5	11.6	724	7	US-11-360-355-131955	Sequence 131955,
81	68.5	11.6	827	6	US-10-438-246-20733	Sequence 20733, A
82	68.5	11.6	1081	7	US-11-649-663A-308	Sequence 308, App
83	68.5	11.6	1112	7	US-11-709-841-51	Sequence 51, Appl
84	68.5	11.6	1133	7	US-11-709-841-56	Sequence 56, Appl
85	68.5	11.6	1375	7	US-11-625-272-144	Sequence 144, App
86	68.5	11.6	3392	7	US-11-649-663A-1654	Sequence 1654, App
87	68	11.5	121	7	US-11-689-173-5816	Sequence 5816, Ap
88	68	11.5	121	7	US-11-689-173-9242	Sequence 9242, Ap
89	68	11.5	1300	7	US-11-649-663A-112	Sequence 112, App
90	68	11.5	1302	7	US-11-649-663A-2152	Sequence 2152, Ap
91	67.5	11.5	117	7	US-11-689-173-11210	Sequence 11210, A
92	67.5	11.5	169	6	US-10-767-701-56401	Sequence 56401, A
93	67.5	11.5	222	6	US-10-767-701-56855	Sequence 56855, A
94	67.5	11.5	863	7	US-11-713-768-82720	Sequence 82720, A
95	67.5	11.5	893	7	US-11-713-768-82719	Sequence 82719, A
96	67.5	11.5	894	7	US-11-649-663A-1892	Sequence 1892, Ap
97	67.5	11.5	895	7	US-11-713-768-82718	Sequence 82718, A
98	67.5	11.5	957	7	US-11-649-663A-1976	Sequence 1976, Ap
99	67.5	11.5	1094	7	US-11-649-663A-1356	Sequence 1356, Ap
100	67.5	11.5	1641	7	US-11-649-663A-760	Sequence 760, App

101	67	11.4	148	7	US-11-786-368-14	Sequence 14, Appl	174	65	11.0	1437	7	US-11-649-663A-2302	Sequence 2302, Ap
102	67	11.4	148	7	US-11-786-369-14	Sequence 14, Appl	175	65	11.0	1438	7	US-11-649-663A-1716	Sequence 1716, Ap
103	67	11.4	984	7	US-11-649-663A-2022	Sequence 2022, Ap	176	65	11.0	1596	7	US-11-649-663A-792	Sequence 792, App
104	67	11.4	1293	7	US-11-633-858-133	Sequence 133, App	177	65	11.0	1601	7	US-11-649-663A-2686	Sequence 2686, Ap
105	67	11.4	1290	7	US-11-633-858-133	Sequence 133, App	178	65	11.0	1801	7	US-11-649-663A-2660	Sequence 2660, Ap
106	67	11.4	1379	7	US-11-649-663A-832	Sequence 832, App	179	65	11.0	1944	7	US-11-649-663A-2442	Sequence 2442, Ap
107	67	11.4	1861	7	US-11-649-663A-1744	Sequence 1744, App	180	65	11.0	2508	7	US-11-649-663A-1998	Sequence 1998, Ap
108	67	11.4	1873	7	US-11-649-663A-846	Sequence 846, App	181	65	11.0	2628	7	US-11-649-663A-2692	Sequence 2692, Ap
109	67	11.4	2321	7	US-11-633-858-216	Sequence 216, App	182	65	11.0	4147	7	US-11-726-028-3	Sequence 3, Appl
110	66.5	11.3	959	7	US-11-649-663A-5346	Sequence 5346, Ap	183	65	11.0	4655	7	US-11-542-670-17	Sequence 17, Appl
111	66.5	11.3	1070	7	US-11-649-663A-2300	Sequence 2300, Ap	184	65	11.0	4659	7	US-11-649-663A-1816	Sequence 1816, Ap
112	66.5	11.3	1232	7	US-11-649-663A-2840	Sequence 2840, Ap	185	64.5	11.0	141	7	US-11-713-768-67485	Sequence 67485, A
113	66.5	11.3	1233	7	US-11-649-663A-734	Sequence 734, App	186	64.5	11.0	229	7	US-11-713-768-67483	Sequence 67483, A
114	66.5	11.3	1289	7	US-11-649-663A-434	Sequence 434, App	187	64.5	11.0	264	6	US-10-438-246-10848	Sequence 10848, A
115	66.5	11.3	1375	6	US-10-529-351A-4026	Sequence 4026, Ap	188	64.5	11.0	873	7	US-11-649-663A-1646	Sequence 1646, A
116	66.5	11.3	1737	7	US-11-649-663A-2046	Sequence 2046, Ap	189	64.5	11.0	914	6	US-10-438-246-20254	Sequence 20254, A
117	66.5	11.3	1918	7	US-11-649-663A-692	Sequence 692, App	190	64.5	11.0	1042	7	US-11-649-663A-356	Sequence 356, App
118	66	11.2	85	7	US-11-214-372B-520	Sequence 520, App	191	64.5	11.0	1060	7	US-11-649-663A-2216	Sequence 2216, Ap
119	66	11.2	158	7	US-11-689-173-10535	Sequence 10535, A	192	64.5	11.0	1388	7	US-11-649-663A-1842	Sequence 1842, Ap
120	66	11.2	158	7	US-11-689-173-10537	Sequence 10537, A	193	64.5	11.0	1391	7	US-11-649-663A-566	Sequence 566, App
121	66	11.2	777	7	US-11-218-035-3	Sequence 3, Appl	194	64.5	11.0	1564	7	US-11-649-663A-798	Sequence 798, App
122	66	11.2	1215	7	US-11-649-663A-2800	Sequence 2800, Ap	195	64.5	11.0	1617	7	US-11-649-663A-2448	Sequence 2448, Ap
123	66	11.2	1220	7	US-11-649-663A-1044	Sequence 1044, Ap	196	64.5	11.0	1659	7	US-11-649-663A-1436	Sequence 1436, Ap
124	66	11.2	1263	7	US-11-649-663A-2848	Sequence 2848, Ap	197	64.5	11.0	2000	6	US-11-649-663A-422	Sequence 422, App
125	66	11.2	1269	7	US-11-649-663A-232	Sequence 232, App	198	64.5	11.0	2037	7	US-11-649-663A-4852	Sequence 4852, Ap
126	66	11.2	1296	7	US-11-649-663A-750	Sequence 750, App	199	64.5	11.0	2214	6	US-10-539-443-2	Sequence 2, Appl
127	66	11.2	1419	7	US-11-649-663A-132	Sequence 132, App	200	64.5	11.0	2279	6	US-10-533-069-990	Sequence 990, App
128	66	11.2	1489	7	US-11-649-663A-2422	Sequence 2422, Ap	201	64.5	11.0	2344	7	US-11-649-663A-1496	Sequence 1496, Ap
129	66	11.2	1490	7	US-11-649-663A-2534	Sequence 2534, Ap	202	64.5	11.0	3331	7	US-11-649-663A-1574	Sequence 1574, Ap
130	66	11.2	1491	7	US-11-649-663A-382	Sequence 382, App	203	64	10.9	412	7	US-11-529-826-13	Sequence 13, Appl
131	66	11.2	1492	7	US-11-649-663A-2094	Sequence 2094, Ap	204	64	10.9	426	7	US-11-713-768-24730	Sequence 24730, A
132	66	11.2	1509	7	US-11-649-663A-1838	Sequence 1838, Ap	205	64	10.9	475	6	US-10-533-069-458	Sequence 458, App
133	66	11.2	1510	7	US-11-649-663A-838	Sequence 838, App	206	64	10.9	475	6	US-11-649-663A-5446	Sequence 5446, Ap
134	66	11.2	1511	7	US-11-649-663A-1120	Sequence 1120, Ap	207	64	10.9	625	7	US-10-587-253-5	Sequence 5, Appl
135	66	11.2	1527	7	US-11-649-663A-1326	Sequence 1326, Ap	208	64	10.9	1143	6	US-11-649-663A-2290	Sequence 2290, Ap
136	66	11.2	1527	7	US-11-649-663A-866	Sequence 866, App	209	64	10.9	1365	7	US-11-649-663A-622	Sequence 622, App
137	66	11.2	1686	7	US-11-649-663A-2224	Sequence 2224, App	210	64	10.9	1375	7	US-11-649-663A-466	Sequence 466, App
138	65.5	11.1	166	7	US-11-713-768-65783	Sequence 65783, A	211	64	10.9	1396	7	US-11-649-663A-2522	Sequence 2522, Ap
139	65.5	11.1	173	7	US-11-689-173-10538	Sequence 10538, A	212	64	10.9	1754	7	US-11-649-663A-2600	Sequence 2600, Ap
140	65.5	11.1	179	7	US-11-751-886-177	Sequence 177, App	213	64	10.9	1758	7	US-11-649-663A-940	Sequence 940, App
141	65.5	11.1	183	7	US-11-713-768-65781	Sequence 65781, A	214	64	10.9	1859	7	US-11-649-663A-1078	Sequence 1078, Ap
142	65.5	11.1	189	7	US-11-689-173-11209	Sequence 11209, A	215	64	10.9	1914	7	US-11-649-663A-1384	Sequence 1384, Ap
143	65.5	11.1	241	7	US-11-689-173-11207	Sequence 11207, A	216	64	10.9	2128	7	US-11-649-663A-90	Sequence 90, Appl
144	65.5	11.1	241	7	US-11-689-173-11208	Sequence 11208, A	217	64	10.9	2568	7	US-11-649-663A-58	Sequence 58, Appl
145	65.5	11.1	259	6	US-10-529-351A-5585	Sequence 5585, Ap	218	64	10.9	2643	7	US-11-649-663A-1528	Sequence 1528, Ap
146	65.5	11.1	262	7	US-11-689-173-7990	Sequence 7990, Ap	219	64	10.9	1011	7	US-11-649-663A-4164	Sequence 4164, Ap
147	65.5	11.1	262	7	US-11-689-173-9112	Sequence 9112, Ap	220	64	10.9	1307	7	US-11-649-663A-2234	Sequence 2234, Ap
148	65.5	11.1	262	7	US-11-689-173-9112	Sequence 9112, Ap	221	63.5	10.8	1611	7	US-11-649-663A-2552	Sequence 2552, Ap
149	65.5	11.1	269	7	US-11-537-235-532	Sequence 532, App	222	63.5	10.8	1611	7	US-11-649-663A-1340	Sequence 1340, Ap
150	65.5	11.1	269	7	US-11-553-810-332	Sequence 532, App	223	63.5	10.8	1641	7	US-11-649-663A-598	Sequence 598, App
151	65.5	11.1	303	7	US-11-689-173-10536	Sequence 10536, A	224	63.5	10.8	1685	7	US-11-649-663A-762	Sequence 762, App
152	65.5	11.1	1271	7	US-11-649-663A-2618	Sequence 2618, Ap	225	63.5	10.8	1691	7	US-11-649-663A-2086	Sequence 2086, Ap
153	65.5	11.1	1272	7	US-11-649-663A-422	Sequence 422, App	226	63.5	10.8	1708	7	US-11-649-663A-2750	Sequence 2750, Ap
154	65.5	11.1	1274	7	US-11-649-663A-1848	Sequence 1848, Ap	227	63.5	10.8	1744	7	US-11-649-663A-1438	Sequence 1438, Ap
155	65.5	11.1	1660	7	US-11-649-663A-2132	Sequence 2132, Ap	228	63.5	10.8	1779	7	US-11-649-663A-1478	Sequence 1478, Ap
156	65.5	11.1	1661	7	US-11-649-663A-1792	Sequence 1792, Ap	229	63.5	10.8	1830	7	US-11-649-663A-2350	Sequence 2350, Ap
157	65.5	11.1	1942	7	US-11-649-663A-1296	Sequence 1296, Ap	230	63.5	10.8	1832	7	US-11-649-663A-1980	Sequence 1980, Ap
158	65.5	11.1	2556	6	US-10-767-701-42785	Sequence 42785, A	231	63.5	10.8	1845	7	US-11-649-663A-4998	Sequence 4998, Ap
159	65	11.0	95	6	US-10-767-701-42785	Sequence 42785, A	232	63.5	10.8	1870	7	US-11-649-663A-5510	Sequence 5510, Ap
160	65	11.0	397	6	US-10-767-701-51471	Sequence 51471, A	233	63.5	10.8	2247	7	US-11-649-663A-138	Sequence 138, App
161	65	11.0	504	7	US-11-360-355-120732	Sequence 120732, A	234	63.5	10.8	2499	7	US-11-625-272-139	Sequence 139, App
162	65	11.0	504	7	US-11-360-355-120732	Sequence 120732, A	235	63.5	10.8	3707	7	US-11-713-768-6149	Sequence 6149, Ap
163	65	11.0	575	7	US-11-689-173-6159	Sequence 6159, Ap	236	63	10.7	298	7	US-11-713-768-6148	Sequence 6148, Ap
164	65	11.0	575	7	US-11-689-173-6159	Sequence 6159, Ap	237	63	10.7	386	7	US-11-713-768-6148	Sequence 6148, Ap
165	65	11.0	1135	7	US-11-649-663A-2204	Sequence 2204, Ap	238	63	10.7	562	7	US-11-649-663A-3662	Sequence 3662, Ap
166	65	11.0	1209	7	US-11-649-663A-1610	Sequence 1610, Ap	239	63	10.7	738	7	US-11-649-663A-816	Sequence 816, App
167	65	11.0	1218	6	US-10-594-211-169	Sequence 169, App	240	63	10.7	1103	7	US-11-649-663A-2450	Sequence 2450, Ap
168	65	11.0	1218	6	US-10-594-211-245	Sequence 245, App	241	63	10.7	1139	6	US-10-587-253-6	Sequence 6, Appl
169	65	11.0	1218	6	US-10-594-211-252	Sequence 252, App	242	63	10.7	1144	7	US-11-649-663A-2720	Sequence 2720, Ap
170	65	11.0	1218	7	US-11-625-272-154	Sequence 154, App	243	63	10.7	1288	7	US-11-403-116-1110	Sequence 1110, Ap
171	65	11.0	1218	7	US-11-633-858-194	Sequence 194, App	244	63	10.7	1471	7	US-11-649-663A-2316	Sequence 2316, Ap
172	65	11.0	1242	7	US-11-649-663A-1968	Sequence 1968, Ap	245	63	10.7				
173	65	11.0	1416	7	US-11-649-663A-1684	Sequence 1684, Ap	246	63	10.7				

247	63	10.7	1753	7	US-11-649-663A-1198	Sequence 1198, Ap	320	62	10.5	3409	7	US-11-257-477-165	Sequence 165, App
248	63	10.7	1964	7	US-11-649-663A-4458	Sequence 4458, Ap	322	61.5	10.4	159	7	US-11-689-173-7143	Sequence 7143, Ap
249	63	10.7	2105	7	US-11-649-663A-1154	Sequence 1154, Ap	323	61.5	10.4	159	7	US-11-689-173-10034	Sequence 10034, A
250	63	10.7	2117	7	US-11-649-663A-2836	Sequence 2836, Ap	324	61.5	10.4	179	7	US-11-689-173-9587	Sequence 9587, Ap
251	63	10.7	2195	7	US-11-649-663A-5412	Sequence 5412, Ap	325	61.5	10.4	231	7	US-11-360-355-151313	Sequence 151313, Ap
252	63	10.7	4243	7	US-11-649-663A-1722	Sequence 1722, Ap	326	61.5	10.4	256	7	US-11-360-355-1513083	Sequence 1513083, Ap
253	62.5	10.6	179	7	US-11-713-768-61518	Sequence 61518, A	327	61.5	10.4	277	6	US-10-533-069-1076	Sequence 1076, Ap
254	62.5	10.6	211	7	US-11-713-768-61517	Sequence 61517, A	328	61.5	10.4	282	6	US-10-533-069-1230	Sequence 1230, Ap
255	62.5	10.6	213	7	US-11-649-663A-2784	Sequence 2784, Ap	329	61.5	10.4	282	6	US-10-529-351A-5217	Sequence 5217, Ap
256	62.5	10.6	466	7	US-11-649-663A-1342	Sequence 1342, Ap	330	61.5	10.4	282	7	US-11-537-235-312	Sequence 312, App
257	62.5	10.6	703	6	US-10-663-431-147	Sequence 147, App	331	61.5	10.4	282	7	US-11-553-810-312	Sequence 312, App
258	62.5	10.6	705	6	US-10-589-677-55	Sequence 55, App	332	61.5	10.4	303	7	US-11-360-355-150454	Sequence 150454, Ap
259	62.5	10.6	1003	7	US-11-649-663A-2592	Sequence 2592, Ap	333	61.5	10.4	527	7	US-11-360-355-152732	Sequence 152732, Ap
260	62.5	10.6	1049	7	US-11-649-663A-6214	Sequence 6214, App	334	61.5	10.4	710	7	US-11-649-663A-4112	Sequence 4112, Ap
261	62.5	10.6	1164	7	US-11-649-663A-2248	Sequence 2248, Ap	335	61.5	10.4	869	7	US-11-673-351-1200	Sequence 1200, Ap
262	62.5	10.6	1189	7	US-11-649-663A-1964	Sequence 1964, Ap	336	61.5	10.4	1050	7	US-11-649-663A-2762	Sequence 2762, Ap
263	62.5	10.6	1285	7	US-11-649-663A-1124	Sequence 1124, Ap	337	61.5	10.4	1278	7	US-11-649-663A-556	Sequence 556, App
264	62.5	10.6	1298	7	US-11-649-663A-826	Sequence 826, App	338	61.5	10.4	1277	7	US-11-649-663A-784	Sequence 784, App
265	62.5	10.6	1432	7	US-11-649-663A-2846	Sequence 2846, Ap	339	61.5	10.4	1249	7	US-11-649-663A-2566	Sequence 2566, Ap
266	62.5	10.6	1459	7	US-11-649-663A-1332	Sequence 1332, Ap	340	61.5	10.4	1251	7	US-11-649-663A-346	Sequence 346, App
267	62.5	10.6	1493	7	US-11-649-663A-4196	Sequence 4196, Ap	341	61.5	10.4	1277	7	US-11-649-663A-634	Sequence 634, App
268	62.5	10.6	1573	7	US-11-649-663A-770	Sequence 770, App	342	61.5	10.4	1278	7	US-11-649-663A-1626	Sequence 1626, Ap
269	62.5	10.6	1573	7	US-11-649-663A-594	Sequence 594, App	343	61.5	10.4	1303	7	US-11-649-663A-1570	Sequence 1570, Ap
270	62.5	10.6	1600	7	US-11-649-663A-2664	Sequence 2664, Ap	344	61.5	10.4	1357	7	US-11-649-663A-1946	Sequence 1946, Ap
271	62.5	10.6	1680	7	US-11-649-663A-712	Sequence 712, App	345	61.5	10.4	1358	7	US-11-649-663A-2238	Sequence 2238, Ap
272	62.5	10.6	1736	7	US-11-649-663A-2668	Sequence 2668, Ap	346	61.5	10.4	1676	7	US-11-649-663A-628	Sequence 628, App
273	62.5	10.6	1962	7	US-11-649-663A-1446	Sequence 1446, Ap	347	61.5	10.4	1681	7	US-11-649-663A-416	Sequence 416, App
274	62.5	10.6	2052	7	US-11-649-663A-652	Sequence 652, App	348	61.5	10.4	1689	7	US-11-649-663A-2456	Sequence 2456, Ap
275	62.5	10.6	2368	7	US-11-649-663A-2844	Sequence 2844, Ap	349	61.5	10.4	1702	7	US-11-649-663A-2114	Sequence 2114, Ap
276	62.5	10.6	2391	7	US-11-649-663A-1386	Sequence 1386, Ap	350	61.5	10.4	1736	7	US-11-649-663A-664	Sequence 664, App
277	62.5	10.6	2973	7	US-11-649-663A-1754	Sequence 1754, Ap	351	61.5	10.4	1741	7	US-11-649-663A-726	Sequence 726, App
278	62.5	10.6	3018	7	US-11-649-663A-1936	Sequence 1936, Ap	352	61.5	10.4	1776	7	US-11-649-663A-2554	Sequence 2554, Ap
279	62	10.5	48	7	US-11-528-927-307	Sequence 307, App	353	61.5	10.4	1809	7	US-11-649-663A-1302	Sequence 1302, Ap
280	62	10.5	48	7	US-11-528-950-307	Sequence 307, App	354	61.5	10.4	1814	7	US-11-649-663A-1302	Sequence 1302, Ap
281	62	10.5	685	7	US-11-709-841-50	Sequence 50, Appl	355	61.5	10.4	1844	7	US-11-649-663A-930	Sequence 930, App
282	62	10.5	707	7	US-11-709-841-58	Sequence 58, Appl	356	61.5	10.4	1913	6	US-10-529-351A-5	Sequence 5, Appl
283	62	10.5	804	7	US-11-709-841-49	Sequence 49, Appl	357	61.5	10.4	2012	7	US-11-649-663A-528	Sequence 528, App
284	62	10.5	984	7	US-11-649-663A-1592	Sequence 1592, Ap	358	61.5	10.4	2143	7	US-11-649-663A-1284	Sequence 1284, Ap
285	62	10.5	1017	7	US-11-649-663A-956	Sequence 956, App	359	61.5	10.4	2157	7	US-11-550-102-2	Sequence 2, Appl
286	62	10.5	1152	7	US-11-649-663A-2712	Sequence 2712, Ap	360	61.5	10.4	2337	7	US-11-649-663A-1868	Sequence 1868, Ap
287	62	10.5	1170	7	US-11-709-841-44	Sequence 44, Appl	361	61.5	10.4	2440	7	US-11-649-663A-1294	Sequence 1294, Ap
288	62	10.5	1170	7	US-11-709-841-45	Sequence 45, Appl	362	61.5	10.4	2514	7	US-11-649-663A-2064	Sequence 2064, Ap
289	62	10.5	1170	7	US-11-709-841-47	Sequence 47, Appl	363	61.5	10.4	2570	6	US-10-529-351A-1164	Sequence 1164, Ap
290	62	10.5	1170	7	US-11-741-492-138	Sequence 138, App	364	61.5	10.4	2670	7	US-11-649-663A-1786	Sequence 1786, Ap
291	62	10.5	1191	7	US-11-709-841-54	Sequence 54, Appl	365	61.5	10.4	3259	7	US-11-649-663A-1020	Sequence 1020, Ap
292	62	10.5	1192	7	US-11-649-663A-2814	Sequence 2814, Ap	366	61.5	10.4	3259	7	US-11-649-663A-2622	Sequence 2622, Ap
293	62	10.5	1194	7	US-11-649-663A-5030	Sequence 5030, Ap	367	61.5	10.4	3658	7	US-11-649-663A-1668	Sequence 1668, Ap
294	62	10.5	1228	7	US-11-649-663A-980	Sequence 980, App	368	61	10.4	79	7	US-11-537-472-8	Sequence 8, Appl
295	62	10.5	1315	7	US-11-649-663A-610	Sequence 610, App	369	61	10.4	248	7	US-11-360-355-167671	Sequence 167671, Ap
296	62	10.5	1337	7	US-11-649-663A-2460	Sequence 2460, Ap	370	61	10.4	401	7	US-11-360-355-131018	Sequence 131018, Ap
297	62	10.5	1347	7	US-11-649-663A-1066	Sequence 1066, Ap	371	61	10.4	585	7	US-11-649-663A-1978	Sequence 1978, Ap
298	62	10.5	1376	7	US-11-649-663A-378	Sequence 378, App	372	61	10.4	715	6	US-10-529-351A-5533	Sequence 5533, Ap
299	62	10.5	1379	7	US-11-649-663A-1738	Sequence 1738, Ap	373	61	10.4	780	7	US-11-649-663A-1866	Sequence 1866, Ap
300	62	10.5	1462	7	US-11-649-663A-1174	Sequence 1174, Ap	374	61	10.4	787	7	US-11-633-858-172	Sequence 172, App
301	62	10.5	1476	7	US-11-649-663A-972	Sequence 972, App	375	61	10.4	795	7	US-11-741-492-98	Sequence 98, Appl
302	62	10.5	1482	7	US-11-649-663A-1804	Sequence 1804, Ap	376	61	10.4	795	7	US-11-649-663A-1856	Sequence 1856, Ap
303	62	10.5	1486	7	US-11-649-663A-2236	Sequence 2236, Ap	377	61	10.4	923	7	US-11-649-663A-4314	Sequence 4314, Ap
304	62	10.5	1495	7	US-11-649-663A-776	Sequence 776, App	378	61	10.4	936	7	US-11-649-663A-4702	Sequence 4702, Ap
305	62	10.5	1506	7	US-11-649-663A-1870	Sequence 1870, App	379	61	10.4	972	7	US-11-649-663A-1318	Sequence 1318, Ap
306	62	10.5	1532	7	US-11-649-663A-2324	Sequence 2324, Ap	380	61	10.4	978	7	US-11-649-663A-120	Sequence 120, App
307	62	10.5	1542	7	US-11-649-663A-50	Sequence 50, Appl	381	61	10.4	987	7	US-11-649-663A-236	Sequence 236, App
308	62	10.5	1638	7	US-11-649-663A-660	Sequence 660, App	382	61	10.4	1047	7	US-11-649-663A-1534	Sequence 1534, Ap
309	62	10.5	1676	7	US-11-649-663A-546	Sequence 546, App	383	61	10.4	1050	7	US-11-649-663A-720	Sequence 720, App
310	62	10.5	1709	7	US-11-649-663A-3210	Sequence 3210, Ap	384	61	10.4	1052	7	US-11-649-663A-1750	Sequence 1750, Ap
311	62	10.5	1745	7	US-11-649-663A-960	Sequence 960, App	385	61	10.4	1055	7	US-11-649-663A-3194	Sequence 3194, Ap
312	62	10.5	1802	7	US-11-649-663A-1932	Sequence 1932, Ap	386	61	10.4	1117	7	US-11-649-663A-1458	Sequence 1458, Ap
313	62	10.5	1919	7	US-11-649-663A-2170	Sequence 2170, Ap	387	61	10.4	1144	7	US-11-649-663A-506	Sequence 506, App
314	62	10.5	1942	7	US-11-649-663A-2732	Sequence 2732, Ap	388	61	10.4	1170	6	US-10-533-069-155	Sequence 155, App
315	62	10.5	1959	7	US-11-649-663A-1428	Sequence 1428, Ap	389	61	10.4	1212	7	US-11-649-663A-1696	Sequence 1696, Ap
316	62	10.5	1962	7	US-11-649-663A-1748	Sequence 1748, Ap	390	61	10.4	1245	7	US-11-649-663A-1904	Sequence 1904, Ap
317	62	10.5	1962	7	US-11-649-663A-2754	Sequence 2754, Ap	391	61	10.4	1261	7	US-11-649-663A-668	Sequence 668, App
318	62	10.5	2003	7	US-11-649-663A-5496	Sequence 5496, Ap	392	61	10.4	1270	7	US-11-649-663A-1252	Sequence 1252, Ap
319	62	10.5	2762	7	US-11-649-663A-2672	Sequence 2672, Ap	393	61	10.4	1270	7	US-11-649-663A-2730	Sequence 2730, Ap

394	61	10.4	1287	7	US-11-649-663A-444	Sequence 444, App	468	60.5	10.3	2030	7	US-11-649-663A-3682	Sequence 3682, App
395	61	10.4	1367	7	US-11-649-663A-510	Sequence 510, App	469	60.5	10.3	2077	7	US-11-649-663A-2340	Sequence 2340, App
396	61	10.4	1432	7	US-11-649-663A-1100	Sequence 1100, App	470	60.5	10.3	2079	7	US-11-649-663A-2126	Sequence 2126, App
397	61	10.4	1434	7	US-11-649-663A-1194	Sequence 1194, App	471	60.5	10.3	2079	7	US-11-649-663A-2408	Sequence 2408, App
398	61	10.4	1459	7	US-11-649-663A-1350	Sequence 1350, App	472	60.5	10.3	2079	7	US-11-649-663A-1642	Sequence 1642, App
399	61	10.4	1524	7	US-11-649-663A-2656	Sequence 2656, App	473	60.5	10.3	2079	7	US-11-649-663A-2802	Sequence 2802, App
400	61	10.4	1524	7	US-11-649-663A-1596	Sequence 1596, App	474	60	10.2	65	7	US-11-649-663A-2802	Sequence 2802, App
401	61	10.4	1591	7	US-11-649-663A-1132	Sequence 1132, App	475	60	10.2	65	7	US-11-360-355-126465	Sequence 126465,
402	61	10.4	1630	7	US-11-649-663A-2222	Sequence 2222, App	476	60	10.2	659	7	US-11-649-663A-614	Sequence 614, App
403	61	10.4	1660	7	US-11-649-663A-670	Sequence 670, App	477	60	10.2	850	7	US-11-649-663A-534	Sequence 534, App
404	61	10.4	1660	7	US-11-649-663A-2926	Sequence 2926, App	478	60	10.2	850	7	US-11-649-663A-1470	Sequence 1470, App
405	61	10.4	1751	7	US-11-649-663A-570	Sequence 570, App	479	60	10.2	1033	7	US-11-649-663A-596	Sequence 596, App
406	61	10.4	1751	7	US-11-649-663A-2426	Sequence 2426, App	480	60	10.2	1077	7	US-11-649-663A-1630	Sequence 1630, App
407	61	10.4	1856	7	US-11-649-663A-332	Sequence 332, App	481	60	10.2	1132	7	US-11-649-663A-394	Sequence 394, App
408	61	10.4	1865	7	US-11-649-663A-2174	Sequence 2174, App	482	60	10.2	1132	7	US-11-649-663A-1832	Sequence 1832, App
409	61	10.4	1915	7	US-11-649-663A-1702	Sequence 1702, App	483	60	10.2	1257	7	US-11-649-663A-24	Sequence 24, Appl
410	61	10.4	1957	7	US-11-649-663A-2192	Sequence 2192, App	484	60	10.2	1263	7	US-11-649-663A-1290	Sequence 1290, App
411	61	10.4	2016	7	US-11-649-663A-2188	Sequence 2188, App	485	60	10.2	1298	7	US-11-649-663A-2774	Sequence 2774, App
412	61	10.4	2124	7	US-11-649-663A-1184	Sequence 1184, App	486	60	10.2	1326	7	US-11-649-663A-1514	Sequence 1514, App
413	61	10.4	2124	7	US-11-649-663A-2768	Sequence 2768, App	487	60	10.2	1329	7	US-11-649-663A-914	Sequence 914, App
414	61	10.4	2682	7	US-11-649-663A-88	Sequence 88, Appl	488	60	10.2	1363	7	US-11-649-663A-358	Sequence 358, App
415	61	10.4	2773	7	US-11-649-663A-1466	Sequence 1466, App	489	60	10.2	1363	7	US-11-649-663A-2430	Sequence 2430, App
416	61	10.4	2791	7	US-11-649-663A-2826	Sequence 2826, App	490	60	10.2	1396	7	US-11-649-663A-1102	Sequence 1102, App
417	61	10.4	3060	7	US-11-649-663A-1532	Sequence 1532, App	491	60	10.2	1404	7	US-11-649-663A-1240	Sequence 1240, App
418	60.5	10.3	112	6	US-10-767-701-40551	Sequence 40551, A	492	60	10.2	1413	7	US-11-649-663A-654	Sequence 654, App
419	60.5	10.3	115	7	US-11-649-663A-5376	Sequence 5376, App	493	60	10.2	1422	7	US-11-649-663A-690	Sequence 690, App
420	60.5	10.3	289	7	US-11-713-768-43817	Sequence 43817, A	494	60	10.2	1452	7	US-11-649-663A-4154	Sequence 4154, App
421	60.5	10.3	289	7	US-11-713-768-45249	Sequence 45249, A	495	60	10.2	1481	7	US-11-649-663A-1190	Sequence 1190, App
422	60.5	10.3	289	7	US-11-713-768-48211	Sequence 48211, A	496	60	10.2	1484	7	US-11-649-663A-424	Sequence 424, App
423	60.5	10.3	349	6	US-10-594-211-180	Sequence 180, App	497	60	10.2	1502	7	US-11-649-663A-1380	Sequence 1380, App
424	60.5	10.3	349	7	US-11-676-830-4	Sequence 4, Appl	498	60	10.2	1516	7	US-11-649-663A-4074	Sequence 4074, App
425	60.5	10.3	395	7	US-11-360-355-120911	Sequence 120911, A	499	60	10.2	1575	7	US-11-649-663A-2648	Sequence 2648, App
426	60.5	10.3	438	7	US-11-649-663A-1434	Sequence 1434, App	500	60	10.2	1577	7	US-11-649-663A-396	Sequence 396, App
427	60.5	10.3	464	7	US-11-689-173-8731	Sequence 8731, App	501	60	10.2	1655	7	US-11-649-663A-3630	Sequence 3630, App
428	60.5	10.3	723	6	US-10-533-069-2074	Sequence 2074, App	502	60	10.2	1656	7	US-11-649-663A-3004	Sequence 3004, App
429	60.5	10.3	723	7	US-11-537-235-346	Sequence 346, App	503	60	10.2	1689	7	US-11-649-663A-908	Sequence 908, App
430	60.5	10.3	723	7	US-11-625-272-100	Sequence 100, App	504	60	10.2	1723	7	US-11-649-663A-2034	Sequence 2034, App
431	60.5	10.3	723	7	US-11-553-810-346	Sequence 346, App	505	60	10.2	1764	7	US-11-649-663A-1220	Sequence 1220, App
433	60.5	10.3	849	7	US-11-649-663A-1686	Sequence 1686, App	506	60	10.2	1768	7	US-11-649-663A-1652	Sequence 1652, App
434	60.5	10.3	891	7	US-11-649-663A-1484	Sequence 1484, App	507	60	10.2	1782	7	US-11-649-663A-2856	Sequence 2856, App
435	60.5	10.3	1015	7	US-11-649-663A-1834	Sequence 1834, App	508	60	10.2	1825	7	US-11-649-663A-882	Sequence 882, App
436	60.5	10.3	1026	7	US-11-649-663A-2500	Sequence 2500, App	509	60	10.2	1825	7	US-11-649-663A-978	Sequence 978, App
437	60.5	10.3	1042	7	US-11-649-663A-1228	Sequence 1228, App	510	60	10.2	2045	7	US-11-649-663A-2726	Sequence 2726, App
438	60.5	10.3	1069	7	US-11-649-663A-1016	Sequence 1016, App	511	60	10.2	2196	7	US-11-536-461-122	Sequence 122, App
439	60.5	10.3	1168	7	US-11-649-663A-1218	Sequence 1218, App	512	60	10.2	2196	7	US-11-691-000-122	Sequence 122, App
440	60.5	10.3	1169	7	US-11-649-663A-2532	Sequence 2532, App	513	60	10.2	2433	7	US-11-649-663A-1618	Sequence 1618, App
441	60.5	10.3	1170	7	US-11-649-663A-1300	Sequence 1300, App	514	60	10.2	2574	7	US-11-649-663A-1990	Sequence 1990, App
442	60.5	10.3	1199	7	US-11-649-663A-2390	Sequence 2390, App	515	60	10.2	2633	7	US-11-649-663A-1414	Sequence 1414, App
443	60.5	10.3	1245	7	US-11-649-663A-1602	Sequence 1602, App	516	60	10.2	3312	6	US-10-529-351A-1133	Sequence 1133, App
444	60.5	10.3	1299	7	US-11-649-663A-1524	Sequence 1524, App	517	60	10.2	5109	7	US-11-649-663A-1520	Sequence 1520, App
445	60.5	10.3	1313	7	US-11-649-663A-2312	Sequence 2312, App	518	60	10.2	5176	7	US-11-360-355-132135	Sequence 132135,
446	60.5	10.3	1378	7	US-11-649-663A-432	Sequence 432, App	519	60	10.1	176	7	US-11-438-246-8755	Sequence 8755, App
447	60.5	10.3	1424	7	US-11-649-663A-504	Sequence 504, App	520	59.5	10.1	197	6	US-10-438-246-8760	Sequence 8760, App
448	60.5	10.3	1436	7	US-11-649-663A-2906	Sequence 2906, App	521	59.5	10.1	412	6	US-11-360-355-126876	Sequence 126876,
449	60.5	10.3	1506	7	US-11-649-663A-1992	Sequence 1992, App	522	59.5	10.1	428	7	US-11-360-355-126876	Sequence 3800, App
450	60.5	10.3	1507	7	US-11-649-663A-608	Sequence 608, App	523	59.5	10.1	475	7	US-11-649-663A-3272	Sequence 3272, App
451	60.5	10.3	1549	7	US-11-649-663A-494	Sequence 494, App	524	59.5	10.1	521	7	US-11-649-663A-144	Sequence 144, App
452	60.5	10.3	1565	7	US-11-649-663A-1824	Sequence 1824, App	525	59.5	10.1	612	7	US-11-360-355-152972	Sequence 152972,
453	60.5	10.3	1567	7	US-11-649-663A-2116	Sequence 2116, App	526	59.5	10.1	729	7	US-11-649-663A-230	Sequence 230, App
454	60.5	10.3	1571	7	US-11-649-663A-2074	Sequence 2074, App	527	59.5	10.1	802	7	US-11-649-663A-5486	Sequence 5486, App
455	60.5	10.3	1592	7	US-11-649-663A-5088	Sequence 5088, App	528	59.5	10.1	839	7	US-11-649-663A-2580	Sequence 2580, App
456	60.5	10.3	1655	7	US-11-649-663A-962	Sequence 962, App	529	59.5	10.1	873	7	US-11-649-663A-1072	Sequence 1072, App
457	60.5	10.3	1761	7	US-11-649-663A-1526	Sequence 1526, App	530	59.5	10.1	876	7	US-11-649-663A-144	Sequence 144, App
458	60.5	10.3	1782	7	US-11-649-663A-780	Sequence 780, App	531	59.5	10.1	1038	7	US-11-649-663A-2356	Sequence 2356, App
459	60.5	10.3	1796	7	US-11-649-663A-910	Sequence 910, App	532	59.5	10.1	1050	7	US-11-649-663A-724	Sequence 724, App
460	60.5	10.3	1811	7	US-11-649-663A-924	Sequence 924, App	533	59.5	10.1	1075	7	US-11-649-663A-3060	Sequence 3060, App
461	60.5	10.3	1867	7	US-11-649-663A-406	Sequence 406, App	534	59.5	10.1	1132	7	US-11-649-663A-892	Sequence 892, App
462	60.5	10.3	1867	7	US-11-649-663A-2604	Sequence 2604, App	535	59.5	10.1	1136	7	US-11-649-663A-2400	Sequence 2400, App
463	60.5	10.3	1884	7	US-11-649-663A-2588	Sequence 2588, App	536	59.5	10.1	1146	7	US-11-649-663A-476	Sequence 476, App
464	60.5	10.3	1897	7	US-11-649-663A-2884	Sequence 2884, App	537	59.5	10.1	1155	7	US-11-649-663A-644	Sequence 644, App
465	60.5	10.3	1942	7	US-11-649-663A-1096	Sequence 1096, App	538	59.5	10.1	1180	7	US-11-649-663A-1546	Sequence 1546, App
466	60.5	10.3	1948	7	US-11-649-663A-2702	Sequence 2702, App	539	59.5	10.1	1212	7	US-11-649-663A-1676	Sequence 1676, App
467	60.5	10.3	1988	7	US-11-649-663A-2860	Sequence 2860, App	540	59.5	10.1	1212	7	US-11-649-663A-3094	Sequence 3094, App
							541	59.5	10.1	1232	7	US-11-649-663A-524	Sequence 524, App

542	59.5	10.1	1270	7	US-11-649-663A-364	Sequence 364, App	615	59	10.0	1393	7	US-11-649-663A-606	Sequence 606, App
543	59.5	10.1	1284	7	US-11-649-663A-1880	Sequence 1880, App	616	59	10.0	1425	7	US-11-649-663A-706	Sequence 706, App
544	59.5	10.1	1298	7	US-11-649-663A-970	Sequence 970, App	617	59	10.0	1444	7	US-11-649-663A-2626	Sequence 2626, App
545	59.5	10.1	1299	7	US-11-649-663A-1640	Sequence 1640, App	618	59	10.0	1445	7	US-11-649-663A-1452	Sequence 1452, App
546	59.5	10.1	1316	7	US-11-649-663A-1812	Sequence 1812, App	619	59	10.0	1448	7	US-11-649-663A-2194	Sequence 2194, App
547	59.5	10.1	1317	7	US-11-649-663A-306	Sequence 306, App	620	59	10.0	1465	7	US-11-649-663A-1720	Sequence 1720, App
548	59.5	10.1	1318	7	US-11-649-663A-2184	Sequence 2184, App	621	59	10.0	1479	7	US-11-649-663A-758	Sequence 758, App
549	59.5	10.1	1323	7	US-11-649-663A-326	Sequence 326, App	622	59	10.0	1503	7	US-11-649-663A-130	Sequence 130, App
550	59.5	10.1	1353	7	US-11-649-663A-1502	Sequence 1502, App	623	59	10.0	1504	7	US-11-649-663A-932	Sequence 932, App
551	59.5	10.1	1370	7	US-11-649-663A-858	Sequence 858, App	624	59	10.0	1518	7	US-11-649-663A-742	Sequence 742, App
552	59.5	10.1	1408	7	US-11-649-663A-2196	Sequence 2196, App	625	59	10.0	1522	7	US-11-649-663A-1154	Sequence 1154, App
553	59.5	10.1	1449	7	US-11-649-663A-134	Sequence 134, App	626	59	10.0	1530	7	US-11-649-663A-854	Sequence 854, App
554	59.5	10.1	1449	7	US-11-649-663A-336	Sequence 336, App	627	59	10.0	1560	7	US-11-649-663A-1846	Sequence 1846, App
555	59.5	10.1	1478	7	US-11-649-663A-710	Sequence 710, App	628	59	10.0	1636	7	US-11-649-663A-3042	Sequence 3042, App
556	59.5	10.1	1495	7	US-11-649-663A-1656	Sequence 1656, App	629	59	10.0	1703	7	US-11-649-663A-558	Sequence 558, App
557	59.5	10.1	1530	7	US-11-649-663A-1862	Sequence 1862, App	630	59	10.0	1706	7	US-11-649-663A-2322	Sequence 2322, App
558	59.5	10.1	1553	7	US-11-649-663A-380	Sequence 380, App	631	59	10.0	1707	7	US-11-649-663A-2322	Sequence 2322, App
559	59.5	10.1	1587	7	US-11-649-663A-2652	Sequence 2652, App	632	59	10.0	1706	7	US-11-649-663A-2342	Sequence 2342, App
560	59.5	10.1	1595	7	US-11-649-663A-4562	Sequence 4562, App	633	59	10.0	1709	7	US-11-649-663A-2970	Sequence 2970, App
561	59.5	10.1	1614	7	US-11-649-663A-1770	Sequence 1770, App	634	59	10.0	1742	7	US-11-649-663A-1238	Sequence 1238, App
562	59.5	10.1	1642	7	US-11-649-663A-1424	Sequence 1424, App	635	59	10.0	1773	7	US-11-649-663A-1710	Sequence 1710, App
563	59.5	10.1	1665	7	US-11-649-663A-1726	Sequence 1726, App	636	59	10.0	1783	7	US-11-649-663A-902	Sequence 902, App
564	59.5	10.1	1696	7	US-11-649-663A-3178	Sequence 3178, App	637	59	10.0	1786	7	US-11-649-663A-602	Sequence 602, App
565	59.5	10.1	1707	7	US-11-649-663A-2636	Sequence 2636, App	638	59	10.0	1814	7	US-11-649-663A-1182	Sequence 1182, App
566	59.5	10.1	1708	7	US-11-649-663A-2076	Sequence 2076, App	639	59	10.0	1880	7	US-11-649-663A-2102	Sequence 2102, App
567	59.5	10.1	1722	7	US-11-649-663A-350	Sequence 350, App	640	59	10.0	1881	7	US-11-649-663A-520	Sequence 520, App
568	59.5	10.1	1733	7	US-11-649-663A-814	Sequence 814, App	641	59	10.0	1883	7	US-11-649-663A-1756	Sequence 1756, App
569	59.5	10.1	1753	7	US-11-649-663A-1222	Sequence 1222, App	642	59	10.0	1991	7	US-11-649-663A-2144	Sequence 2144, App
570	59.5	10.1	1772	7	US-11-649-663A-4212	Sequence 4212, App	643	59	10.0	1991	7	US-11-649-663A-2570	Sequence 2570, App
571	59.5	10.1	1821	7	US-11-649-663A-2108	Sequence 2108, App	644	59	10.0	2047	7	US-11-649-663A-680	Sequence 680, App
572	59.5	10.1	1828	7	US-11-649-663A-2544	Sequence 2544, App	645	59	10.0	2062	7	US-11-649-663A-876	Sequence 876, App
573	59.5	10.1	1831	7	US-11-649-663A-2120	Sequence 2120, App	646	59	10.0	2085	7	US-11-649-663A-954	Sequence 954, App
574	59.5	10.1	1860	7	US-11-649-663A-612	Sequence 612, App	647	59	10.0	2088	7	US-11-649-663A-4996	Sequence 4996, App
575	59.5	10.1	1868	7	US-11-649-663A-2266	Sequence 2266, App	648	59	10.0	2142	7	US-11-649-663A-2118	Sequence 2118, App
576	59.5	10.1	1896	7	US-11-649-663A-1376	Sequence 1376, App	649	59	10.0	2143	7	US-11-649-663A-2550	Sequence 2550, App
577	59.5	10.1	1945	7	US-11-649-663A-1972	Sequence 1972, App	650	59	10.0	2205	7	US-11-649-663A-1876	Sequence 1876, App
578	59.5	10.1	2061	7	US-11-649-663A-1216	Sequence 1216, App	651	59	10.0	2472	7	US-11-649-663A-1716	Sequence 1716, App
579	59.5	10.1	2325	7	US-11-649-663A-5472	Sequence 5472, App	652	59	10.0	3062	7	US-11-649-663A-228	Sequence 228, App
580	59.5	10.1	2430	7	US-11-649-663A-96	Sequence 96, App	653	59	10.0	3362	7	US-11-649-663A-2314	Sequence 2314, App
581	59.5	10.1	2841	7	US-11-649-663A-1630	Sequence 1630, App	654	59	10.0	143	6	US-10-767-701-60902	Sequence 25639, A
582	59	10.0	167	6	US-10-767-701-61680	Sequence 25310, A	655	58.5	9.9	176	6	US-10-767-701-60902	Sequence 60902, A
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584	59	10.0	314	7	US-11-713-768-88093	Sequence 88093, A	657	58.5	9.9	213	7	US-11-621-022-1	Sequence 1, Appl
585	59	10.0	315	7	US-11-728-567-994	Sequence 994, App	658	58.5	9.9	251	6	US-10-566-929-15	Sequence 15, Appl
586	59	10.0	315	7	US-11-713-768-88092	Sequence 88092, A	659	58.5	9.9	258	7	US-11-257-477-28	Sequence 28, Appl
587	59	10.0	348	7	US-11-234-694-74	Sequence 74, Appl	660	58.5	9.9	280	7	US-11-713-768-74373	Sequence 74373, A
588	59	10.0	448	7	US-11-799-117-12	Sequence 12, Appl	661	58.5	9.9	280	7	US-11-713-768-107866	Sequence 107866, A
589	59	10.0	482	6	US-10-573-962-15	Sequence 15, Appl	662	58.5	9.9	281	7	US-11-713-768-74372	Sequence 74372, A
590	59	10.0	516	7	US-11-649-663A-2272	Sequence 2272, App	663	58.5	9.9	281	7	US-11-713-768-107865	Sequence 107865, A
591	59	10.0	644	7	US-11-649-663A-4416	Sequence 4416, App	664	58.5	9.9	305	6	US-10-438-246-33140	Sequence 33140, A
592	59	10.0	687	7	US-11-649-663A-5016	Sequence 5016, App	665	58.5	9.9	322	7	US-11-713-768-107864	Sequence 107864, A
593	59	10.0	858	7	US-11-649-663A-156	Sequence 156, App	666	58.5	9.9	323	7	US-11-713-768-74371	Sequence 74371, A
594	59	10.0	906	7	US-11-649-663A-1492	Sequence 1492, App	667	58.5	9.9	417	7	US-11-799-117-6	Sequence 6, Appl
595	59	10.0	954	7	US-11-649-663A-1922	Sequence 1922, App	668	58.5	9.9	426	7	US-11-615-609A-37	Sequence 37, Appl
596	59	10.0	983	7	US-11-649-663A-2434	Sequence 2434, App	669	58.5	9.9	455	6	US-10-529-351A-3481	Sequence 3481, App
597	59	10.0	1001	7	US-11-649-663A-1460	Sequence 1460, App	670	58.5	9.9	455	6	US-10-551-004-65	Sequence 65, Appl
598	59	10.0	1017	7	US-11-649-663A-3140	Sequence 3140, App	671	58.5	9.9	455	7	US-11-625-272-149	Sequence 149, App
599	59	10.0	1060	7	US-11-649-663A-2474	Sequence 2474, App	672	58.5	9.9	455	7	US-11-799-117-2	Sequence 2, Appl
600	59	10.0	1096	7	US-11-649-663A-4668	Sequence 4668, App	673	58.5	9.9	486	7	US-11-649-663A-82	Sequence 82, Appl
601	59	10.0	1141	7	US-11-787-713-35	Sequence 35, Appl	674	58.5	9.9	503	7	US-11-656-720-2	Sequence 2, Appl
602	59	10.0	1159	7	US-11-649-663A-1666	Sequence 1666, App	675	58.5	9.9	547	6	US-10-566-929-17	Sequence 17, Appl
603	59	10.0	1194	7	US-11-649-663A-2328	Sequence 2328, App	676	58.5	9.9	547	6	US-10-566-929-19	Sequence 19, Appl
604	59	10.0	1220	7	US-11-649-663A-1542	Sequence 1542, App	677	58.5	9.9	584	7	US-11-403-116-468	Sequence 468, App
605	59	10.0	1221	7	US-11-649-663A-1672	Sequence 1672, App	678	58.5	9.9	584	7	US-11-403-116-470	Sequence 470, App
606	59	10.0	1223	7	US-11-649-663A-2472	Sequence 2472, App	679	58.5	9.9	678	7	US-11-649-663A-3924	Sequence 3924, App
607	59	10.0	1245	7	US-11-649-663A-850	Sequence 850, App	681	58.5	9.9	787	7	US-11-552-437-90	Sequence 90, Appl
608	59	10.0	1259	7	US-11-649-663A-5038	Sequence 5038, App	682	58.5	9.9	915	7	US-11-649-663A-702	Sequence 702, App
609	59	10.0	1281	7	US-11-649-663A-1826	Sequence 1826, App	683	58.5	9.9	929	7	US-11-649-663A-3988	Sequence 3988, App
610	59	10.0	1303	7	US-11-649-663A-430	Sequence 430, App	684	58.5	9.9	992	6	US-10-566-929-16	Sequence 16, Appl
611	59	10.0	1310	7	US-11-649-663A-1186	Sequence 1186, App	685	58.5	9.9	992	6	US-10-566-929-18	Sequence 18, Appl
612	59	10.0	1310	7	US-11-649-663A-3450	Sequence 3450, App	686	58.5	9.9	1026	7	US-11-649-663A-1518	Sequence 1518, App
613	59	10.0	1350	7	US-11-649-663A-3966	Sequence 3966, App	687	58.5	9.9	1076	7	US-11-649-663A-3980	Sequence 3980, App
614	59	10.0	1377	7	US-11-649-663A-518	Sequence 518, App	688	58.5	9.9	1111	7	US-11-510-314-4	Sequence 4, Appl

689	58.5	9.9	1146	7	US-11-649-663A-84	Sequence 84, Appl	762	58	9.8	1285	7	US-11-649-663A-2386	Sequence 2386, Ap
690	58.5	9.9	1193	7	US-11-510-314-2	Sequence 2, Appl	763	58	9.8	1331	7	US-11-649-663A-2766	Sequence 2766, Ap
691	58.5	9.9	1283	7	US-11-649-663A-578	Sequence 578, App	764	58	9.8	1348	7	US-11-649-663A-2452	Sequence 2452, Ap
692	58.5	9.9	1291	7	US-11-649-663A-1080	Sequence 1080, Ap	765	58	9.8	1359	7	US-11-649-663A-1994	Sequence 1994, Ap
693	58.5	9.9	1333	7	US-11-649-663A-1258	Sequence 1258, Ap	766	58	9.8	1391	7	US-11-649-663A-2252	Sequence 2252, Ap
694	58.5	9.9	1335	7	US-11-649-663A-1106	Sequence 1106, Ap	767	58	9.8	1431	7	US-11-649-663A-1112	Sequence 1112, Ap
695	58.5	9.9	1337	7	US-11-649-663A-896	Sequence 896, App	768	58	9.8	1431	7	US-11-649-663A-2332	Sequence 2332, Ap
696	58.5	9.9	1346	7	US-11-649-663A-3818	Sequence 3818, Ap	769	58	9.8	1449	7	US-11-649-663A-790	Sequence 790, App
697	58.5	9.9	1368	7	US-11-649-663A-116	Sequence 116, App	770	58	9.8	1460	7	US-11-649-663A-5280	Sequence 5280, Ap
698	58.5	9.9	1368	7	US-11-649-663A-4560	Sequence 4560, App	771	58	9.8	1464	7	US-11-649-663A-2038	Sequence 2038, Ap
699	58.5	9.9	1407	7	US-11-649-663A-464	Sequence 464, App	772	58	9.8	1467	7	US-11-649-663A-1854	Sequence 1854, Ap
700	58.5	9.9	1408	7	US-11-649-663A-2510	Sequence 2510, Ap	773	58	9.8	1480	7	US-11-649-663A-752	Sequence 752, App
701	58.5	9.9	1416	7	US-11-649-663A-1480	Sequence 1480, Ap	774	58	9.8	1485	7	US-11-649-663A-2206	Sequence 2206, Ap
702	58.5	9.9	1433	7	US-11-649-663A-1920	Sequence 1920, Ap	775	58	9.8	1516	7	US-11-649-663A-2358	Sequence 2358, Ap
703	58.5	9.9	1467	7	US-11-649-663A-4592	Sequence 4592, Ap	776	58	9.8	1521	7	US-11-649-663A-36	Sequence 36, Appl
704	58.5	9.9	1471	7	US-11-649-663A-1160	Sequence 1160, Ap	777	58	9.8	1522	7	US-11-649-663A-1098	Sequence 1098, Ap
705	58.5	9.9	1558	7	US-11-649-663A-1366	Sequence 1366, App	778	58	9.8	1523	7	US-11-649-663A-786	Sequence 786, App
706	58.5	9.9	1558	7	US-11-649-663A-856	Sequence 856, App	779	58	9.8	1533	7	US-11-649-663A-2056	Sequence 2056, Ap
707	58.5	9.9	1576	7	US-11-649-663A-2886	Sequence 2886, Ap	780	58	9.8	1552	7	US-11-649-663A-1110	Sequence 1110, Ap
708	58.5	9.9	1600	7	US-11-649-663A-544	Sequence 544, App	781	58	9.8	1572	7	US-11-649-663A-1926	Sequence 1926, Ap
709	58.5	9.9	1628	7	US-11-649-663A-2748	Sequence 2748, App	782	58	9.8	1664	7	US-11-649-663A-5028	Sequence 5028, Ap
710	58.5	9.9	1652	7	US-11-649-663A-1188	Sequence 1188, App	783	58	9.8	1674	7	US-11-649-663A-1328	Sequence 1328, Ap
711	58.5	9.9	1663	7	US-11-649-663A-938	Sequence 938, App	784	58	9.8	1696	7	US-11-649-663A-630	Sequence 630, App
712	58.5	9.9	1692	7	US-11-649-663A-4190	Sequence 4190, Ap	785	58	9.8	1730	7	US-11-649-663A-5198	Sequence 5198, Ap
713	58.5	9.9	1693	7	US-11-649-663A-2728	Sequence 2728, Ap	786	58	9.8	1744	7	US-11-649-663A-580	Sequence 580, App
714	58.5	9.9	1784	7	US-11-649-663A-1774	Sequence 1774, Ap	787	58	9.8	1791	7	US-11-649-663A-2026	Sequence 2026, Ap
715	58.5	9.9	1785	7	US-11-649-663A-2834	Sequence 2834, Ap	788	58	9.8	1826	7	US-11-649-663A-1322	Sequence 1322, Ap
716	58.5	9.9	1788	7	US-11-649-663A-2834	Sequence 2834, Ap	789	58	9.8	1917	7	US-11-649-663A-2172	Sequence 2172, Ap
717	58.5	9.9	1845	7	US-11-649-663A-1310	Sequence 1310, Ap	790	58	9.8	1929	7	US-11-649-663A-2462	Sequence 2462, Ap
718	58.5	9.9	1848	7	US-11-649-663A-1372	Sequence 1372, Ap	791	58	9.8	2097	7	US-11-649-663A-148	Sequence 148, App
719	58.5	9.9	1907	7	US-11-649-663A-2770	Sequence 2770, Ap	792	58	9.8	2149	7	US-11-649-663A-3214	Sequence 3214, Ap
720	58.5	9.9	1925	7	US-11-649-663A-2362	Sequence 2362, Ap	793	58	9.8	2365	7	US-11-649-663A-804	Sequence 804, App
721	58.5	9.9	1961	7	US-11-649-663A-1714	Sequence 1714, Ap	794	58	9.8	2598	7	US-11-649-663A-1488	Sequence 1488, Ap
722	58.5	9.9	1965	7	US-11-649-663A-1092	Sequence 1092, Ap	795	58	9.8	2643	7	US-11-649-663A-1864	Sequence 1864, Ap
723	58.5	9.9	2010	7	US-11-649-663A-1358	Sequence 1358, Ap	796	58	9.8	3291	7	US-11-649-663A-2666	Sequence 2666, Ap
724	58.5	9.9	2052	7	US-11-649-663A-516	Sequence 516, App	797	57.5	9.8	152	6	US-10-767-701-43109	Sequence 43109, A
725	58.5	9.9	2064	7	US-11-649-663A-2494	Sequence 2494, Ap	798	57.5	9.8	264	7	US-11-689-173-6813	Sequence 6813, A
726	58.5	9.9	2411	7	US-11-649-663A-4618	Sequence 4618, Ap	799	57.5	9.8	280	7	US-11-656-491-5395	Sequence 5395, Ap
727	58.5	9.9	2445	7	US-11-649-663A-2052	Sequence 2052, Ap	800	57.5	9.8	310	7	US-11-713-768-9759	Sequence 9759, Ap
728	58.5	9.9	4709	7	US-11-649-663A-2292	Sequence 2292, Ap	801	57.5	9.8	328	7	US-11-713-768-9512	Sequence 9512, Ap
729	58	9.8	46	7	US-11-214-372B-120	Sequence 120, App	802	57.5	9.8	395	7	US-11-673-351-1776	Sequence 1776, Ap
730	58	9.8	83	6	US-10-767-701-40042	Sequence 40042, A	803	57.5	9.8	420	7	US-11-713-768-9511	Sequence 9511, Ap
731	58	9.8	115	7	US-10-689-173-8506	Sequence 8506, Ap	804	57.5	9.8	442	7	US-11-689-173-9303	Sequence 9303, Ap
732	58	9.8	119	6	US-10-438-246-25519	Sequence 25519, A	805	57.5	9.8	493	7	US-11-713-768-9510	Sequence 9510, Ap
733	58	9.8	127	6	US-10-767-701-45809	Sequence 45809, A	807	57.5	9.8	565	7	US-11-542-670-53	Sequence 53, Appl
734	58	9.8	166	6	US-10-438-246-18567	Sequence 18567, A	808	57.5	9.8	586	7	US-11-584-820-90	Sequence 90, Appl
735	58	9.8	192	6	US-10-438-246-18588	Sequence 18588, A	809	57.5	9.8	651	7	US-11-649-663A-3918	Sequence 3918, Ap
736	58	9.8	224	6	US-10-438-246-25518	Sequence 25518, A	810	57.5	9.8	657	7	US-11-649-663A-512	Sequence 512, App
737	58	9.8	299	6	US-10-438-246-18090	Sequence 18090, A	811	57.5	9.8	745	7	US-11-537-235-68	Sequence 68, Appl
738	58	9.8	301	6	US-10-438-246-25229	Sequence 25229, A	812	57.5	9.8	745	7	US-11-553-810-68	Sequence 68, Appl
739	58	9.8	359	7	US-11-360-355-120013	Sequence 120013, A	813	57.5	9.8	895	7	US-11-649-663A-1408	Sequence 1408, Ap
740	58	9.8	363	6	US-10-438-246-18056	Sequence 18056, A	814	57.5	9.8	907	7	US-11-649-663A-1040	Sequence 1040, Ap
741	58	9.8	369	6	US-10-767-701-47121	Sequence 47121, A	815	57.5	9.8	977	7	US-11-649-663A-1418	Sequence 1418, Ap
742	58	9.8	513	7	US-11-649-663A-3284	Sequence 3284, Ap	816	57.5	9.8	986	7	US-11-649-663A-2680	Sequence 2680, Ap
743	58	9.8	525	7	US-11-713-768-76541	Sequence 76541, A	817	57.5	9.8	991	6	US-10-481-700-5	Sequence 5, Appl
744	58	9.8	528	7	US-11-649-663A-2320	Sequence 2320, Ap	818	57.5	9.8	1058	7	US-11-649-663A-420	Sequence 420, App
745	58	9.8	539	7	US-11-713-768-76540	Sequence 76540, A	819	57.5	9.8	1058	7	US-11-649-663A-1586	Sequence 1586, Ap
746	58	9.8	600	6	US-10-438-246-8944	Sequence 8944, Ap	820	57.5	9.8	1125	7	US-11-649-663A-650	Sequence 650, App
747	58	9.8	901	7	US-11-360-355-146763	Sequence 146763, A	821	57.5	9.8	1136	7	US-11-649-663A-2504	Sequence 2504, Ap
748	58	9.8	944	7	US-11-649-663A-2280	Sequence 2280, Ap	822	57.5	9.8	1146	7	US-11-649-663A-2372	Sequence 2372, Ap
749	58	9.8	950	7	US-11-649-663A-2002	Sequence 2002, Ap	823	57.5	9.8	1167	7	US-11-649-663A-2734	Sequence 2734, Ap
750	58	9.8	1023	7	US-11-649-663A-1554	Sequence 1554, Ap	824	57.5	9.8	1175	7	US-11-649-663A-3288	Sequence 3288, Ap
751	58	9.8	1050	7	US-11-649-663A-2020	Sequence 2020, Ap	825	57.5	9.8	1188	7	US-11-649-663A-1544	Sequence 1544, Ap
752	58	9.8	1092	7	US-11-649-663A-912	Sequence 912, App	826	57.5	9.8	1231	7	US-11-649-663A-1962	Sequence 1962, Ap
753	58	9.8	1092	7	US-11-649-663A-2066	Sequence 2066, Ap	827	57.5	9.8	1252	7	US-11-649-663A-5316	Sequence 5316, App
754	58	9.8	1179	7	US-11-649-663A-508	Sequence 508, App	828	57.5	9.8	1263	7	US-11-649-663A-1510	Sequence 1510, Ap
755	58	9.8	1187	7	US-11-649-663A-2394	Sequence 2394, Ap	829	57.5	9.8	1269	7	US-11-649-663A-164	Sequence 164, App
756	58	9.8	1187	7	US-11-649-663A-2092	Sequence 2092, Ap	830	57.5	9.8	1275	7	US-11-649-663A-1886	Sequence 1886, Ap
757	58	9.8	1214	7	US-11-649-663A-986	Sequence 986, App	831	57.5	9.8	1292	7	US-11-649-663A-2482	Sequence 2482, Ap
758	58	9.8	1220	7	US-11-649-663A-1048	Sequence 1048, Ap	832	57.5	9.8	1296	7	US-11-649-663A-1734	Sequence 1734, Ap
759	58	9.8	1234	7	US-11-649-663A-656	Sequence 656, App	833	57.5	9.8	1323	7	US-11-649-663A-450	Sequence 450, App
760	58	9.8	1242	7	US-11-649-663A-98	Sequence 98, Appl	834	57.5	9.8	1325	7	US-11-649-663A-2050	Sequence 2050, Ap
761	58	9.8					835	57.5	9.8	1329	7		

836	57.5	9.8	1356	7	US-11-649-663A-64	Sequence 64, Appl	910	57	9.7	1143	7	US-11-649-663A-1918	Sequence 1918, Ap
837	57.5	9.8	1356	7	US-11-716-794-17	Sequence 17, Appl	911	57	9.7	1156	7	US-11-649-663A-756	Sequence 756, App
838	57.5	9.8	1370	7	US-11-649-663A-2124	Sequence 2124, Ap	912	57	9.7	1168	7	US-11-649-663A-316	Sequence 316, App
839	57.5	9.8	1395	7	US-11-649-663A-1130	Sequence 1130, Ap	913	57	9.7	1181	7	US-11-649-663A-2684	Sequence 2684, Ap
840	57.5	9.8	1463	7	US-11-649-663A-1308	Sequence 1308, Ap	914	57	9.7	1224	7	US-11-649-663A-1844	Sequence 1844, Ap
841	57.5	9.8	1469	7	US-11-649-663A-1890	Sequence 1890, Ap	915	57	9.7	1227	7	US-11-649-663A-486	Sequence 486, App
842	57.5	9.8	1470	7	US-11-649-663A-1280	Sequence 1280, Ap	916	57	9.7	1233	7	US-11-649-663A-1468	Sequence 1468, Ap
843	57.5	9.8	1483	7	US-11-649-663A-5082	Sequence 5082, Ap	917	57	9.7	1242	7	US-11-649-663A-1678	Sequence 1678, Ap
844	57.5	9.8	1486	7	US-11-649-663A-684	Sequence 684, App	918	57	9.7	1259	7	US-11-649-663A-1126	Sequence 1126, Ap
845	57.5	9.8	1494	7	US-11-649-663A-820	Sequence 820, App	919	57	9.7	1260	7	US-11-649-663A-1794	Sequence 1794, Ap
846	57.5	9.8	1527	7	US-11-649-663A-2694	Sequence 2694, Ap	920	57	9.7	1268	7	US-11-649-663A-744	Sequence 744, App
847	57.5	9.8	1534	7	US-11-649-663A-2156	Sequence 2156, Ap	921	57	9.7	1277	7	US-11-649-663A-888	Sequence 888, App
848	57.5	9.8	1537	7	US-11-649-663A-716	Sequence 716, App	922	57	9.7	1296	7	US-11-649-663A-2080	Sequence 2080, Ap
849	57.5	9.8	1557	7	US-11-649-663A-1244	Sequence 1244, Ap	923	57	9.7	1314	7	US-11-649-663A-736	Sequence 736, App
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851	57.5	9.8	1591	7	US-11-649-663A-576	Sequence 576, App	925	57	9.7	1322	7	US-11-649-663A-592	Sequence 592, App
852	57.5	9.8	1592	7	US-11-649-663A-1172	Sequence 1172, Ap	926	57	9.7	1325	7	US-11-649-663A-454	Sequence 454, App
853	57.5	9.8	1600	7	US-11-649-663A-636	Sequence 636, App	927	57	9.7	1337	7	US-11-649-663A-304	Sequence 304, App
854	57.5	9.8	1627	7	US-11-390-828-4	Sequence 4, Appl	928	57	9.7	1340	7	US-11-649-663A-2412	Sequence 2412, Ap
855	57.5	9.8	1652	7	US-11-649-663A-1450	Sequence 1450, Ap	929	57	9.7	1352	7	US-11-649-663A-1090	Sequence 1090, Ap
856	57.5	9.8	1662	7	US-11-649-663A-1966	Sequence 1966, Ap	930	57	9.7	1357	7	US-11-649-663A-1426	Sequence 1426, Ap
857	57.5	9.8	1673	7	US-11-649-663A-812	Sequence 812, App	931	57	9.7	1358	7	US-11-649-663A-320	Sequence 320, App
858	57.5	9.8	1713	7	US-11-649-663A-4894	Sequence 4894, Ap	932	57	9.7	1358	7	US-11-649-663A-2628	Sequence 2628, Ap
859	57.5	9.8	1722	7	US-11-649-663A-2838	Sequence 2838, Ap	933	57	9.7	1358	7	US-11-649-663A-2640	Sequence 2640, Ap
860	57.5	9.8	1737	7	US-11-649-663A-674	Sequence 674, App	934	57	9.7	1369	7	US-11-649-663A-2492	Sequence 2492, Ap
861	57.5	9.8	1740	7	US-11-649-663A-1390	Sequence 1390, Ap	935	57	9.7	1371	7	US-11-649-663A-2624	Sequence 2624, Ap
862	57.5	9.8	1753	7	US-11-649-663A-802	Sequence 802, App	936	57	9.7	1395	7	US-11-649-663A-2624	Sequence 2624, Ap
863	57.5	9.8	1765	7	US-11-649-663A-2282	Sequence 2282, Ap	937	57	9.7	1396	7	US-11-649-663A-366	Sequence 366, App
864	57.5	9.8	1800	7	US-11-649-663A-1392	Sequence 1392, Ap	938	57	9.7	1410	7	US-11-649-663A-964	Sequence 964, App
865	57.5	9.8	1818	7	US-11-649-663A-2842	Sequence 2842, Ap	939	57	9.7	1412	7	US-11-649-663A-3072	Sequence 3072, Ap
866	57.5	9.8	1847	7	US-11-649-663A-2852	Sequence 2852, Ap	940	57	9.7	1413	7	US-11-649-663A-1582	Sequence 1582, Ap
867	57.5	9.8	1933	7	US-11-649-663A-2226	Sequence 2226, Ap	941	57	9.7	1416	7	US-11-649-663A-2646	Sequence 2646, Ap
868	57.5	9.8	1962	7	US-11-649-663A-998	Sequence 998, App	942	57	9.7	1418	7	US-11-649-663A-950	Sequence 950, App
869	57.5	9.8	2046	7	US-11-649-663A-3456	Sequence 3456, Ap	943	57	9.7	1439	7	US-11-649-663A-604	Sequence 604, App
870	57.5	9.8	2119	7	US-11-649-663A-4798	Sequence 4798, Ap	944	57	9.7	1482	7	US-11-649-663A-880	Sequence 880, App
871	57.5	9.8	2124	7	US-11-649-663A-3446	Sequence 3446, Ap	945	57	9.7	1522	7	US-11-649-663A-1928	Sequence 1928, Ap
872	57.5	9.8	2250	7	US-11-649-663A-1394	Sequence 1394, Ap	946	57	9.7	1533	7	US-11-649-663A-78	Sequence 78, Appl
873	57.5	9.8	2274	7	US-11-649-663A-56	Sequence 56, Appl	947	57	9.7	1535	7	US-11-649-663A-944	Sequence 944, App
874	57.5	9.8	2355	7	US-11-625-272-147	Sequence 147, App	948	57	9.7	1536	7	US-11-649-663A-1218	Sequence 1218, Ap
875	57.5	9.8	2386	7	US-11-707-223-32	Sequence 32, Appl	949	57	9.7	1540	7	US-11-649-663A-2418	Sequence 2418, Ap
876	57.5	9.8	2394	7	US-11-649-663A-2722	Sequence 2722, Ap	950	57	9.7	1549	7	US-11-649-663A-2258	Sequence 2258, Ap
877	57.5	9.8	2616	7	US-11-649-663A-1680	Sequence 1680, Ap	951	57	9.7	1597	7	US-11-649-663A-618	Sequence 618, App
878	57.5	9.8	2740	7	US-11-649-663A-1234	Sequence 1234, Ap	952	57	9.7	1605	7	US-11-649-663A-1410	Sequence 1410, Ap
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884	57	9.7	303	7	US-11-713-768-55599	Sequence 55599, A	958	57	9.7	1721	7	US-11-649-663A-968	Sequence 968, App
885	57	9.7	309	7	US-11-713-768-55598	Sequence 55598, A	959	57	9.7	1735	7	US-11-649-663A-2246	Sequence 2246, Ap
886	57	9.7	443	7	US-11-537-235-318	Sequence 318, App	960	57	9.7	1738	7	US-11-649-663A-864	Sequence 864, App
887	57	9.7	443	7	US-11-537-235-318	Sequence 318, App	961	57	9.7	1766	7	US-11-649-663A-5194	Sequence 5194, Ap
888	57	9.7	549	6	US-10-438-246-33486	Sequence 33486, A	962	57	9.7	1775	7	US-11-649-663A-526	Sequence 526, App
889	57	9.7	598	7	US-11-403-116-465	Sequence 465, App	963	57	9.7	1822	6	US-10-529-351A-4964	Sequence 4964, Ap
890	57	9.7	619	7	US-11-649-663A-194	Sequence 194, App	964	57	9.7	1872	7	US-11-649-663A-1664	Sequence 1664, Ap
891	57	9.7	655	6	US-10-529-351A-1871	Sequence 1871, Ap	965	57	9.7	1910	7	US-11-649-663A-2256	Sequence 2256, Ap
892	57	9.7	838	7	US-11-649-663A-808	Sequence 808, App	966	57	9.7	1951	7	US-11-649-663A-3118	Sequence 3118, Ap
893	57	9.7	856	7	US-11-649-663A-5482	Sequence 5482, Ap	967	57	9.7	1968	7	US-11-649-663A-730	Sequence 730, App
895	57	9.7	893	7	US-11-649-663A-1942	Sequence 1942, Ap	968	57	9.7	2017	7	US-11-649-663A-2682	Sequence 2682, Ap
896	57	9.7	903	7	US-11-649-663A-574	Sequence 574, App	969	57	9.7	2180	7	US-11-649-663A-530	Sequence 530, App
897	57	9.7	904	7	US-11-649-663A-2616	Sequence 2616, Ap	970	57	9.7	6498	7	US-11-726-028-8	Sequence 8, Appl
898	57	9.7	906	7	US-11-649-663A-2610	Sequence 2610, Ap	971	56.5	9.6	62	7	US-11-518-530-508	Sequence 508, App
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903	57	9.7	994	7	US-11-649-663A-918	Sequence 918, App	976	56.5	9.6	423	6	US-10-438-246-25468	Sequence 25468, A
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905	57	9.7	1027	7	US-11-649-663A-4296	Sequence 4296, Ap	978	56.5	9.6	462	7	US-11-713-768-6831	Sequence 6831, Ap
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907	57	9.7	1049	7	US-11-649-663A-468	Sequence 468, App	980	56.5	9.6	480	7	US-11-713-768-6830	Sequence 6830, Ap
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909	57	9.7	1055	7	US-11-649-663A-2854	Sequence 2854, Ap	982	56.5	9.6	642	7	US-11-112-327-11	Sequence 11, Appl

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985	56.5	9.6	871	7	US-11-445-001-86	Sequence 86, Appl	1058	56	9.5	135	6	US-10-767-701-162533	Sequence 62533, A
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994	56.5	9.6	1125	7	US-11-649-663A-54	Sequence 54, Appl	1067	56	9.5	264	7	US-11-728-567-710	Sequence 710, App
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1002	56.5	9.6	1234	7	US-11-649-663A-1046	Sequence 1046, App	1075	56	9.5	503	7	US-11-649-663A-86	Sequence 86, Appl
1003	56.5	9.6	1253	7	US-11-649-663A-1276	Sequence 1276, App	1076	56	9.5	515	7	US-11-360-355-132122	Sequence 132122, A
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1005	56.5	9.6	1277	7	US-11-649-663A-440	Sequence 440, App	1078	56	9.5	572	7	US-11-649-663A-5524	Sequence 5524, App
1006	56.5	9.6	1280	7	US-11-649-663A-2512	Sequence 2512, App	1079	56	9.5	628	7	US-11-649-663A-3552	Sequence 3552, App
1007	56.5	9.6	1292	7	US-11-649-663A-514	Sequence 514, App	1080	56	9.5	754	7	US-11-713-768-81272	Sequence 81272, A
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1015	56.5	9.6	1394	7	US-11-649-663A-640	Sequence 640, App	1088	56	9.5	967	7	US-11-649-663A-412	Sequence 412, App
1016	56.5	9.6	1436	6	US-10-438-246-19057	Sequence 19057, A	1089	56	9.5	997	7	US-11-649-663A-4404	Sequence 4404, App
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1018	56.5	9.6	1459	7	US-11-649-663A-3196	Sequence 3196, App	1091	56	9.5	1160	7	US-11-649-663A-2370	Sequence 2370, App
1019	56.5	9.6	1462	7	US-11-649-663A-1412	Sequence 1412, App	1092	56	9.5	1187	7	US-11-649-663A-1728	Sequence 1728, App
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1021	56.5	9.6	1487	7	US-11-649-663A-696	Sequence 696, App	1094	56	9.5	1209	7	US-11-649-663A-2564	Sequence 2564, App
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1026	56.5	9.6	1521	7	US-11-649-663A-1956	Sequence 1956, App	1099	56	9.5	1251	7	US-11-649-663A-1888	Sequence 1888, App
1027	56.5	9.6	1531	7	US-11-649-663A-170	Sequence 170, App	1100	56	9.5	1265	7	US-11-649-663A-428	Sequence 426, App
1028	56.5	9.6	1535	7	US-11-673-351-48	Sequence 48, Appl	1101	56	9.5	1265	7	US-11-649-663A-678	Sequence 478, App
1029	56.5	9.6	1545	7	US-11-649-663A-1584	Sequence 1584, App	1102	56	9.5	1283	7	US-11-649-663A-678	Sequence 678, App
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1031	56.5	9.6	1553	7	US-11-649-663A-1432	Sequence 1432, App	1104	56	9.5	1292	7	US-11-649-663A-1736	Sequence 1736, App
1032	56.5	9.6	1577	7	US-11-649-663A-1118	Sequence 1118, App	1105	56	9.5	1293	7	US-11-649-663A-824	Sequence 824, App
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1039	56.5	9.6	1711	7	US-11-649-663A-2190	Sequence 2190, App	1112	56	9.5	1403	7	US-11-649-663A-738	Sequence 738, App
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1047	56.5	9.6	1940	7	US-11-649-663A-728	Sequence 728, App	1120	56	9.5	1518	7	US-11-649-663A-1982	Sequence 1982, App
1048	56.5	9.6	1955	7	US-11-649-663A-1590	Sequence 1590, App	1121	56	9.5	1527	7	US-11-649-663A-1278	Sequence 1278, App
1049	56.5	9.6	1970	7	US-11-649-663A-1984	Sequence 1984, App	1122	56	9.5	1556	7	US-11-649-663A-2208	Sequence 2208, App
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1053	56.5	9.6	93	6	US-10-767-701-43275	Sequence 43275, A	1126	56	9.5	1653	7	US-11-649-663A-626	Sequence 626, App
1054	56	9.5	124	7	US-11-713-768-17338	Sequence 17338, A	1127	56	9.5	1669	7	US-11-649-663A-1758	Sequence 1758, App
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1133	56	9.5	1747	7	US-11-649-663A-2700	Sequence 2700, Ap	1208	55.5	9.4	1219	7	US-11-649-663A-1462	Sequence 1462, Ap
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1136	56	9.5	1767	7	US-11-649-663A-900	Sequence 900, App	1210	55.5	9.4	1224	7	US-11-649-663A-1616	Sequence 1616, App
1137	56	9.5	1792	7	US-11-649-663A-1192	Sequence 1192, Ap	1211	55.5	9.4	1244	7	US-11-649-663A-488	Sequence 488, App
1138	56	9.5	1816	7	US-11-649-663A-590	Sequence 590, App	1212	55.5	9.4	1245	7	US-11-649-663A-3982	Sequence 3982, Ap
1139	56	9.5	1863	7	US-11-649-663A-1830	Sequence 1830, Ap	1213	55.5	9.4	1258	7	US-11-649-663A-1612	Sequence 1612, Ap
1140	56	9.5	1869	7	US-11-649-663A-746	Sequence 746, App	1214	55.5	9.4	1291	7	US-11-649-663A-1206	Sequence 1206, Ap
1141	56	9.5	1884	7	US-11-649-663A-234	Sequence 234, App	1215	55.5	9.4	1298	7	US-11-649-663A-5050	Sequence 5050, Ap
1142	56	9.5	1919	7	US-11-649-663A-4028	Sequence 4028, Ap	1216	55.5	9.4	1309	7	US-11-649-663A-2670	Sequence 2670, Ap
1143	56	9.5	1934	7	US-11-649-663A-1742	Sequence 1742, Ap	1217	55.5	9.4	1320	7	US-11-649-663A-2270	Sequence 2270, Ap
1144	56	9.5	1937	7	US-11-649-663A-3074	Sequence 3074, Ap	1218	55.5	9.4	1351	7	US-11-649-663A-2808	Sequence 2808, Ap
1145	56	9.5	2062	7	US-11-649-663A-1454	Sequence 1454, Ap	1219	55.5	9.4	1375	7	US-11-649-663A-2318	Sequence 2318, Ap
1146	56	9.5	2068	7	US-11-649-663A-2662	Sequence 2662, Ap	1220	55.5	9.4	1382	7	US-11-649-663A-2276	Sequence 2276, Ap
1147	56	9.5	2077	7	US-11-649-663A-324	Sequence 324, App	1221	55.5	9.4	1382	7	US-11-649-663A-828	Sequence 828, App
1148	56	9.5	2101	7	US-11-649-663A-778	Sequence 778, App	1222	55.5	9.4	1382	7	US-11-649-663A-2402	Sequence 2402, Ap
1149	56	9.5	2110	7	US-11-649-663A-2010	Sequence 2010, Ap	1223	55.5	9.4	1407	7	US-11-649-663A-1498	Sequence 1498, Ap
1150	56	9.5	2127	7	US-11-649-663A-748	Sequence 748, App	1224	55.5	9.4	1410	7	US-11-649-663A-1062	Sequence 1062, Ap
1151	56	9.5	2205	7	US-11-649-663A-1504	Sequence 1504, Ap	1225	55.5	9.4	1436	7	US-11-649-663A-958	Sequence 958, App
1152	56	9.5	2235	7	US-11-649-663A-2036	Sequence 2036, Ap	1226	55.5	9.4	1446	7	US-11-649-663A-662	Sequence 662, App
1153	56	9.5	2280	7	US-11-649-663A-1878	Sequence 1878, Ap	1227	55.5	9.4	1447	7	US-11-649-663A-3646	Sequence 3646, Ap
1154	56	9.5	2328	7	US-11-649-663A-1936	Sequence 1936, Ap	1228	55.5	9.4	1472	7	US-11-649-663A-1344	Sequence 1344, Ap
1155	56	9.5	2384	7	US-11-649-663A-1740	Sequence 1740, Ap	1229	55.5	9.4	1481	7	US-11-649-663A-1162	Sequence 1162, Ap
1156	56	9.5	2415	7	US-11-649-663A-1564	Sequence 1564, Ap	1230	55.5	9.4	1512	7	US-11-649-663A-550	Sequence 550, App
1157	56	9.5	2436	7	US-11-649-663A-1790	Sequence 1790, Ap	1231	55.5	9.4	1513	7	US-11-649-663A-2306	Sequence 2306, Ap
1158	56	9.5	2459	7	US-11-649-663A-1578	Sequence 1578, Ap	1232	55.5	9.4	1529	7	US-11-649-663A-1114	Sequence 1114, Ap
1159	56	9.5	2487	7	US-11-649-663A-1608	Sequence 1608, Ap	1233	55.5	9.4	1537	7	US-11-649-663A-2736	Sequence 2736, Ap
1160	56	9.5	2782	7	US-11-649-663A-722	Sequence 722, App	1234	55.5	9.4	1538	7	US-11-649-663A-2654	Sequence 2654, Ap
1161	56	9.5	2973	7	US-11-649-663A-1566	Sequence 1566, Ap	1235	55.5	9.4	1553	7	US-11-649-663A-1430	Sequence 1430, Ap
1162	56	9.5	3159	7	US-11-649-663A-1916	Sequence 1916, Ap	1236	55.5	9.4	1566	7	US-11-649-663A-222	Sequence 222, App
1163	56	9.5	3652	7	US-11-649-663A-2760	Sequence 2760, Ap	1237	55.5	9.4	1619	7	US-11-649-663A-2228	Sequence 2228, Ap
1164	56	9.5	5405	7	US-11-625-927-151	Sequence 151, App	1238	55.5	9.4	1632	7	US-11-649-663A-3990	Sequence 3990, Ap
1165	55.5	9.4	42	7	US-11-528-927-571	Sequence 571, App	1239	55.5	9.4	1657	7	US-11-649-663A-642	Sequence 642, App
1166	55.5	9.4	42	7	US-11-528-950-571	Sequence 571, App	1240	55.5	9.4	1659	7	US-11-649-663A-984	Sequence 984, App
1167	55.5	9.4	97	6	US-10-438-246-32293	Sequence 32293, A	1241	55.5	9.4	1713	7	US-11-649-663A-3720	Sequence 3720, Ap
1168	55.5	9.4	168	7	US-11-713-768-91545	Sequence 91545, A	1242	55.5	9.4	1746	7	US-11-649-663A-2742	Sequence 2742, Ap
1169	55.5	9.4	168	7	US-11-713-768-95301	Sequence 95301, A	1243	55.5	9.4	1771	7	US-11-649-663A-928	Sequence 928, App
1170	55.5	9.4	183	6	US-10-767-701-32134	Sequence 32134, A	1244	55.5	9.4	1773	7	US-11-649-663A-2658	Sequence 2658, Ap
1171	55.5	9.4	184	6	US-10-767-701-45523	Sequence 45523, A	1245	55.5	9.4	1779	7	US-11-649-663A-2160	Sequence 2160, Ap
1172	55.5	9.4	264	7	US-11-713-768-89430	Sequence 89430, A	1246	55.5	9.4	1794	7	US-11-649-663A-2164	Sequence 2164, Ap
1173	55.5	9.4	264	7	US-11-713-768-93186	Sequence 93186, A	1247	55.5	9.4	1824	7	US-11-649-663A-1444	Sequence 1444, Ap
1174	55.5	9.4	439	7	US-11-713-768-6544	Sequence 6544, Ap	1248	55.5	9.4	1847	7	US-11-649-663A-1242	Sequence 1242, Ap
1175	55.5	9.4	470	7	US-11-713-768-6543	Sequence 6543, Ap	1249	55.5	9.4	1855	7	US-11-649-663A-2478	Sequence 2478, Ap
1176	55.5	9.4	505	7	US-11-713-768-6542	Sequence 6542, Ap	1250	55.5	9.4	1864	7	US-11-649-663A-794	Sequence 794, App
1177	55.5	9.4	558	7	US-11-649-663A-174	Sequence 174, App	1251	55.5	9.4	1868	7	US-11-649-663A-4320	Sequence 4320, Ap
1178	55.5	9.4	582	7	US-11-649-663A-3088	Sequence 3088, Ap	1252	55.5	9.4	1942	7	US-11-649-663A-1076	Sequence 1076, Ap
1179	55.5	9.4	684	7	US-11-514-773-3	Sequence 3, Appli	1253	55.5	9.4	1973	7	US-11-649-663A-1378	Sequence 1378, Ap
1181	55.5	9.4	685	7	US-11-514-773-1	Sequence 1, Appli	1254	55.5	9.4	2013	7	US-11-649-663A-1226	Sequence 1226, Ap
1182	55.5	9.4	685	7	US-11-514-773-1	Sequence 1, Appli	1255	55.5	9.4	2228	7	US-11-649-663A-920	Sequence 920, App
1183	55.5	9.4	685	7	US-11-537-235-88	Sequence 88, Appl	1256	55.5	9.4	2499	7	US-11-649-663A-268	Sequence 268, App
1184	55.5	9.4	685	7	US-11-537-235-88	Sequence 88, Appl	1257	55	9.3	98	7	US-11-360-355-168355	Sequence 168355,
1185	55.5	9.4	863	7	US-11-649-663A-2446	Sequence 2446, Ap	1258	55	9.3	98	7	US-11-360-355-170437	Sequence 170437,
1186	55.5	9.4	919	6	US-10-481-700-2	Sequence 2, Appli	1259	55	9.3	136	7	US-11-360-355-164877	Sequence 164877,
1187	55.5	9.4	946	7	US-11-676-042-2	Sequence 1628, Ap	1260	55	9.3	136	6	US-10-767-701-60421	Sequence 60421, A
1188	55.5	9.4	963	7	US-11-676-042-2	Sequence 2, Appli	1261	55	9.3	156	6	US-10-438-246-6500	Sequence 6500, Ap
1189	55.5	9.4	1005	7	US-11-649-663A-1158	Sequence 1158, Ap	1262	55	9.3	160	7	US-11-360-355-134059	Sequence 134059,
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1191	55.5	9.4	1061	7	US-11-649-663A-328	Sequence 328, App	1264	55	9.3	176	6	US-10-438-246-16685	Sequence 16685, A
1192	55.5	9.4	1066	7	US-11-649-663A-1402	Sequence 1402, Ap	1265	55	9.3	196	6	US-10-767-701-40420	Sequence 40420, A
1193	55.5	9.4	1068	7	US-11-649-663A-3134	Sequence 3134, Ap	1266	55	9.3	200	6	US-10-438-246-6484	Sequence 6484, Ap
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1195	55.5	9.4	1089	7	US-11-649-663A-62	Sequence 62, Appl	1268	55	9.3	222	7	US-11-552-437-48	Sequence 48, Appl
1196	55.5	9.4	1098	7	US-11-649-663A-2414	Sequence 2414, Ap	1269	55	9.3	230	6	US-10-438-246-24892	Sequence 24892, A
1197	55.5	9.4	1099	7	US-11-649-663A-400	Sequence 400, App	1270	55	9.3	360	7	US-11-360-355-157607	Sequence 157607,
1198	55.5	9.4	1122	7	US-11-649-663A-2524	Sequence 2524, Ap	1271	55	9.3	370	7	US-11-787-713-37	Sequence 37, Appl
1199	55.5	9.4	1126	7	US-11-649-663A-568	Sequence 568, App	1272	55	9.3	387	6	US-10-438-246-16684	Sequence 16684, A
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1202	55.5	9.4	1187	7	US-11-649-663A-1142	Sequence 1142, Ap	1275	55	9.3	484	7	US-11-713-768-94848	Sequence 94848, A
1203	55.5	9.4	1192	7	US-11-649-663A-694	Sequence 694, App	1276	55	9.3	485	7	US-11-713-768-91091	Sequence 91091, A
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1278	55	9.3	485	7	US-11-713-768-94847	Sequence 94847, A	1351	55	9.3	1475	7	US-11-649-663A-1474	Sequence 1474, Ap
1279	55	9.3	486	7	US-11-713-768-91090	Sequence 91090, A	1352	55	9.3	1479	7	US-11-649-663A-460	Sequence 460, App
1280	55	9.3	487	7	US-11-713-768-94846	Sequence 94846, A	1353	55	9.3	1481	7	US-11-649-663A-878	Sequence 878, App
1281	55	9.3	505	7	US-11-649-663A-4872	Sequence 4872, Ap	1354	55	9.3	1518	7	US-11-714-684-212	Sequence 212, App
1282	55	9.3	538	7	US-11-370-191-8	Sequence 8, Appl1	1355	55	9.3	1518	7	US-11-714-684-212	Sequence 212, App
1283	55	9.3	587	7	US-11-713-768-43888	Sequence 43888, A	1356	55	9.3	1535	7	US-11-649-663A-572	Sequence 572, App
1284	55	9.3	618	6	US-10-529-351A-5433	Sequence 5433, Ap	1357	55	9.3	1535	7	US-11-649-663A-2384	Sequence 2384, Ap
1285	55	9.3	619	7	US-11-649-663A-522	Sequence 522, App	1358	55	9.3	1601	7	US-11-649-663A-2364	Sequence 2364, Ap
1286	55	9.3	794	7	US-11-713-768-45043	Sequence 45043, A	1359	55	9.3	1609	7	US-11-625-272-146	Sequence 146, App
1287	55	9.3	794	7	US-11-713-768-46386	Sequence 46386, A	1360	55	9.3	1623	7	US-11-649-663A-1512	Sequence 1512, Ap
1288	55	9.3	794	7	US-11-713-768-46386	Sequence 46386, A	1361	55	9.3	1626	6	US-10-481-700-12	Sequence 12, Appl1
1289	55	9.3	840	7	US-11-649-663A-44	Sequence 44, Appl1	1362	55	9.3	1629	7	US-11-649-663A-2828	Sequence 2828, Ap
1290	55	9.3	833	7	US-11-713-768-45042	Sequence 45042, A	1363	55	9.3	1633	7	US-11-649-663A-1088	Sequence 1088, Ap
1291	55	9.3	833	7	US-11-713-768-45790	Sequence 45790, A	1364	55	9.3	1633	7	US-11-649-663A-2406	Sequence 2406, Ap
1292	55	9.3	853	7	US-11-713-768-46385	Sequence 46385, A	1365	55	9.3	1659	7	US-11-649-663A-3184	Sequence 3184, Ap
1293	55	9.3	856	7	US-11-713-768-45041	Sequence 45041, A	1366	55	9.3	1668	6	US-10-481-700-7	Sequence 7, Appl1
1294	55	9.3	856	7	US-11-713-768-46384	Sequence 46384, A	1367	55	9.3	1670	7	US-11-649-663A-1006	Sequence 1006, Ap
1295	55	9.3	856	7	US-11-713-768-46384	Sequence 46384, A	1368	55	9.3	1675	7	US-11-649-663A-658	Sequence 658, App
1296	55	9.3	864	7	US-11-649-663A-1674	Sequence 1674, Ap	1369	55	9.3	1679	6	US-10-481-700-11	Sequence 11, Appl1
1297	55	9.3	893	7	US-11-649-663A-1638	Sequence 1638, Ap	1370	55	9.3	1696	7	US-11-649-663A-1464	Sequence 1464, Ap
1298	55	9.3	929	7	US-11-360-355-120849	Sequence 120849, A	1371	55	9.3	1700	7	US-11-649-663A-1010	Sequence 1010, Ap
1299	55	9.3	962	7	US-11-649-663A-922	Sequence 922, App	1372	55	9.3	1701	7	US-11-649-663A-2440	Sequence 2440, Ap
1300	55	9.3	978	7	US-11-649-663A-1692	Sequence 1692, Ap	1373	55	9.3	1721	6	US-10-481-700-10	Sequence 10, Appl1
1301	55	9.3	1038	7	US-11-633-858-230	Sequence 230, App	1374	55	9.3	1721	7	US-11-649-663A-3508	Sequence 3508, Ap
1302	55	9.3	1063	7	US-11-649-663A-2596	Sequence 2596, Ap	1375	55	9.3	1721	7	US-11-649-663A-1128	Sequence 1128, Ap
1303	55	9.3	1065	7	US-11-649-663A-344	Sequence 344, App	1376	55	9.3	1766	7	US-11-649-663A-2614	Sequence 2614, Ap
1304	55	9.3	1067	7	US-11-649-663A-1718	Sequence 1718, Ap	1377	55	9.3	1783	7	US-11-649-663A-1440	Sequence 1440, Ap
1305	55	9.3	1067	7	US-11-649-663A-2718	Sequence 2718, Ap	1378	55	9.3	1883	7	US-11-649-663A-5108	Sequence 5108, Ap
1306	55	9.3	1073	7	US-11-649-663A-1312	Sequence 1312, Ap	1379	55	9.3	1916	7	US-11-649-663A-1530	Sequence 1530, Ap
1307	55	9.3	1089	7	US-11-649-663A-1910	Sequence 1910, Ap	1380	55	9.3	1938	7	US-11-649-663A-996	Sequence 996, App
1308	55	9.3	1097	7	US-11-649-663A-496	Sequence 496, App	1381	55	9.3	1990	7	US-11-649-663A-862	Sequence 862, App
1309	55	9.3	1105	7	US-11-649-663A-1682	Sequence 1682, Ap	1382	55	9.3	2097	7	US-11-649-663A-4144	Sequence 4144, Ap
1310	55	9.3	1109	7	US-11-649-663A-1516	Sequence 1516, Ap	1383	55	9.3	2175	7	US-11-649-663A-2008	Sequence 2008, Ap
1311	55	9.3	1116	7	US-11-649-663A-2606	Sequence 2606, Ap	1384	55	9.3	2262	7	US-11-649-663A-1008	Sequence 1008, Ap
1312	55	9.3	1125	7	US-11-649-663A-2582	Sequence 2582, Ap	1385	55	9.3	2268	7	US-11-649-663A-2062	Sequence 2062, Ap
1313	55	9.3	1126	7	US-11-649-663A-2134	Sequence 2134, Ap	1386	55	9.3	2369	7	US-11-649-663A-4660	Sequence 4660, Ap
1314	55	9.3	1129	7	US-11-649-663A-332	Sequence 332, App	1387	55	9.3	2416	7	US-11-649-663A-4660	Sequence 4660, Ap
1315	55	9.3	1134	7	US-11-649-663A-2104	Sequence 2104, Ap	1388	54.5	9.3	64	7	US-11-689-173-10481	Sequence 10481, A
1316	55	9.3	1134	7	US-11-649-663A-2548	Sequence 2548, Ap	1389	54.5	9.3	83	6	US-10-767-701-33968	Sequence 33968, A
1317	55	9.3	1143	7	US-11-649-663A-492	Sequence 492, App	1390	54.5	9.3	86	7	US-11-689-173-7905	Sequence 7905, Ap
1318	55	9.3	1143	7	US-11-649-663A-348	Sequence 348, App	1391	54.5	9.3	111	6	US-10-767-701-39494	Sequence 39494, A
1319	55	9.3	1161	7	US-11-649-663A-2568	Sequence 2568, Ap	1392	54.5	9.3	123	6	US-10-767-701-48946	Sequence 48946, A
1320	55	9.3	1164	7	US-11-649-663A-338	Sequence 338, App	1393	54.5	9.3	123	6	US-10-767-701-48946	Sequence 48946, A
1321	55	9.3	1197	7	US-11-649-663A-340	Sequence 340, App	1394	54.5	9.3	161	6	US-10-438-246-26350	Sequence 26350, A
1322	55	9.3	1217	7	US-11-649-663A-2612	Sequence 2612, Ap	1395	54.5	9.3	176	7	US-11-360-355-165806	Sequence 165806, A
1323	55	9.3	1218	7	US-11-649-663A-498	Sequence 498, App	1396	54.5	9.3	196	7	US-11-360-355-165806	Sequence 165806, A
1324	55	9.3	1224	7	US-11-649-663A-1958	Sequence 1958, Ap	1397	54.5	9.3	216	6	US-10-438-246-25376	Sequence 25376, A
1325	55	9.3	1252	7	US-11-649-663A-806	Sequence 806, App	1398	54.5	9.3	221	7	US-11-360-355-135854	Sequence 135854, A
1326	55	9.3	1253	7	US-11-649-663A-2590	Sequence 2590, Ap	1399	54.5	9.3	227	7	US-11-510-314-8	Sequence 8, Appl1
1327	55	9.3	1254	7	US-11-649-663A-840	Sequence 840, App	1400	54.5	9.3	259	6	US-10-551-004-45	Sequence 45, Appl1
1328	55	9.3	1267	7	US-11-649-663A-868	Sequence 868, App	1401	54.5	9.3	259	7	US-11-537-235-300	Sequence 300, App
1329	55	9.3	1300	6	US-10-481-700-13	Sequence 13, Appl1	1402	54.5	9.3	259	7	US-11-553-810-300	Sequence 300, App
1330	55	9.3	1300	7	US-11-649-663A-1250	Sequence 1250, Ap	1403	54.5	9.3	305	7	US-11-713-768-56489	Sequence 56489, A
1331	55	9.3	1336	7	US-11-649-663A-1036	Sequence 1036, Ap	1404	54.5	9.3	356	7	US-11-713-768-56488	Sequence 56488, A
1332	55	9.3	1337	7	US-11-649-663A-376	Sequence 376, App	1405	54.5	9.3	371	7	US-11-713-768-56487	Sequence 56487, A
1333	55	9.3	1342	6	US-10-481-700-15	Sequence 15, Appl1	1406	54.5	9.3	384	7	US-11-713-768-70547	Sequence 70547, A
1334	55	9.3	1346	7	US-11-649-663A-1146	Sequence 1146, Ap	1407	54.5	9.3	384	7	US-11-713-768-85617	Sequence 85617, A
1335	55	9.3	1346	7	US-11-649-663A-676	Sequence 676, App	1408	54.5	9.3	469	7	US-11-649-663A-1370	Sequence 1370, Ap
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Sequence 5782, Ap
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Sequence 1221, Ap
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OM protein - protein search, using sw model

Run on: November 29, 2007, 17:21:19 ; Search time 85 Seconds
(without alignments)
1014.355 Million cell updates/sec

Title: US-10-692-299-2

Perfect score: 589

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Scoring table: BLOSUM62

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Searched: 3552611 seqs, 817857308 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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16	589	100.0	105	3	US-09-965-528-11
29	589	100.0	105	3	US-09-997-428-371
33	589	100.0	105	3	US-09-796-753-64
75	589	100.0	105	3	US-09-969-984-11
76	589	100.0	105	4	US-10-016-481-2
77	589	100.0	105	4	US-10-027-603-2
99	589	100.0	105	4	US-10-132-812-16
258	589	100.0	105	4	US-10-223-085-172
264	589	100.0	105	4	US-10-219-065-166
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299	589	100.0	105	4	US-10-212-355-5
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733	498	84.6	86	5	US-10-503-554A-82	Sequence 82, Appl	806	455	77.2	86	6	US-11-048-649-10	Sequence 10, Appl
734	498	84.6	86	5	US-10-343-095A-117	Sequence 117, App	807	455	77.2	86	6	US-11-529-695-28	Sequence 28, Appl
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752	498	84.6	89	4	US-10-323-157-15	Sequence 15, Appl	825	376	63.8	81	4	US-10-417-426-20	Sequence 20, Appl
753	498	84.6	89	5	US-10-713-567-15	Sequence 15, Appl	826	376	63.8	81	5	US-10-680-554-15	Sequence 15, Appl
754	498	84.6	89	5	US-10-811-328-15	Sequence 15, Appl	827	376	63.8	81	5	US-10-713-567-13	Sequence 13, Appl
755	498	84.6	89	5	US-10-912-907-15	Sequence 15, Appl	828	376	63.8	81	5	US-10-811-328-13	Sequence 13, Appl
756	498	84.6	89	5	US-10-415-724-15	Sequence 15, Appl	829	376	63.8	81	5	US-10-912-907-13	Sequence 13, Appl
757	498	84.6	89	5	US-10-415-724-15	Sequence 15, Appl	830	376	63.8	81	5	US-10-415-724-13	Sequence 13, Appl
758	498	84.6	89	6	US-11-529-695-15	Sequence 15, Appl	831	376	63.8	81	5	US-10-977-113-16	Sequence 16, Appl
759	497	84.4	86	4	US-10-333-192-20	Sequence 20, Appl	832	376	63.8	81	5	US-10-871-152-27	Sequence 27, Appl
760	497	84.4	86	5	US-10-503-554A-81	Sequence 81, Appl	833	376	63.8	81	6	US-10-415-724-13	Sequence 13, Appl
761	497	84.4	86	5	US-10-542-664-2	Sequence 2, Appli	834	376	63.8	81	6	US-11-073-420-16	Sequence 16, Appl
762	497	84.4	86	5	US-10-576-066-3	Sequence 3, Appli	835	376	63.8	81	6	US-11-048-649-20	Sequence 20, Appl
763	497	84.4	86	5	US-11-304-129-20	Sequence 20, Appl	836	376	63.8	81	6	US-11-529-695-13	Sequence 13, Appl
764	494	83.9	85	4	US-10-016-481-16	Sequence 16, Appl	837	315	53.5	80	4	US-10-417-426-13	Sequence 13, Appl
765	494	83.9	85	4	US-10-323-157-16	Sequence 16, Appl	838	315	53.5	80	4	US-10-467-019-21	Sequence 21, Appl
766	494	83.9	85	5	US-10-713-567-16	Sequence 16, Appl	839	315	53.5	80	4	US-10-912-907-21	Sequence 21, Appl
767	494	83.9	85	5	US-10-811-328-16	Sequence 16, Appl	840	315	53.5	80	4	US-10-470-951-64	Sequence 64, Appl
768	494	83.9	85	5	US-10-912-907-16	Sequence 16, Appl	841	315	53.5	80	4	US-10-333-132-34	Sequence 34, Appl
769	494	83.9	85	5	US-10-415-724-16	Sequence 16, Appl	842	315	53.5	80	5	US-10-977-113-15	Sequence 15, Appl
770	494	83.9	85	5	US-10-415-724-16	Sequence 16, Appl	843	315	53.5	80	5	US-10-503-554A-21	Sequence 21, Appl
771	494	83.9	85	6	US-11-529-695-16	Sequence 16, Appl	844	315	53.5	80	6	US-10-871-152-26	Sequence 26, Appl
772	494	83.9	86	5	US-10-811-328-20	Sequence 20, Appl	845	315	53.5	80	6	US-11-073-420-15	Sequence 15, Appl
773	494	83.9	86	5	US-10-912-907-20	Sequence 20, Appl	846	315	53.5	80	6	US-11-304-129-34	Sequence 34, Appl
774	494	83.9	86	6	US-11-529-695-20	Sequence 20, Appl	847	311.5	52.9	79	3	US-11-048-649-13	Sequence 13, Appl
775	478	81.2	86	4	US-10-016-481-17	Sequence 17, Appl	848	311.5	52.9	79	3	US-09-886-242A-5	Sequence 5, Appli
776	478	81.2	86	4	US-10-323-157-17	Sequence 17, Appl	849	311.5	52.9	79	5	US-10-692-299-5	Sequence 5, Appli
777	478	81.2	86	5	US-10-713-567-17	Sequence 17, Appl	850	311.5	52.9	79	6	US-11-537-382-5	Sequence 5, Appli
778	478	81.2	86	5	US-10-811-328-17	Sequence 17, Appl	851	310.5	52.7	81	4	US-10-016-481-12	Sequence 12, Appl
779	478	81.2	86	5	US-10-912-907-17	Sequence 17, Appl	852	310.5	52.7	81	4	US-10-132-812-19	Sequence 19, Appl
780	478	81.2	86	5	US-10-415-724-17	Sequence 17, Appl	853	310.5	52.7	81	4	US-10-323-157-12	Sequence 12, Appl
781	478	81.2	86	5	US-10-415-724-17	Sequence 17, Appl	854	310.5	52.7	81	5	US-10-680-554-12	Sequence 12, Appl
782	478	81.2	86	6	US-10-415-724-17	Sequence 17, Appl	855	310.5	52.7	81	5	US-10-713-567-12	Sequence 12, Appl
783	476	80.8	82	5	US-11-529-695-17	Sequence 17, Appl	856	310.5	52.7	81	5	US-10-811-328-12	Sequence 12, Appl
784	473	80.3	86	4	US-10-977-113-11	Sequence 11, Appl	857	310.5	52.7	81	5	US-10-912-907-12	Sequence 12, Appl
785	473	80.3	86	4	US-10-470-951-37	Sequence 37, Appl	858	310.5	52.7	81	5	US-10-415-724-12	Sequence 12, Appl
786	473	80.3	86	5	US-10-362-504-49	Sequence 49, Appl	859	310.5	52.7	81	5	US-10-415-724-12	Sequence 12, Appl
787	473	80.3	86	5	US-10-680-554-10	Sequence 10, Appl	860	310.5	52.7	81	6	US-11-529-695-12	Sequence 12, Appl
788	473	80.3	86	5	US-10-713-567-30	Sequence 30, Appl	861	306	52.0	100	3	US-09-886-242A-4	Sequence 4, Appli
789	473	80.3	86	5	US-10-811-328-30	Sequence 30, Appl	862	306	52.0	100	4	US-10-027-603-4	Sequence 4, Appli
790	473	80.3	86	6	US-10-503-554A-138	Sequence 138, App	863	306	52.0	100	5	US-10-692-299-4	Sequence 4, Appli
791	469	79.6	86	4	US-11-529-695-30	Sequence 30, Appl	864	306	52.0	100	6	US-11-537-382-4	Sequence 4, Appli
792	469	79.6	86	4	US-10-470-951-41	Sequence 41, Appl	865	303	51.4	108	4	US-10-016-481-5	Sequence 5, Appli
793	469	79.6	86	5	US-10-362-504-53	Sequence 53, Appl	866	303	51.4	108	4	US-10-231-411-4	Sequence 4, Appli
794	467	79.3	86	4	US-10-503-554A-142	Sequence 142, App	867	303	51.4	108	4	US-10-212-355-2	Sequence 2, Appli
795	467	79.3	86	4	US-10-470-951-39	Sequence 39, Appl	868	303	51.4	108	4	US-10-323-137-5	Sequence 5, Appli
796	467	79.3	86	4	US-10-362-504-51	Sequence 51, Appl	869	303	51.4	108	4	US-10-212-201-2	Sequence 2, Appli
797	455	77.2	86	5	US-10-503-554A-140	Sequence 140, App	870	303	51.4	108	4	US-10-467-019-17	Sequence 17, Appl
798	455	77.2	86	4	US-10-417-426-10	Sequence 10, Appl	871	303	51.4	108	4	US-10-680-755A-2	Sequence 2, Appli
799	455	77.2	86	5	US-10-470-951-8	Sequence 8, Appli	872	303	51.4	108	4	US-10-680-800A-2	Sequence 2, Appli

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878	303	51.4	108	5	US-10-503-554A-17	Sequence 17, Appl	951	287.5	48.8	96	5	US-10-811-328-11	Sequence 11, Appl
879	303	51.4	108	5	US-10-982-168-2	Sequence 2, Appli	952	287.5	48.8	96	5	US-10-912-907-11	Sequence 11, Appl
880	303	51.4	108	5	US-10-504-588-6	Sequence 6, Appli	953	287.5	48.8	96	5	US-10-415-724-11	Sequence 11, Appl
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882	303	51.4	108	5	US-10-549-241-4	Sequence 4, Appli	955	287.5	48.8	96	6	US-11-529-695-11	Sequence 11, Appl
883	303	51.4	108	6	US-11-384-222-4	Sequence 4, Appli	956	286	48.6	80	5	US-10-977-113-10	Sequence 10, Appl
884	303	51.4	108	6	US-11-549-232-2	Sequence 2, Appli	957	286	48.6	80	6	US-11-073-420-10	Sequence 10, Appl
885	303	51.4	108	6	US-11-549-227-2	Sequence 2, Appli	958	286	48.6	81	4	US-10-417-426-7	Sequence 7, Appli
886	303	51.4	108	6	US-11-548-814-2	Sequence 2, Appli	959	286	48.6	81	4	US-10-467-019-39	Sequence 39, Appl
887	303	51.4	108	6	US-11-550-982-2	Sequence 2, Appli	960	286	48.6	81	4	US-10-362-504-71	Sequence 71, Appl
888	303	51.4	108	6	US-11-549-237-2	Sequence 2, Appli	961	286	48.6	81	5	US-10-680-554-9	Sequence 9, Appli
889	303	51.4	108	6	US-11-549-222-2	Sequence 2, Appli	962	286	48.6	81	5	US-10-680-554-11	Sequence 11, Appl
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891	303	51.4	108	6	US-11-550-993-2	Sequence 2, Appli	964	286	48.6	81	5	US-10-713-567-31	Sequence 31, Appl
892	303	51.4	108	6	US-11-551-002-2	Sequence 2, Appli	965	286	48.6	81	5	US-10-811-328-29	Sequence 29, Appl
893	303	51.4	108	6	US-11-548-810-2	Sequence 2, Appli	966	286	48.6	81	5	US-10-811-328-31	Sequence 31, Appl
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896	303	51.4	108	6	US-11-529-695-5	Sequence 5, Appli	969	286	48.6	81	6	US-11-048-649-7	Sequence 7, Appli
897	303	51.4	108	6	US-11-548-830-2	Sequence 2, Appli	970	286	48.6	81	6	US-11-529-695-29	Sequence 29, Appl
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899	303	51.4	108	6	US-11-548-826-2	Sequence 2, Appli	972	284	48.2	81	6	US-11-073-420-37	Sequence 37, Appl
900	303	51.4	108	6	US-11-551-008-2	Sequence 2, Appli	973	282.5	48.0	129	4	US-10-132-812-14	Sequence 14, Appl
901	303	51.4	108	6	US-11-549-241-2	Sequence 2, Appli	974	282.5	48.0	129	4	US-10-231-411-2	Sequence 2, Appli
902	303	51.4	116	4	US-10-680-755A-26	Sequence 26, Appl	975	282.5	48.0	129	4	US-10-680-755A-29	Sequence 29, Appl
903	303	51.4	116	4	US-10-680-800A-26	Sequence 26, Appl	976	282.5	48.0	129	4	US-10-680-800A-29	Sequence 29, Appl
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909	303	51.4	116	6	US-11-548-810-26	Sequence 26, Appl	982	282.5	48.0	129	6	US-11-550-983-29	Sequence 29, Appl
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911	303	51.4	116	6	US-11-548-824-26	Sequence 26, Appl	984	282.5	48.0	129	6	US-11-548-810-29	Sequence 29, Appl
912	303	51.4	116	6	US-11-548-830-26	Sequence 26, Appl	985	282.5	48.0	129	6	US-11-548-819-29	Sequence 29, Appl
913	303	51.4	116	6	US-11-548-826-26	Sequence 26, Appl	986	282.5	48.0	129	6	US-11-548-824-29	Sequence 29, Appl
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918	298	50.6	107	4	US-10-132-812-10	Sequence 10, Appl	991	278.5	47.3	77	5	US-10-680-554-14	Sequence 14, Appl
919	298	50.6	107	4	US-10-231-411-6	Sequence 6, Appli	992	278.5	47.3	77	5	US-10-713-567-32	Sequence 32, Appl
920	298	50.6	107	4	US-10-467-019-37	Sequence 37, Appl	993	278.5	47.3	77	6	US-10-811-328-32	Sequence 32, Appl
921	298	50.6	107	4	US-10-467-019-55	Sequence 55, Appl	994	278.5	47.3	77	6	US-11-529-695-32	Sequence 32, Appl
922	298	50.6	107	4	US-10-362-504-59	Sequence 69, Appl	995	270.5	45.9	102	5	US-10-680-554-6	Sequence 6, Appli
923	298	50.6	107	5	US-10-503-554A-37	Sequence 37, Appl	996	267.5	45.4	77	4	US-10-417-426-11	Sequence 11, Appl
924	298	50.6	107	5	US-10-503-554A-55	Sequence 55, Appl	997	267.5	45.4	77	5	US-10-680-554-13	Sequence 13, Appl
925	298	50.6	107	5	US-10-549-241-6	Sequence 6, Appli	998	267.5	45.4	77	5	US-10-977-113-14	Sequence 14, Appl
926	298	50.6	107	6	US-11-384-222-6	Sequence 6, Appli	999	267.5	45.4	77	5	US-10-871-152-24	Sequence 24, Appl
927	291	49.4	80	4	US-10-467-019-22	Sequence 22, Appl	1000	267.5	45.4	77	6	US-11-073-420-14	Sequence 14, Appl
928	291	49.4	80	5	US-10-503-554A-22	Sequence 22, Appl	1001	267.5	45.4	77	6	US-11-048-649-11	Sequence 11, Appl
929	291	49.4	81	4	US-10-016-481-6	Sequence 6, Appli	1002	265.5	45.1	102	4	US-10-417-426-8	Sequence 8, Appli
930	291	49.4	81	4	US-10-323-157-6	Sequence 6, Appli	1003	265.5	45.1	102	5	US-10-871-152-21	Sequence 21, Appl
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932	291	49.4	81	4	US-10-467-019-19	Sequence 19, Appl	1005	251.5	42.7	100	4	US-10-417-426-6	Sequence 6, Appli
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937	291	49.4	81	5	US-10-415-724-6	Sequence 6, Appli	1010	250.5	42.5	75	5	US-10-871-152-25	Sequence 25, Appl
938	291	49.4	81	5	US-10-977-113-9	Sequence 9, Appli	1011	250.5	42.5	75	6	US-11-073-420-13	Sequence 13, Appl
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941	291	49.4	81	5	US-10-415-724-6	Sequence 6, Appli	1014	109	18.5	23	4	US-10-680-755A-9	Sequence 9, Appli
942	291	49.4	81	5	US-10-542-664-3	Sequence 3, Appli	1015	109	18.5	23	4	US-10-680-800A-9	Sequence 9, Appli
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944	291	49.4	81	6	US-11-073-420-9	Sequence 9, Appli	1017	109	18.5	23	6	US-11-550-982-9	Sequence 9, Appli
945	291	49.4	81	6	US-11-048-649-5	Sequence 5, Appli	1018	109	18.5	23	6	US-11-548-805-9	Sequence 9, Appli

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1021	109	18.5	23	6	US-11-548-810-9	Sequence 9, Appli
1022	109	18.5	23	6	US-11-548-819-9	Sequence 9, Appli
1023	109	18.5	23	6	US-11-548-824-9	Sequence 9, Appli
1024	109	18.5	23	6	US-11-548-830-9	Sequence 9, Appli
1025	109	18.5	23	6	US-11-548-826-9	Sequence 9, Appli
1026	109	18.5	23	6	US-11-551-008-9	Sequence 9, Appli
1027	108.5	18.4	221	5	US-10-579-596-5	Sequence 5, Appli
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1030	107.5	18.3	180	4	US-10-287-971-34	Sequence 34, Appl
1031	107.5	18.3	224	3	US-09-976-736-14	Sequence 14, Appl
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1034	107.5	18.3	224	4	US-10-295-027-628	Sequence 628, App
1035	107.5	18.3	224	4	US-10-287-971-28	Sequence 28, Appl
1036	107.5	18.3	224	4	US-10-408-765A-335	Sequence 335, App
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1038	107.5	18.3	224	5	US-10-998-271-14	Sequence 14, Appl
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1042	107.5	18.3	224	6	US-11-069-137-5	Sequence 5, Appli
1043	107.5	18.3	224	6	US-11-443-428A-879994	Sequence 879994,
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1052	105.5	17.9	223	6	US-11-465-956-4	Sequence 11, Appl
1053	102	17.3	179	3	US-09-972-473-11	Sequence 11, Appl
1054	102	17.3	179	3	US-09-972-473-11	Sequence 6, Appli
1055	102	17.3	179	4	US-10-351-275-6	Sequence 11, Appl
1056	102	17.3	179	5	US-10-819-054-11	Sequence 11, Appl
1057	102	17.3	179	6	US-11-255-790-11	Sequence 11, Appl
1058	102	17.3	179	6	US-11-069-137-11	Sequence 11, Appl
1059	102	17.3	186	5	US-10-940-774-7146	Sequence 7146, Ap
1060	102	17.3	207	3	US-09-976-736-13	Sequence 13, Appl
1061	102	17.3	207	5	US-10-998-271-13	Sequence 13, Appl
1062	102	17.3	255	6	US-11-443-428A-772896	Sequence 772896,
1063	102	17.3	259	3	US-09-976-736-12	Sequence 12, Appl

Search completed: November 29, 2007, 17:24:31
Job time : 113.66 secs

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OM protein - protein search, using sw model

Run on: November 29, 2007, 17:17:13 ; Search time 37 Seconds

(without alignments)
328.583 Million cell updates/sec

Title: US-10-692-299-2_COPY_20_105

Perfect score: 498

Sequence: 1 AVITGACERDVQCGAGTCCA.....CSRFPDGRYRCMDLKNINP 86

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 983262 seqs, 142787483 residues

Total number of hits satisfying chosen parameters: 983262

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : Issued Patents AA.*
1: /EMC Celerra_SIDS2/ptodata/1/iaa/5-COMB.pep.*
2: /EMC Celerra_SIDS2/ptodata/1/iaa/6-COMB.pep.*
3: /EMC Celerra_SIDS2/ptodata/1/iaa/7-COMB.pep.*
4: /EMC Celerra_SIDS2/ptodata/1/iaa/H-COMB.pep.*
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7: /EMC Celerra_SIDS2/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	498	100.0	86	3	US-10-333-132-21
2	498	100.0	86	3	US-10-323-157A-3
3	498	100.0	86	3	US-10-231-411A-7
4	498	100.0	86	3	US-10-811-328-3
5	498	100.0	87	3	US-10-323-157A-18
6	498	100.0	87	3	US-10-811-328-18
7	498	100.0	89	3	US-10-323-157A-15
8	498	100.0	89	3	US-10-811-328-15
9	498	100.0	105	2	US-09-712-529-5
10	498	100.0	105	2	US-10-212-201A-5
11	498	100.0	105	2	US-10-212-355-5
12	498	100.0	105	2	US-09-991-181-371
13	498	100.0	105	2	US-09-990-444-371
14	498	100.0	105	2	US-09-997-333-371
15	498	100.0	105	2	US-09-992-598-371
16	498	100.0	105	2	US-09-989-735-371
17	498	100.0	105	3	US-09-989-726-371
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19	498	100.0	105	3	US-09-989-728-371
20	498	100.0	105	3	US-09-997-349-371
21	498	100.0	105	3	US-09-997-653-371
22	498	100.0	105	3	US-09-989-231A-371
23	498	100.0	105	3	US-09-989-732-371
24	498	100.0	105	3	US-09-990-441-371
25	498	100.0	105	3	US-10-333-132-23
26	498	100.0	105	3	US-10-123-292-470

27	498	100.0	105	3	US-10-323-157A-2	Sequence 2, Appli
28	498	100.0	105	3	US-09-989-328-371	Sequence 371, App
29	498	100.0	105	3	US-09-989-724-371	Sequence 371, App
30	498	100.0	105	3	US-09-989-733-371	Sequence 371, App
31	498	100.0	105	3	US-09-993-583-371	Sequence 371, App
32	498	100.0	105	3	US-10-152-398-470	Sequence 470, App
33	498	100.0	105	3	US-09-989-279-371	Sequence 371, App
34	498	100.0	105	3	US-10-123-907-470	Sequence 470, App
35	498	100.0	105	3	US-10-147-512-470	Sequence 470, App
36	498	100.0	105	3	US-10-147-485-470	Sequence 470, App
37	498	100.0	105	3	US-09-991-157-371	Sequence 371, App
38	498	100.0	105	3	US-10-124-814-470	Sequence 470, App
39	498	100.0	105	3	US-10-124-822-470	Sequence 470, App
40	498	100.0	105	3	US-09-990-439-371	Sequence 371, App
41	498	100.0	105	3	US-09-997-641-371	Sequence 371, App
42	498	100.0	105	3	US-10-223-081-172	Sequence 172, App
43	498	100.0	105	3	US-10-811-328-2	Sequence 2, Appli
44	498	100.0	105	3	US-09-997-384-371	Sequence 371, App
45	498	100.0	105	3	US-10-982-168-5	Sequence 5, Appli
46	498	100.0	105	3	US-10-219-074-166	Sequence 166, App
47	498	100.0	105	3	US-10-227-873-166	Sequence 166, App
48	498	100.0	105	3	US-10-223-087-172	Sequence 172, App
49	498	100.0	105	3	US-10-131-833A-470	Sequence 470, App
50	498	100.0	105	3	US-10-218-849-166	Sequence 166, App
51	498	100.0	105	3	US-10-142-419-470	Sequence 470, App
52	498	100.0	105	3	US-09-989-730-371	Sequence 371, App
53	498	100.0	105	3	US-10-216-168-166	Sequence 166, App
54	498	100.0	105	3	US-10-152-375-470	Sequence 470, App
55	498	100.0	105	3	US-10-223-082-172	Sequence 172, App
56	498	100.0	105	3	US-10-223-084-172	Sequence 172, App
57	498	100.0	105	3	US-09-997-585-371	Sequence 371, App
58	498	100.0	105	3	US-10-131-818A-470	Sequence 470, App
59	498	100.0	105	3	US-10-990-246-5	Sequence 5, Appli
60	498	100.0	105	3	US-10-145-873-470	Sequence 470, App
61	498	100.0	105	3	US-10-152-395-470	Sequence 470, App
62	498	100.0	105	3	US-10-131-822A-470	Sequence 470, App
63	498	100.0	105	3	US-10-142-763-470	Sequence 470, App
64	498	100.0	105	3	US-10-128-694A-470	Sequence 470, App
65	498	100.0	105	3	US-09-997-601-371	Sequence 371, App
66	498	100.0	105	3	US-10-123-213-470	Sequence 470, App
67	498	100.0	105	3	US-10-123-909-470	Sequence 470, App
68	498	100.0	105	3	US-10-131-826A-470	Sequence 470, App
69	498	100.0	105	3	US-10-680-755A-5	Sequence 5, Appli
70	498	100.0	105	3	US-10-147-513-470	Sequence 470, App
71	498	100.0	105	3	US-10-121-043-470	Sequence 470, App
72	498	100.0	105	3	US-09-997-666-371	Sequence 371, App
73	498	100.0	105	3	US-10-139-980-470	Sequence 470, App
74	498	100.0	105	3	US-10-223-090-172	Sequence 172, App
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76	497	99.8	105	3	US-10-333-132-22	Sequence 22, Appl
77	497	99.8	105	3	US-10-467-554-3	Sequence 3, Appli
78	494	99.2	85	3	US-10-323-157A-16	Sequence 16, Appl
79	494	99.2	85	3	US-10-811-328-16	Sequence 16, Appl
80	494	99.2	86	3	US-10-811-328-20	Sequence 20, Appl
81	486	97.6	105	2	US-09-621-976-5350	Sequence 5350, Ap
82	478	96.0	86	3	US-10-323-157A-17	Sequence 17, Appl
83	478	96.0	86	3	US-10-811-328-17	Sequence 17, Appl
84	473	95.0	86	3	US-10-811-328-30	Sequence 30, Appl
85	455	91.4	86	3	US-10-811-328-28	Sequence 28, Appl
86	413	82.9	86	3	US-10-323-157A-14	Sequence 14, Appl
87	413	82.9	86	3	US-10-811-328-14	Sequence 14, Appl
88	376	75.5	81	3	US-10-323-157A-13	Sequence 13, Appl
89	376	75.5	81	3	US-10-811-328-13	Sequence 13, Appl
90	357	71.7	80	2	US-09-513-999C-4698	Sequence 4698, Ap
91	357	71.7	80	3	US-10-793-479-4698	Sequence 4698, Ap
92	315	63.3	80	3	US-10-333-132-34	Sequence 34, Appl
93	310.5	62.3	81	3	US-10-323-157A-12	Sequence 12, Appl
94	310.5	62.3	81	3	US-10-811-328-12	Sequence 12, Appl
95	291	58.4	81	3	US-10-323-157A-6	Sequence 6, Appli
96	291	58.4	81	3	US-10-811-328-6	Sequence 6, Appli
97	291	58.4	108	2	US-09-712-529-2	Sequence 2, Appli
98	291	58.4	108	2	US-10-212-201A-2	Sequence 2, Appli
99	291	58.4	108	2	US-10-212-355-2	Sequence 2, Appli

100	291	58.4	108	3	US-10-323-157A-5	Sequence 5, Appli	173	100.5	20.2	350	2	US-09-905-381A-236	Sequence 236, App
101	291	58.4	108	3	US-10-231-411A-4	Sequence 4, Appli	174	100.5	20.2	350	2	US-09-906-618-236	Sequence 236, App
102	291	58.4	108	3	US-10-811-328-5	Sequence 5, Appli	175	100.5	20.2	350	2	US-09-906-646-236	Sequence 236, App
103	291	58.4	108	3	US-10-982-168-2	Sequence 2, Appli	176	100.5	20.2	350	2	US-09-904-462-236	Sequence 236, App
104	291	58.4	108	3	US-10-990-246-2	Sequence 2, Appli	177	100.5	20.2	350	2	US-09-902-736A-236	Sequence 236, App
105	291	58.4	108	3	US-10-680-755A-2	Sequence 2, Appli	178	100.5	20.2	350	2	US-09-906-722A-236	Sequence 236, App
106	291	58.4	116	3	US-10-680-755A-26	Sequence 26, Appl	179	100.5	20.2	350	2	US-09-905-449-236	Sequence 236, App
107	286	57.4	81	3	US-10-811-328-29	Sequence 29, Appl	180	100.5	20.2	350	2	US-09-903-562B-236	Sequence 236, App
108	286	57.4	81	3	US-10-811-328-31	Sequence 31, Appl	181	100.5	20.2	350	3	US-09-906-679A-236	Sequence 236, App
109	286	57.4	107	3	US-10-231-411A-6	Sequence 6, Appli	182	100.5	20.2	350	3	US-09-907-841-236	Sequence 2, Appli
110	278.5	55.9	77	3	US-10-811-328-32	Sequence 32, Appl	183	100.5	20.2	350	3	US-09-906-838B-236	Sequence 236, App
111	270.5	54.3	129	3	US-10-231-411A-2	Sequence 2, Appli	184	100.5	20.2	350	3	US-09-909-320-236	Sequence 236, App
112	270.5	54.3	129	3	US-10-680-755A-29	Sequence 29, Appl	185	100.5	20.2	350	3	US-10-063-639A-8	Sequence 8, Appli
113	267.5	53.7	96	3	US-10-323-157A-11	Sequence 11, Appl	186	100.5	20.2	350	3	US-09-907-942-236	Sequence 236, App
114	267.5	53.7	96	3	US-10-811-328-11	Sequence 11, Appl	187	100.5	20.2	350	3	US-09-906-815C-236	Sequence 8, Appli
115	109	21.9	23	3	US-10-680-755A-9	Sequence 9, Appli	188	100.5	20.2	350	3	US-10-063-638A-8	Sequence 8, Appli
116	107.5	21.6	224	2	US-09-161-241-14	Sequence 14, Appl	189	100.5	20.2	350	3	US-10-063-510-8	Sequence 50, Appli
117	107.5	21.6	224	2	US-09-972-473-5	Sequence 5, Appli	190	100.5	20.2	350	3	US-10-223-081-50	Sequence 8, Appli
118	107.5	21.6	350	3	US-09-972-473-38	Sequence 38, Appl	191	100.5	20.2	350	3	US-10-063-741-8	Sequence 8, Appli
119	102	20.5	179	3	US-09-972-473-11	Sequence 11, Appl	192	100.5	20.2	350	3	US-10-063-584-8	Sequence 8, Appli
120	102	20.5	186	2	US-09-949-016-7146	Sequence 7146, Ap	193	100.5	20.2	350	3	US-10-223-087-50	Sequence 50, Appli
121	102	20.5	207	2	US-09-161-241-13	Sequence 13, Appl	194	100.5	20.2	350	3	US-09-903-749A-236	Sequence 236, App
122	102	20.5	259	2	US-09-161-241-12	Sequence 12, Appl	195	100.5	20.2	350	3	US-09-904-532B-236	Sequence 236, App
123	102	20.5	259	2	US-09-949-016-6872	Sequence 6872, Ap	196	100.5	20.2	350	3	US-10-006-867-8	Sequence 8, Appli
124	102	20.5	259	2	US-10-012-231A-70	Sequence 70, Appl	197	100.5	20.2	350	3	US-10-223-082-50	Sequence 50, Appli
125	102	20.5	259	2	US-10-015-389A-70	Sequence 70, Appl	198	100.5	20.2	350	3	US-09-905-075-236	Sequence 236, App
126	102	20.5	259	2	US-10-006-768A-70	Sequence 70, Appl	199	100.5	20.2	350	3	US-10-063-659-8	Sequence 8, Appli
127	102	20.5	259	2	US-10-015-671A-70	Sequence 70, Appl	200	100.5	20.2	350	3	US-10-063-742-8	Sequence 8, Appli
128	102	20.5	259	2	US-10-015-393A-70	Sequence 70, Appl	201	100.5	20.2	350	3	US-10-063-703-8	Sequence 8, Appli
129	102	20.5	259	2	US-10-011-833A-70	Sequence 70, Appl	202	100.5	20.2	350	3	US-10-063-709-8	Sequence 8, Appli
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131	102	20.5	259	2	US-10-012-064A-70	Sequence 70, Appl	204	100.5	20.2	350	3	US-10-063-583-8	Sequence 8, Appli
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133	102	20.5	259	2	US-10-011-795B-70	Sequence 70, Appl	206	100.5	20.2	350	3	US-10-063-646-8	Sequence 8, Appli
134	102	20.5	259	2	US-10-015-386A-70	Sequence 70, Appl	207	100.5	20.2	350	3	US-10-063-647-8	Sequence 8, Appli
135	102	20.5	259	2	US-10-012-121A-70	Sequence 70, Appl	208	100.5	20.2	350	3	US-10-063-661-8	Sequence 8, Appli
136	102	20.5	259	2	US-10-006-485A-70	Sequence 70, Appl	209	100.5	20.2	350	3	US-10-063-651-8	Sequence 8, Appli
137	102	20.5	259	2	US-10-006-746A-70	Sequence 70, Appl	210	100.5	20.2	350	3	US-10-063-540-8	Sequence 8, Appli
138	102	20.5	259	2	US-10-012-752A-70	Sequence 70, Appl	211	100.5	20.2	350	3	US-10-063-648-8	Sequence 8, Appli
139	102	20.5	259	2	US-10-017-253A-70	Sequence 70, Appl	212	100.5	20.2	350	3	US-10-063-657-8	Sequence 8, Appli
140	102	20.5	259	2	US-10-015-519A-70	Sequence 70, Appl	213	100.5	20.2	350	3	US-10-063-702-8	Sequence 8, Appli
141	102	20.5	259	2	US-10-015-715A-70	Sequence 70, Appl	214	100.5	20.2	350	3	US-10-063-529-8	Sequence 8, Appli
142	102	20.5	259	2	US-10-007-236A-70	Sequence 70, Appl	215	100.5	20.2	350	3	US-10-063-644-8	Sequence 8, Appli
143	102	20.5	259	2	US-10-012-149A-70	Sequence 70, Appl	216	100.5	20.2	350	3	US-10-063-516-8	Sequence 8, Appli
144	102	20.5	259	2	US-10-007-194A-70	Sequence 70, Appl	217	100.5	20.2	350	3	US-10-063-519A-8	Sequence 8, Appli
145	102	20.5	259	2	US-10-013-910A-70	Sequence 70, Appl	218	100.5	20.2	350	3	US-10-063-522-8	Sequence 8, Appli
146	102	20.5	259	2	US-10-006-117A-70	Sequence 70, Appl	219	100.5	20.2	350	3	US-10-063-654-8	Sequence 8, Appli
147	102	20.5	259	2	US-10-015-480A-70	Sequence 70, Appl	220	100.5	20.2	350	3	US-10-063-582-8	Sequence 8, Appli
148	102	20.5	259	2	US-10-006-172A-70	Sequence 70, Appl	221	100.5	20.2	350	3	US-10-063-524-8	Sequence 8, Appli
149	102	20.5	259	2	US-10-015-395A-70	Sequence 70, Appl	222	100.5	20.2	350	3	US-09-903-640A-236	Sequence 236, App
150	102	20.5	259	2	US-10-174-576-250	Sequence 250, App	223	100.5	20.2	350	3	US-10-448-580-236	Sequence 8, Appli
151	102	20.5	259	2	US-10-015-610A-70	Sequence 70, Appl	224	100.5	20.2	350	3	US-10-972-317-8	Sequence 8, Appli
152	102	20.5	259	2	US-10-180-998-250	Sequence 250, App	225	100.5	20.2	350	3	US-10-063-551-8	Sequence 8, Appli
153	102	20.5	259	2	US-10-201-769-250	Sequence 250, App	226	100.5	20.2	350	3	US-10-063-650-8	Sequence 8, Appli
154	102	20.5	259	2	US-10-006-130A-70	Sequence 70, Appl	227	100.5	20.2	350	3	US-10-063-523-8	Sequence 8, Appli
155	102	20.5	259	2	US-10-174-576-250	Sequence 250, App	228	100.5	20.2	350	3	US-10-063-705-8	Sequence 8, Appli
156	102	20.5	259	2	US-10-015-869A-70	Sequence 70, Appl	229	100.5	20.2	350	3	US-10-063-467-236	Sequence 8, Appli
157	102	20.5	259	2	US-10-207-916-250	Sequence 250, App	230	100.5	20.2	350	3	US-10-063-554-8	Sequence 8, Appli
158	102	20.5	259	2	US-10-015-869A-70	Sequence 70, Appl	231	100.5	20.2	350	3	US-10-063-597-8	Sequence 8, Appli
159	102	20.5	259	2	US-10-015-869A-70	Sequence 250, App	232	100.5	20.2	350	3	US-10-063-600-8	Sequence 8, Appli
160	102	20.5	259	2	US-10-174-583-250	Sequence 250, App	233	100.5	20.2	350	3	US-10-063-652A-8	Sequence 8, Appli
161	102	20.5	263	3	US-10-187-745-250	Sequence 21, Appl	234	100.5	20.2	350	3	US-10-063-602-8	Sequence 8, Appli
162	101	20.3	259	2	US-09-972-473-21	Sequence 21, Appl	235	100.5	20.2	350	3	US-10-063-560-8	Sequence 8, Appli
163	101	20.3	272	2	US-09-972-473-36	Sequence 36, Appl	236	100.5	20.2	350	3	US-10-063-517-8	Sequence 8, Appli
164	100.5	20.2	215	2	US-10-104-047-2196	Sequence 2196, Ap	237	100.5	20.2	350	3	US-10-063-548-8	Sequence 8, Appli
165	100.5	20.2	350	2	US-09-161-241-9	Sequence 9, Appli	238	100.5	20.2	350	3	US-10-063-598-8	Sequence 8, Appli
166	100.5	20.2	350	2	US-09-907-754A-236	Sequence 236, App	239	100.5	20.2	350	3	US-10-063-597-8	Sequence 8, Appli
167	100.5	20.2	350	2	US-09-905-125A-236	Sequence 236, App	240	100.5	20.2	350	3	US-10-063-600-8	Sequence 8, Appli
168	100.5	20.2	350	2	US-09-902-775A-236	Sequence 236, App	241	100.5	20.2	350	3	US-10-063-652A-8	Sequence 8, Appli
169	100.5	20.2	350	2	US-09-906-700-236	Sequence 236, App	242	100.5	20.2	350	3	US-10-063-602-8	Sequence 8, Appli
170	100.5	20.2	350	2	US-09-903-603A-236	Sequence 236, App	243	100.5	20.2	350	3	US-10-063-560-8	Sequence 8, Appli
171	100.5	20.2	350	2	US-09-904-920A-236	Sequence 236, App	244	100.5	20.2	350	3	US-10-063-517-8	Sequence 8, Appli
172	100.5	20.2	350	2	US-09-903-064-236	Sequence 236, App	245	100.5	20.2	350	3	US-10-063-548-8	Sequence 8, Appli

246	100.5	20.2	350	3	US-10-063-553-8	Sequence 8, Appli	319	75.5	15.2	1664	3	US-10-055-877-212	Sequence 212, App
247	100.5	20.2	350	3	US-10-063-553A-8	Sequence 8, Appli	320	74.5	15.0	425	3	US-10-108-260A-4381	Sequence 4381, Ap
248	100.5	20.2	350	3	US-10-448-923-236	Sequence 236, App	321	74.5	15.0	451	3	US-10-915-160-6	Sequence 6, Appli
249	100.5	20.2	350	3	US-10-063-595-8	Sequence 8, Appli	322	73	14.7	87	3	US-09-972-473-25	Sequence 25, Appli
250	100.5	20.2	350	3	US-10-063-587-8	Sequence 8, Appli	323	73	14.7	124	2	US-09-949-016-11293	Sequence 11293, A
251	100.5	20.2	350	3	US-10-063-586-8	Sequence 8, Appli	324	72.5	14.6	163	1	US-08-219-237B-5	Sequence 5, Appli
252	100.5	20.2	350	3	US-10-223-090-50	Sequence 50, Appli	325	72.5	14.6	163	2	US-08-477-347-13	Sequence 13, Appli
253	100.5	20.2	375	2	US-09-949-016-7856	Sequence 7856, Ap	326	72.5	14.6	163	2	US-08-476-862-4	Sequence 4, Appli
254	100.5	20.2	375	2	US-09-949-016-7857	Sequence 7857, Ap	327	72.5	14.6	163	2	US-08-468-560C-5	Sequence 5, Appli
255	100.5	20.2	375	2	US-09-949-016-7858	Sequence 7858, Ap	328	72.5	14.6	163	2	US-08-828-683A-13	Sequence 13, Appli
256	98.5	19.8	349	2	US-09-161-241-8	Sequence 8, Appli	329	72.5	14.6	163	2	US-09-800-909-4	Sequence 4, Appli
257	98.5	19.8	349	2	US-09-972-473-17	Sequence 17, Appli	330	72.5	14.6	163	2	US-09-800-908-13	Sequence 13, Appli
258	97	19.5	266	2	US-09-161-241-10	Sequence 10, Appli	331	72.5	14.6	163	2	US-09-523-323-54	Sequence 54, Appli
259	97	19.5	266	2	US-09-976-594-1086	Sequence 1086, Ap	332	72.5	14.6	163	2	US-09-884-987-5	Sequence 5, Appli
260	97	19.5	266	2	US-09-999-833A-456	Sequence 456, App	333	72.5	14.6	163	2	US-08-232-087A-9	Sequence 9, Appli
261	97	19.5	266	2	US-10-020-445A-456	Sequence 456, App	334	72.5	14.6	163	2	US-09-422-680A-25	Sequence 25, Appli
262	97	19.5	266	2	US-09-978-189-456	Sequence 456, App	335	72.5	14.6	189	2	US-10-703-032-156619	Sequence 156619,
263	97	19.5	266	2	US-10-017-085A-456	Sequence 456, App	336	72.5	14.6	197	3	US-08-974-022-48	Sequence 48, Appli
264	97	19.5	266	3	US-10-145-129A-456	Sequence 456, App	337	72.5	14.6	227	2	US-08-795-445A-48	Sequence 48, Appli
265	97	19.5	266	3	US-10-013-929A-456	Sequence 456, App	338	72.5	14.6	227	2	US-08-795-447A-48	Sequence 48, Appli
266	97	19.5	266	3	US-10-013-917A-456	Sequence 456, App	339	72.5	14.6	227	2	US-08-974-186-48	Sequence 48, Appli
267	97	19.5	266	3	US-10-013-925A-456	Sequence 456, App	340	72.5	14.6	227	2	US-08-795-446B-48	Sequence 48, Appli
268	97	19.5	266	3	US-10-123-292-428	Sequence 428, App	341	72.5	14.6	227	2	US-08-706-945D-134	Sequence 134, App
269	97	19.5	266	3	US-09-972-473-8	Sequence 8, Appli	342	72.5	14.6	227	2	US-08-577-788C-48	Sequence 48, Appli
270	97	19.5	266	3	US-10-162-521A-456	Sequence 456, App	343	72.5	14.6	227	3	US-09-613-591F-131	Sequence 131, App
271	97	19.5	266	3	US-10-145-016A-456	Sequence 456, App	344	72.5	14.6	235	2	US-09-326-394-4	Sequence 4, Appli
272	97	19.5	266	3	US-10-013-926A-456	Sequence 456, App	345	72.5	14.6	235	2	US-09-580-235-2	Sequence 2, Appli
273	97	19.5	266	3	US-10-152-398-428	Sequence 428, App	346	72.5	14.6	235	2	US-09-580-235-4	Sequence 4, Appli
274	97	19.5	266	3	US-10-162-522A-456	Sequence 456, App	347	72.5	14.6	235	2	US-09-580-235-6	Sequence 6, Appli
275	97	19.5	266	3	US-10-123-907-428	Sequence 428, App	348	72.5	14.6	235	2	US-09-580-235-8	Sequence 8, Appli
276	97	19.5	266	3	US-10-147-512-428	Sequence 428, App	349	72.5	14.6	235	2	US-09-580-181-2	Sequence 2, Appli
277	97	19.5	266	3	US-10-147-485-428	Sequence 428, App	350	72.5	14.6	235	2	US-09-580-181-4	Sequence 4, Appli
278	97	19.5	266	3	US-10-124-814-428	Sequence 428, App	351	72.5	14.6	235	2	US-09-580-181-6	Sequence 6, Appli
279	97	19.5	266	3	US-10-143-029A-456	Sequence 456, App	352	72.5	14.6	235	2	US-09-580-181-8	Sequence 8, Appli
280	97	19.5	266	3	US-10-124-822-428	Sequence 428, App	353	72.5	14.6	235	2	US-09-102-530-2	Sequence 2, Appli
281	97	19.5	266	3	US-10-165-247A-456	Sequence 456, App	354	72.5	14.6	235	2	US-09-102-530-4	Sequence 4, Appli
282	97	19.5	266	3	US-10-017-086A-456	Sequence 456, App	355	72.5	14.6	235	2	US-09-102-530-6	Sequence 6, Appli
283	97	19.5	266	3	US-09-999-832A-456	Sequence 456, App	356	72.5	14.6	235	2	US-09-102-530-8	Sequence 8, Appli
284	97	19.5	266	3	US-10-131-833A-428	Sequence 428, App	357	72.5	14.6	235	2	US-09-882-735A-16	Sequence 16, Appli
285	97	19.5	266	3	US-10-142-419-428	Sequence 428, App	358	72.5	14.6	235	3	US-10-243-230-2	Sequence 2, Appli
286	97	19.5	266	3	US-10-152-375-428	Sequence 428, App	359	72.5	14.6	235	3	US-10-243-230-4	Sequence 4, Appli
287	97	19.5	266	3	US-10-143-031A-456	Sequence 456, App	360	72.5	14.6	235	3	US-10-243-230-6	Sequence 6, Appli
288	97	19.5	266	3	US-10-131-818A-428	Sequence 428, App	361	72.5	14.6	235	3	US-10-243-230-8	Sequence 8, Appli
289	97	19.5	266	3	US-10-013-923A-456	Sequence 456, App	362	72.5	14.6	257	2	US-09-579-845-10	Sequence 10, Appli
290	97	19.5	266	3	US-10-013-927A-456	Sequence 456, App	363	72.5	14.6	439	2	US-10-360-101-226	Sequence 226, App
291	97	19.5	266	3	US-10-145-873-428	Sequence 428, App	364	72.5	14.6	461	1	US-08-385-229-2	Sequence 2, Appli
292	97	19.5	266	3	US-10-152-395-428	Sequence 428, App	365	72.5	14.6	461	1	US-08-650-000-2	Sequence 2, Appli
293	97	19.5	266	3	US-10-131-822A-428	Sequence 428, App	366	72.5	14.6	461	2	US-09-042-785A-7	Sequence 7, Appli
294	97	19.5	266	3	US-10-142-763-428	Sequence 428, App	367	72.5	14.6	461	2	US-08-477-347-3	Sequence 3, Appli
295	97	19.5	266	3	US-10-128-694A-428	Sequence 428, App	368	72.5	14.6	461	2	US-09-006-353A-4	Sequence 4, Appli
296	97	19.5	266	3	US-10-123-213-428	Sequence 428, App	369	72.5	14.6	461	2	US-08-476-862-2	Sequence 2, Appli
297	97	19.5	266	3	US-10-123-909-428	Sequence 428, App	370	72.5	14.6	461	2	US-09-573-986-4	Sequence 4, Appli
298	97	19.5	266	3	US-09-978-564A-456	Sequence 456, App	371	72.5	14.6	461	2	US-08-406-824A-2	Sequence 2, Appli
299	97	19.5	266	3	US-09-978-564A-456	Sequence 456, App	372	72.5	14.6	461	2	US-08-800-909-2	Sequence 2, Appli
300	97	19.5	266	3	US-09-978-375A-456	Sequence 456, App	373	72.5	14.6	461	2	US-09-758-124-2	Sequence 2, Appli
301	97	19.5	266	3	US-10-165-353A-456	Sequence 456, App	374	72.5	14.6	461	2	US-09-800-908-3	Sequence 3, Appli
302	97	19.5	266	3	US-10-143-030A-456	Sequence 456, App	375	72.5	14.6	461	2	US-08-896-096A-17	Sequence 17, Appli
303	97	19.5	266	3	US-10-131-826A-428	Sequence 428, App	376	72.5	14.6	461	2	US-09-949-016-6019	Sequence 6019, Ap
304	97	19.5	266	3	US-10-145-089A-456	Sequence 456, App	377	72.5	14.6	461	2	US-10-046-433-6	Sequence 6, Appli
305	97	19.5	266	3	US-10-170-481A-456	Sequence 456, App	378	72.5	14.6	461	3	US-09-826-212A-4	Sequence 4, Appli
306	97	19.5	266	3	US-10-147-513-428	Sequence 428, App	379	72.5	14.6	461	3	US-10-420-785A-2	Sequence 2, Appli
307	97	19.5	266	3	US-10-121-043-428	Sequence 428, App	380	72.5	14.6	461	3	US-09-526-437-5	Sequence 5, Appli
308	97	19.5	266	3	US-10-160-502A-456	Sequence 456, App	381	72.5	14.6	461	3	US-08-469-637A-3	Sequence 3, Appli
309	97	19.5	266	3	US-10-139-980A-428	Sequence 428, App	382	72.5	14.6	461	3	US-10-411-037-32	Sequence 32, Appli
310	95.5	19.2	259	3	US-09-972-473-37	Sequence 37, Appli	383	72.5	14.6	461	3	US-10-287-994-32	Sequence 32, Appli
311	83.5	16.8	508	2	US-10-915-160-2	Sequence 2, Appli	384	72.5	14.6	461	3	US-10-775-204-462	Sequence 462, App
312	81.5	16.4	446	2	US-10-104-047-2665	Sequence 2665, Ap	385	72.5	14.6	461	3	US-10-775-204-467	Sequence 467, App
313	81	16.3	1964	2	US-09-467-937-1	Sequence 1, Appli	386	72.5	14.6	461	3	US-10-410-937-32	Sequence 32, Appli
314	79.5	16.0	446	3	US-10-108-260A-3580	Sequence 3580, Ap	387	72.5	14.6	461	3	US-10-410-962-32	Sequence 32, Appli
315	77	15.5	145	3	US-10-703-032-196520	Sequence 196520,	388	72.5	14.6	461	3	US-10-410-987A-32	Sequence 32, Appli
316	76.5	15.4	1342	2	US-09-561-709B-13	Sequence 13, Appli	389	72.5	14.6	461	3	US-09-518-931-6	Sequence 6, Appli
317	76	15.3	14	3	US-10-323-157A-19	Sequence 19, Appli	390	72.5	14.6	461	3	US-10-775-180-152	Sequence 152, App
318	76	15.3	14	3	US-10-811-328-19	Sequence 19, Appli	391	72.5	14.6	461	3	US-10-775-180-155	Sequence 155, App

392	72.5	14.6	461	3	US-10-410-945A-32	Sequence 32, Appl	465	68	13.7	224	2	US-08-795-446B-50	Sequence 50, Appl
393	72.5	14.6	461	3	US-10-410-930A-32	Sequence 32, Appl	466	68	13.7	224	2	US-08-706-945D-137	Sequence 137, App
394	72.5	14.6	461	3	US-11-393-893-152	Sequence 152, App	466	68	13.7	224	2	US-08-577-788C-51	Sequence 51, Appl
395	72.5	14.6	461	3	US-11-393-893-155	Sequence 155, App	468	68	13.7	224	3	US-09-613-591F-134	Sequence 134, App
396	72.5	14.6	461	3	US-11-393-893-155	Sequence 155, App	468	68	13.7	224	3	US-09-613-591F-134	Sequence 134, App
397	72.5	14.6	461	3	US-11-429-373-467	Sequence 467, App	469	68	13.7	427	2	US-09-086-483A-4	Sequence 4, Appl
398	72.5	14.6	461	3	US-11-429-373-467	Sequence 467, App	470	68	13.7	427	2	US-09-041-886-2	Sequence 2, Appl
399	72.5	14.6	461	7	5395760-2	Patent No. 5395760	471	68	13.7	427	2	US-09-006-353A-5	Sequence 5, Appl
400	72.5	14.6	471	3	US-10-966-673-66	Sequence 66, Appl	472	68	13.7	427	2	US-09-573-986-5	Sequence 5, Appl
401	72.5	14.6	471	3	US-10-966-673-67	Sequence 67, Appl	473	68	13.7	427	2	US-09-580-212-4	Sequence 4, Appl
402	72.5	14.6	471	3	US-10-966-673-68	Sequence 68, Appl	474	68	13.7	427	2	US-09-769-402-4	Sequence 4, Appl
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404	72.5	14.6	490	3	US-10-363-427-4	Sequence 4, Appl	476	68	13.7	427	2	US-09-949-016-6233	Sequence 24, Appl
405	72.5	14.6	491	2	US-09-949-016-7840	Sequence 7840, Ap	477	68	13.7	427	2	US-08-681-219A-24	Sequence 24, Appl
406	72.5	14.6	501	1	US-09-285-531A-2	Sequence 2, Appl	479	68	13.7	427	3	US-10-280-047-4	Sequence 4, Appl
407	72.5	14.6	518	2	US-08-385-229-4	Sequence 4, Appl	480	68	13.7	427	3	US-09-836-212A-5	Sequence 5, Appl
408	72.5	14.6	518	2	US-09-579-845-1	Sequence 1, Appl	481	68	13.7	455	2	US-09-518-931-7	Sequence 7, Appl
409	72.5	14.6	518	3	US-09-579-845-3	Sequence 3, Appl	482	68	13.7	455	2	US-09-527-236A-4	Sequence 4, Appl
410	72.5	14.6	659	3	US-10-423-507-1	Sequence 12, Appl	483	68	13.7	455	2	US-09-756-854-4	Sequence 4, Appl
411	72.5	14.6	720	3	US-10-363-427-8	Sequence 8, Appl	484	68	13.7	455	2	US-10-041-574-4	Sequence 4, Appl
412	72.5	14.6	844	3	US-10-775-204-246	Sequence 246, App	485	68	13.7	464	2	US-09-095-094-4	Sequence 4, Appl
413	72.5	14.6	844	3	US-10-775-204-251	Sequence 251, App	486	68	13.7	464	2	US-09-949-016-9441	Sequence 9441, Ap
414	72.5	14.6	844	3	US-10-775-180-83	Sequence 83, Appl	487	68	13.7	483	2	US-09-252-991A-19884	Sequence 19884, A
415	72.5	14.6	844	3	US-10-775-180-86	Sequence 86, Appl	488	68	13.7	3075	1	US-08-460-309-5	Sequence 5, Appl
416	72.5	14.6	844	3	US-11-393-893-83	Sequence 83, Appl	489	68	13.7	3075	1	US-08-125-077-5	Sequence 5, Appl
417	72.5	14.6	844	3	US-11-393-893-86	Sequence 86, Appl	490	67	13.5	317	2	US-09-383-586-20	Sequence 20, Appl
418	72.5	14.6	844	3	US-11-429-373-246	Sequence 246, App	491	67	13.5	317	2	US-09-823-038A-20	Sequence 5, Appl
419	72.5	14.6	844	3	US-11-429-373-251	Sequence 251, App	492	67	13.5	1101	2	US-09-561-709B-5	Sequence 5, Appl
420	71.5	14.4	453	2	US-09-171-461-48	Sequence 48, Appl	493	67	13.5	1398	3	US-10-055-877-46	Sequence 46, Appl
421	71.5	14.4	453	2	US-09-970-711-48	Sequence 48, Appl	494	67	13.5	1403	3	US-10-055-877-52	Sequence 52, Appl
422	71.5	14.4	470	2	US-10-915-160-4	Sequence 4, Appl	495	67	13.5	1404	3	US-10-055-877-44	Sequence 44, Appl
423	71.5	14.4	1574	3	US-10-055-877-211	Sequence 211, App	496	67	13.5	1450	3	US-10-055-877-48	Sequence 48, Appl
424	71	14.3	593	1	US-07-668-648-4	Sequence 4, Appl	497	67	13.5	1577	3	US-10-055-877-54	Sequence 54, Appl
425	71	14.3	593	1	US-08-429-998-4	Sequence 4, Appl	498	67	13.5	1620	2	US-10-055-877-213	Sequence 213, App
426	71	14.3	593	1	US-08-431-333-4	Sequence 4, Appl	499	67	13.5	1761	2	US-09-561-709B-1	Sequence 1, Appl
427	71	14.3	593	2	US-09-91-862-17	Sequence 17, Appl	500	67	13.5	2321	2	US-09-230-652-2	Sequence 2, Appl
428	71	14.3	593	2	US-09-813-156-17	Sequence 17, Appl	501	67	13.5	2321	2	US-09-612-226B-2	Sequence 2, Appl
429	71	14.3	593	2	US-09-456-886-17	Sequence 17, Appl	502	66.5	13.4	589	1	US-10-356-625-2	Sequence 2, Appl
430	71	14.3	593	2	US-09-824-647-17	Sequence 17, Appl	503	66.5	13.4	589	1	US-07-668-648-6	Sequence 6, Appl
431	71	14.3	593	2	US-09-880-842-17	Sequence 17, Appl	504	66.5	13.4	589	1	US-08-429-998-6	Sequence 6, Appl
432	71	14.3	593	3	US-10-281-160-17	Sequence 4, Appl	505	66.5	13.4	589	1	US-08-429-998-6	Sequence 6, Appl
433	71	14.3	593	5	PCT-US91-02321-4	Sequence 9775, Ap	506	66.5	13.4	589	1	US-08-431-333-2	Sequence 2, Appl
434	71	14.3	613	2	US-09-949-016-9775	Sequence 11264, A	507	66.5	13.4	589	1	US-08-431-333-6	Sequence 6, Appl
435	69	13.9	575	2	US-09-949-016-11264	Sequence 11264, A	508	66.5	13.4	589	2	US-08-991-862-2	Sequence 2, Appl
436	69	13.9	575	2	US-09-949-016-11265	Sequence 11265, A	509	66.5	13.4	589	2	US-08-991-862-2	Sequence 2, Appl
437	69	13.9	575	2	US-09-949-016-11265	Sequence 11265, A	510	66.5	13.4	589	2	US-08-991-862-2	Sequence 2, Appl
438	69	13.9	575	2	US-09-949-016-11267	Sequence 11267, A	511	66.5	13.4	589	2	US-09-456-886-2	Sequence 2, Appl
439	69	13.9	575	2	US-09-949-016-11267	Sequence 11267, A	512	66.5	13.4	589	2	US-09-456-886-2	Sequence 2, Appl
440	69	13.9	657	2	US-09-949-016-11365	Sequence 11365, A	513	66.5	13.4	589	2	US-09-824-647-2	Sequence 2, Appl
441	69	13.9	657	2	US-09-949-016-11367	Sequence 11367, A	514	66.5	13.4	589	2	US-09-880-842-2	Sequence 2, Appl
442	69	13.9	657	2	US-09-949-016-11368	Sequence 11368, A	515	66.5	13.4	589	3	US-10-281-160-2	Sequence 2, Appl
443	69	13.9	657	2	US-09-949-016-11368	Sequence 11368, A	516	66.5	13.4	589	3	PCT-US91-02321-6	Sequence 6, Appl
444	69	13.9	677	2	US-09-949-016-11369	Sequence 11369, A	517	66.5	13.4	589	3	US-10-042-865-108	Sequence 108, App
445	69	13.9	677	2	US-09-949-016-11370	Sequence 11370, A	518	66.5	13.4	1587	2	US-09-561-709B-3	Sequence 3, Appl
446	69	13.9	677	2	US-09-949-016-11371	Sequence 11371, A	519	66.5	13.4	1587	2	US-09-750-972-2	Sequence 2, Appl
447	68.5	13.8	1172	3	US-09-949-016-11372	Sequence 11372, A	520	66.5	13.4	1587	2	US-09-750-972-2	Sequence 2, Appl
448	68	13.7	122	2	US-10-296-733A-24	Sequence 24, Appl	521	66.5	13.4	1587	2	US-09-750-972-2	Sequence 2, Appl
449	68	13.7	159	1	US-08-477-347-15	Sequence 15, Appl	522	66	13.3	1172	1	US-08-625-137B-2	Sequence 19, Appl
450	68	13.7	159	2	US-08-477-347-15	Sequence 15, Appl	523	66	13.3	1172	1	US-08-313-288B-19	Sequence 6333, Ap
451	68	13.7	159	2	US-08-476-862-6	Sequence 6, Appl	524	66	13.3	1172	2	US-09-949-016-6333	Sequence 26, Appl
452	68	13.7	159	2	US-08-468-560C-6	Sequence 6, Appl	525	66	13.3	3712	2	US-10-296-733A-26	Sequence 48, Appl
453	68	13.7	159	2	US-08-828-683A-16	Sequence 16, Appl	526	66	13.3	3712	2	US-10-037-417-48	Sequence 51, Appl
454	68	13.7	159	2	US-09-800-909-6	Sequence 6, Appl	527	66	13.3	3712	2	US-10-037-417-51	Sequence 128595,
455	68	13.7	159	2	US-09-800-909-15	Sequence 15, Appl	528	65.5	13.2	144	3	US-10-703-032-128595	Sequence 132027,
456	68	13.7	159	2	US-09-884-987-6	Sequence 8, Appl	529	65.5	13.2	178	3	US-10-703-032-132027	Sequence 177, App
457	68	13.7	179	1	US-07-668-648-8	Sequence 8, Appl	530	65.5	13.2	179	2	US-09-148-545-177	Sequence 177, App
458	68	13.7	179	1	US-08-429-998-8	Sequence 8, Appl	531	65.5	13.2	179	2	US-09-621-011-177	Sequence 177, App
459	68	13.7	179	1	US-08-431-333-8	Sequence 8, Appl	532	65.5	13.2	182	2	US-09-981-876-177	Sequence 3287, Ap
460	68	13.7	179	5	PCT-US91-02321-8	Sequence 8, Appl	533	65.5	13.2	182	2	US-10-104-047-3287	Sequence 198, App
461	68	13.7	224	2	US-08-974-022-50	Sequence 50, Appl	534	65.5	13.2	683	2	US-08-979-847B-198	Sequence 200, App
462	68	13.7	224	2	US-08-795-445A-50	Sequence 50, Appl	535	65.5	13.2	683	2	US-08-979-847B-208	Sequence 208, App
463	68	13.7	224	2	US-08-795-447A-50	Sequence 50, Appl	536	65.5	13.2	683	2	US-08-979-847B-210	Sequence 210, Appl
464	68	13.7	224	2	US-08-974-186-50	Sequence 50, Appl	537	65.5	13.2	720	2	US-08-872-855-4	Sequence 4, Appl

538	65.5	13.2	722	2	US-08-981-392-12	Sequence 12, Appl	611	62	12.4	415	1	US-08-833-642A-5	Sequence 5, Appli
539	65.5	13.2	722	2	US-09-908-322-12	Sequence 12, Appl	612	62	12.4	415	2	US-08-709-974A-4	Sequence 1, Appli
540	65.5	13.2	722	2	US-09-310-685-14	Sequence 14, Appl	613	62	12.4	415	2	US-09-069-632-1	Sequence 4, Appli
541	65.5	13.2	722	3	US-09-783-931C-12	Sequence 12, Appl	614	62	12.4	435	1	US-08-361-920-27	Sequence 27, Appl
542	65.5	13.2	722	3	US-10-042-865-107	Sequence 107, App	615	62	12.4	435	1	US-08-479-939-27	Sequence 27, Appl
543	65.5	13.2	768	2	US-08-979-847B-89	Sequence 89, Appl	616	62	12.4	435	1	US-08-483-432-27	Sequence 27, Appl
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545	65.5	13.2	2471	1	US-08-185-432-16	Sequence 16, Appl	618	62	12.4	578	2	US-08-981-392-13	Sequence 13, Appl
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547	65.5	13.2	2471	2	US-08-534-384-19	Sequence 19, Appl	620	62	12.4	578	3	US-09-783-931C-13	Sequence 13, Appl
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549	65.5	13.2	2471	2	US-09-121-457-1	Sequence 1, Appli	622	62	12.4	831	2	US-09-939-853A-97	Sequence 97, Appl
550	65	13.1	116	3	US-10-703-032-156175	Sequence 156175, Ap	623	62	12.4	831	2	US-09-939-853A-98	Sequence 98, Appl
551	65	13.1	142	2	US-10-094-749-1973	Sequence 1973, Ap	624	62	12.4	998	1	US-08-449-645A-20	Sequence 20, Appl
552	65	13.1	166	3	US-10-703-032-117513	Sequence 117513, Ap	625	62	12.4	998	1	US-08-702-367A-20	Sequence 20, Appl
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556	65	13.1	993	2	US-09-192-435-1	Sequence 1, Appli	629	62	12.4	1068	2	US-09-113-825-2	Sequence 2, Appli
557	65	13.1	993	2	US-09-558-340-1	Sequence 1, Appli	630	62	12.4	1113	2	US-09-959-392-4	Sequence 4, Appli
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559	64.5	13.0	77	2	US-09-627-775-2	Sequence 2, Appli	632	62	12.4	1170	1	US-08-313-288B-20	Sequence 20, Appl
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561	64.5	13.0	299	2	US-09-188-930-332	Sequence 332, App	634	62	12.4	1833	2	US-09-592-685-2	Sequence 2, Appli
562	64.5	13.0	299	2	US-09-312-283C-192	Sequence 192, App	635	62	12.4	1833	5	PCT-US95-02251-18	Sequence 18, Appl
563	64.5	13.0	299	2	US-09-312-283C-332	Sequence 332, App	636	62	12.4	2556	1	US-08-185-432-17	Sequence 17, Appl
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565	64.5	13.0	1581	2	US-09-949-002-414	Sequence 414, App	638	62	12.4	2556	2	US-08-532-384-20	Sequence 20, Appl
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573	64	12.9	425	2	US-09-748-537-14	Sequence 14, Appl	646	61.5	12.3	277	2	US-09-006-353A-12	Sequence 12, Appl
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575	63.5	12.8	94	2	US-09-950-933A-44	Sequence 44, Appl	648	61.5	12.3	277	2	US-09-573-986-12	Sequence 12, Appl
576	63.5	12.8	94	3	US-10-976-102-44	Sequence 44, Appl	649	61.5	12.3	277	2	US-09-880-939-2	Sequence 2, Appli
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585	63.5	12.8	729	2	US-08-872-855-8	Sequence 8, Appli	658	61.5	12.3	2157	3	US-10-960-275-2	Sequence 2, Appli
586	63.5	12.8	841	2	US-08-897-427A-2	Sequence 2, Appli	659	61.5	12.3	3571	2	US-09-911-842A-2	Sequence 2, Appli
587	63.5	12.8	841	3	US-10-770-127-197	Sequence 197, App	660	61.5	12.3	3571	3	US-10-150-821-2	Sequence 2, Appli
588	63.5	12.8	841	3	US-10-726-568-17	Sequence 17, Appl	661	61	12.2	233	3	US-10-703-032-114880	Sequence 114880, A
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591	63.5	12.8	2743	2	US-10-037-182-36	Sequence 36, Appl	664	61	12.2	1170	2	US-09-949-002-350	Sequence 350, App
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593	63.5	12.8	3695	2	US-10-037-182-2	Sequence 2, Appli	666	61	12.2	1251	1	US-08-199-780-3	Sequence 3, Appli
594	63	12.7	129	2	US-10-104-047-2669	Sequence 2669, Ap	667	61	12.2	1252	1	US-08-316-650-3	Sequence 3, Appli
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596	63	12.7	3597	2	US-10-037-417-6	Sequence 6, Appli	669	60.5	12.1	2476	1	US-10-703-032-122834	Sequence 122834, A
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600	62.5	12.6	297	2	US-09-270-767-44071	Sequence 44071, A	673	60.5	12.1	515	2	US-09-635-872A-6	Sequence 6, Appli
601	62.5	12.6	1080	2	US-09-904-380-2	Sequence 2, Appli	674	60.5	12.1	515	2	US-09-636-077A-6	Sequence 6, Appli
602	62.5	12.6	1140	3	US-10-055-877-215	Sequence 215, App	675	60.5	12.1	515	2	US-09-636-060C-6	Sequence 6, Appli
603	62.5	12.6	5179	2	US-09-538-092-1258	Sequence 1258, Ap	676	60.5	12.1	515	2	US-09-986-552-6	Sequence 6, Appli
604	62	12.4	248	2	US-09-252-991A-32322	Sequence 32322, A	677	60.5	12.1	515	2	US-09-636-596C-6	Sequence 6, Appli
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691	60.5	12.1	702	3	US-09-595-593A-4	Sequence 4, Appli	764	60	12.0	623	3	US-10-696-900-5	Sequence 5, Appli
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693	60.5	12.1	702	3	US-11-051-631-4	Sequence 4, Appli	766	60	12.0	651	1	US-08-264-101-2	Sequence 2, Appli
694	60.5	12.1	723	2	US-09-068-740A-9	Sequence 9, Appli	767	60	12.0	651	5	PCT-US95-07295-2	Sequence 2, Appli
695	60.5	12.1	723	2	US-09-423-753-27	Sequence 27, Appl	768	60	12.0	734	1	US-08-765-243-2	Sequence 8, Appli
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697	60.5	12.1	723	3	US-10-241-476-27	Sequence 27, Appl	770	60	12.0	735	3	US-10-232-972E-10	Sequence 10, Appl
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703	60.5	12.1	723	3	US-10-124-814-346	Sequence 346, App	776	59.5	11.9	230	2	US-09-252-991A-28812	Sequence 28812, A
704	60.5	12.1	723	3	US-10-124-822-346	Sequence 346, App	777	59.5	11.9	275	3	US-10-703-032-141333	Sequence 141333, A
705	60.5	12.1	723	3	US-09-595-593A-9	Sequence 9, Appli	778	59.5	11.9	340	2	US-09-252-991A-18667	Sequence 18667, A
706	60.5	12.1	723	3	US-10-131-833A-346	Sequence 346, App	779	59.5	11.9	405	3	US-09-540-209B-9253	Sequence 9253, Ap
707	60.5	12.1	723	3	US-10-142-419-346	Sequence 346, App	780	59.5	11.9	886	2	US-09-110-116-3	Sequence 3, Appli
708	60.5	12.1	723	3	US-10-142-375-346	Sequence 346, App	781	59.5	11.9	886	2	US-09-631-603-14	Sequence 14, Appl
709	60.5	12.1	723	3	US-10-131-818A-346	Sequence 346, App	782	59.5	11.9	4544	1	US-08-469-658-52	Sequence 52, Appl
710	60.5	12.1	723	3	US-11-043-357-9	Sequence 9, Appli	783	59.5	11.9	4544	1	US-08-469-658-52	Sequence 52, Appl
711	60.5	12.1	723	3	US-10-145-873-346	Sequence 346, App	784	59	11.8	149	3	US-10-703-032-152836	Sequence 9, Appli
712	60.5	12.1	723	3	US-10-152-395-346	Sequence 346, App	785	59	11.8	258	2	US-09-579-845-9	Sequence 9, Appli
713	60.5	12.1	723	3	US-10-131-822A-346	Sequence 346, App	786	59	11.8	298	2	US-09-902-540-12595	Sequence 12595, A
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715	60.5	12.1	723	3	US-10-128-694A-346	Sequence 346, App	788	59	11.8	315	3	US-10-225-066A-994	Sequence 994, App
716	60.5	12.1	723	3	US-10-123-213-346	Sequence 346, App	789	59	11.8	335	2	US-09-252-991A-32163	Sequence 32163, A
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722	60.5	12.1	723	3	US-10-139-980-346	Sequence 346, App	795	59	11.8	349	3	US-10-305-278-296	Sequence 296, App
723	60.5	12.1	1073	3	US-09-949-016-9771	Sequence 9771, Ap	796	59	11.8	372	2	US-09-252-991A-20108	Sequence 20108, A
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725	60.5	12.1	1104	1	US-08-828-584-5	Sequence 5, Appli	798	59	11.8	474	1	US-09-042-785A-8	Sequence 8, Appli
726	60.5	12.1	1345	2	US-09-949-016-8313	Sequence 8313, Ap	799	59	11.8	474	2	US-09-758-124-4	Sequence 4, Appli
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728	60.5	12.1	1652	2	US-09-436-063C-1	Sequence 1, Appli	801	59	11.8	474	2	5395760-4	Patent No. 5395760
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732	60.5	12.1	1917	3	US-10-156-240-5	Sequence 7, Appli	805	58.5	11.7	84	3	Sequence 206, App	Sequence 206, App
733	60.5	12.1	2508	2	US-09-627-650B-7	Sequence 7, Appli	806	58.5	11.7	84	3	Sequence 206, App	Sequence 206, App
734	60.5	12.1	2508	2	US-09-436-063C-7	Sequence 7, Appli	807	58.5	11.7	84	3	Sequence 192, App	Sequence 192, App
735	60.5	12.1	2508	3	US-10-156-240-7	Sequence 7, Appli	808	58.5	11.7	99	3	Sequence 3259, Ap	Sequence 3259, Ap
736	60.5	12.1	2544	2	US-09-627-650B-3	Sequence 3, Appli	809	58.5	11.7	139	3	Sequence 3302, A	Sequence 3302, A
737	60.5	12.1	2544	2	US-09-436-063C-3	Sequence 3, Appli	810	58.5	11.7	143	2	Sequence 48519, A	Sequence 48519, A
738	60.5	12.1	2544	3	US-10-156-240-3	Sequence 3, Appli	811	58.5	11.7	143	2	Sequence 182470	Sequence 182470
739	60.5	12.1	2601	2	US-09-627-650B-9	Sequence 9, Appli	812	58.5	11.7	164	3	Sequence 205, App	Sequence 205, App
740	60.5	12.1	2601	2	US-09-436-063C-9	Sequence 9, Appli	813	58.5	11.7	164	3	Sequence 205, App	Sequence 205, App
741	60.5	12.1	2601	3	US-10-156-240-9	Sequence 9, Appli	814	58.5	11.7	189	3	Sequence 205, App	Sequence 205, App
742	60.5	12.1	2703	2	US-08-185-432-19	Sequence 19, Appl	815	58.5	11.7	189	3	Sequence 47, Appl	Sequence 47, Appl
743	60.5	12.1	2703	2	US-08-899-232-4	Sequence 4, Appli	816	58.5	11.7	207	2	Sequence 47, Appl	Sequence 47, Appl
744	60.5	12.1	2703	2	US-09-121-457-4	Sequence 4, Appli	817	58.5	11.7	207	2	Sequence 133, App	Sequence 133, App
745	60	12.0	113	2	US-09-270-767-37873	Sequence 37873, A	818	58.5	11.7	207	2	Sequence 47, Appl	Sequence 47, Appl
746	60	12.0	113	2	US-09-270-767-37873	Sequence 37873, A	819	58.5	11.7	207	2	Sequence 133, App	Sequence 133, App
747	60	12.0	184	1	US-08-464-339A-2	Sequence 2, Appli	820	58.5	11.7	207	2	Sequence 47, Appl	Sequence 47, Appl
748	60	12.0	184	1	US-08-468-847B-18	Sequence 18, Appl	821	58.5	11.7	207	2	Sequence 133, App	Sequence 133, App
749	60	12.0	184	2	US-09-706-722A-2	Sequence 2, Appli	822	58.5	11.7	207	2	Sequence 47, Appl	Sequence 47, Appl
750	60	12.0	184	2	US-09-949-016-6782	Sequence 6782, Ap	823	58.5	11.7	207	2	Sequence 133, App	Sequence 133, App
751	60	12.0	184	5	PCT-US94-14388-2	Sequence 2, Appli	824	58.5	11.7	207	2	Sequence 47, Appl	Sequence 47, Appl
752	60	12.0	202	2	US-09-949-016-10546	Sequence 10546, A	825	58.5	11.7	207	2	Sequence 130, App	Sequence 130, App
753	60	12.0	275	2	US-09-489-039A-7372	Sequence 7372, Ap	826	58.5	11.7	291	3	Sequence 204, App	Sequence 204, App
754	60	12.0	314	3	US-10-108-260A-2665	Sequence 2665, Ap	827	58.5	11.7	291	3	Sequence 204, App	Sequence 204, App
755	60	12.0	399	2	US-09-807-802A-9	Sequence 9, Appli	828	58.5	11.7	291	3	Sequence 204, App	Sequence 204, App
756	60	12.0	399	3	US-10-696-282-9	Sequence 9, Appli	829	58.5	11.7	291	3	Sequence 204, App	Sequence 204, App

830	58.5	11.7	301	2	US-09-252-991A-31214	Sequence 31214, A	903	57.5	11.5	668	1	US-08-786-164-13	Sequence 13, Appl
831	58.5	11.7	325	1	US-08-232-549-2	Sequence 2, Appl	904	57.5	11.5	745	2	US-10-104-047-2955	Sequence 2955, Ap
832	58.5	11.7	325	2	US-09-042-785A-9	Sequence 9, Appl	905	57.5	11.5	745	2	US-10-104-047-2960	Sequence 2960, Ap
833	58.5	11.7	325	5	PCT-US91-02207-2	Sequence 2, Appl	906	57.5	11.5	745	3	US-10-123-292-68	Sequence 68, Appl
834	58.5	11.7	397	3	US-10-000-986A-203	Sequence 203, App	907	57.5	11.5	745	3	US-10-152-398-68	Sequence 68, Appl
835	58.5	11.7	397	3	US-09-992-600B-203	Sequence 203, App	908	57.5	11.5	745	3	US-10-123-907-68	Sequence 68, Appl
836	58.5	11.7	397	3	US-09-999-570A-203	Sequence 203, App	909	57.5	11.5	745	3	US-10-147-512-68	Sequence 68, Appl
837	58.5	11.7	397	3	US-10-001-142C-203	Sequence 203, App	910	57.5	11.5	745	3	US-10-147-485-68	Sequence 68, Appl
838	58.5	11.7	480	3	US-10-703-032-109121	Sequence 109121, A	911	57.5	11.5	745	3	US-10-124-814-68	Sequence 68, Appl
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840	58.5	11.7	721	2	US-08-872-855-7	Sequence 7, Appl	913	57.5	11.5	745	3	US-10-131-833A-68	Sequence 68, Appl
841	58.5	11.7	721	2	US-08-981-392-5	Sequence 5, Appl	914	57.5	11.5	745	3	US-10-142-419-68	Sequence 68, Appl
842	58.5	11.7	721	2	US-09-908-322-5	Sequence 5, Appl	915	57.5	11.5	745	3	US-10-152-375-68	Sequence 68, Appl
843	58.5	11.7	721	3	US-09-310-685-12	Sequence 12, Appl	916	57.5	11.5	745	3	US-10-131-818A-68	Sequence 68, Appl
844	58.5	11.7	721	3	US-09-783-931C-5	Sequence 5, Appl	917	57.5	11.5	745	3	US-10-145-873-68	Sequence 68, Appl
845	58.5	11.7	721	3	US-10-042-865-109	Sequence 109, App	918	57.5	11.5	745	3	US-10-152-395-68	Sequence 68, Appl
846	58.5	11.7	787	2	US-10-000-489-70	Sequence 70, Appl	919	57.5	11.5	745	3	US-10-131-822A-68	Sequence 68, Appl
847	58.5	11.7	787	2	US-09-992-095B-70	Sequence 70, Appl	920	57.5	11.5	745	3	US-10-142-763-68	Sequence 68, Appl
848	58.5	11.7	787	3	US-10-000-986A-70	Sequence 70, Appl	921	57.5	11.5	745	3	US-10-128-694A-68	Sequence 68, Appl
849	58.5	11.7	787	3	US-09-932-600B-70	Sequence 70, Appl	922	57.5	11.5	745	3	US-10-123-213-68	Sequence 68, Appl
850	58.5	11.7	787	3	US-09-924-340-70	Sequence 70, Appl	923	57.5	11.5	745	3	US-10-123-909-68	Sequence 68, Appl
851	58.5	11.7	787	3	US-09-999-570A-70	Sequence 70, Appl	924	57.5	11.5	745	3	US-10-108-260A-3826	Sequence 3826, Ap
852	58.5	11.7	787	3	US-10-001-142C-70	Sequence 70, Appl	925	57.5	11.5	745	3	US-10-131-826A-68	Sequence 68, Appl
853	58.5	11.7	787	3	US-10-219-074-90	Sequence 90, Appl	926	57.5	11.5	745	3	US-10-147-513-68	Sequence 68, Appl
854	58.5	11.7	787	3	US-10-227-873-90	Sequence 90, Appl	927	57.5	11.5	745	3	US-10-141-043-68	Sequence 68, Appl
855	58.5	11.7	787	3	US-10-218-849-90	Sequence 90, Appl	928	57.5	11.5	745	3	US-10-139-980-68	Sequence 68, Appl
856	58.5	11.7	787	3	US-10-216-168-90	Sequence 90, Appl	929	57.5	11.5	745	3	US-09-142-956B-14	Sequence 14, Appl
857	58.5	11.7	1065	1	US-08-400-159-8	Sequence 8, Appl	930	57.5	11.5	767	1	US-08-874-678-2	Sequence 2, Appl
858	58.5	11.7	1148	2	US-08-882-046-4	Sequence 4, Appl	931	57.5	11.5	767	2	US-08-643-839-2	Sequence 2, Appl
859	58.5	11.7	1148	2	US-09-566-047-4	Sequence 4, Appl	932	57.5	11.5	767	2	US-09-348-886-2	Sequence 2, Appl
860	58.5	11.7	1212	2	US-09-214-278-3	Sequence 3, Appl	933	57.5	11.5	767	2	US-10-105-901A-2	Sequence 2, Appl
861	58.5	11.7	1212	2	US-09-855-722-3	Sequence 3, Appl	934	57.5	11.5	788	1	US-08-232-538-15	Sequence 15, Appl
862	58.5	11.7	1212	3	US-10-219-248-3	Sequence 3, Appl	935	57.5	11.5	788	1	US-08-786-164-15	Sequence 15, Appl
863	58.5	11.7	1257	2	US-08-611-729A-8	Sequence 8, Appl	936	57.5	11.5	789	3	US-10-101-018A-15	Sequence 15, Appl
864	58.5	11.7	1257	2	US-09-195-524-8	Sequence 8, Appl	937	57.5	11.5	810	1	US-08-820-170A-34	Sequence 34, Appl
865	58.5	11.7	1257	2	US-09-310-685-6	Sequence 6, Appl	938	57.5	11.5	810	2	US-09-055-699-34	Sequence 34, Appl
866	58.5	11.7	1257	2	US-10-029-217A-24	Sequence 24, Appl	939	57.5	11.5	810	2	US-09-273-565-34	Sequence 34, Appl
867	58.5	11.7	4391	2	US-10-006-011A-2	Sequence 2, Appl	940	57.5	11.5	810	2	US-09-565-538-34	Sequence 34, Appl
868	58.5	11.7	4391	2	US-10-420-270-4	Sequence 4, Appl	941	57.5	11.5	810	2	US-09-661-468-34	Sequence 34, Appl
869	58	11.6	137	3	US-10-703-032-165719	Sequence 165719, A	942	57.5	11.5	810	2	US-09-976-165-34	Sequence 34, Appl
870	58	11.6	137	3	US-09-252-991A-31920	Sequence 31920, A	943	57.5	11.5	880	2	US-10-104-047-2834	Sequence 2834, Ap
871	58	11.6	197	3	US-10-108-260A-3943	Sequence 3943, Ap	944	57.5	11.5	1356	1	US-08-810-116-8	Sequence 8, Appl
872	58	11.6	258	2	US-09-579-845-7	Sequence 7, Appl	945	57.5	11.5	1356	1	US-07-930-548A-8	Sequence 8, Appl
873	58	11.6	487	2	US-09-579-845-14	Sequence 14, Appl	946	57.5	11.5	1356	2	US-09-098-707A-2	Sequence 2, Appl
874	58	11.6	525	5	US-08-688-988-10	Sequence 10, Appl	947	57.5	11.5	1356	2	US-09-483-539-2	Sequence 2, Appl
875	58	11.6	1149	2	US-09-252-991A-25557	Sequence 25557, A	948	57.5	11.5	1356	2	US-09-949-016-6198	Sequence 6198, Ap
876	58	11.6	1686	3	US-10-386-414A-2	Sequence 2, Appl	949	57.5	11.5	1356	2	US-10-100-405A-2	Sequence 2, Appl
877	58	11.6	1788	3	US-09-619-049-777	Sequence 777, App	950	57.5	11.5	1356	2	US-10-022-939-2	Sequence 2, Appl
878	58	11.6	4440	3	US-10-183-001-525	Sequence 525, App	951	57.5	11.5	1356	3	US-10-090-183-2	Sequence 2, Appl
879	58	11.6	4440	3	US-10-180-998-525	Sequence 525, App	952	57.5	11.5	1356	3	US-10-394-322A-66	Sequence 66, Appl
880	58	11.6	4440	3	US-10-201-769-525	Sequence 525, App	953	57.5	11.5	1356	3	US-10-633-742-6	Sequence 6, Appl
881	58	11.6	4440	3	US-10-174-576-525	Sequence 525, App	954	57.5	11.5	1456	2	US-09-949-016-9853	Sequence 9853, Ap
882	58	11.6	4440	3	US-10-174-581-525	Sequence 525, App	955	57.5	11.5	1480	2	US-09-191-647-7	Sequence 7, Appl
883	58	11.6	4440	3	US-10-207-916-525	Sequence 525, App	956	57.5	11.5	1480	2	US-09-540-245A-7	Sequence 7, Appl
884	58	11.6	4440	3	US-10-174-583-525	Sequence 525, App	957	57.5	11.5	1480	2	US-09-540-153-7	Sequence 7, Appl
885	58	11.6	4440	3	US-10-187-745-525	Sequence 525, App	958	57.5	11.5	1480	2	US-09-182-024A-5	Sequence 5, Appl
886	57.5	11.5	63	3	US-09-950-933A-75	Sequence 75, Appl	959	57.5	11.5	1480	2	US-10-289-776-7	Sequence 7, Appl
887	57.5	11.5	63	3	US-10-976-102-75	Sequence 75, Appl	960	57.5	11.5	1480	5	PCT-US91-09055-2	Sequence 2, Appl
888	57.5	11.5	71	3	US-10-703-032-165833	Sequence 165833, A	961	57.5	11.5	1504	2	US-10-037-417-98	Sequence 98, Appl
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890	57.5	11.5	132	2	US-09-523-323-55	Sequence 55, Appl	963	57	11.4	87	3	US-10-703-032-145575	Sequence 145575, A
891	57.5	11.5	187	2	US-09-248-796A-16235	Sequence 16235, A	964	57	11.4	105	3	US-10-703-032-186142	Sequence 186142, A
892	57.5	11.5	207	2	US-10-094-749-2017	Sequence 2017, Ap	965	57	11.4	115	3	US-09-950-933A-39	Sequence 39, Appl
893	57.5	11.5	280	3	US-09-450-969-5395	Sequence 5395, Ap	966	57	11.4	115	3	US-10-976-102-39	Sequence 39, Appl
894	57.5	11.5	280	3	US-10-724-972B-5395	Sequence 5395, Ap	967	57	11.4	147	2	US-09-527-236A-19	Sequence 19, Appl
895	57.5	11.5	293	2	US-09-134-001C-5374	Sequence 5374, Ap	968	57	11.4	147	2	US-09-756-854-19	Sequence 19, Appl
896	57.5	11.5	443	2	US-09-461-325-147	Sequence 147, App	969	57	11.4	147	2	US-10-041-574-19	Sequence 19, Appl
897	57.5	11.5	443	2	US-10-012-542-147	Sequence 147, App	970	57	11.4	147	2	US-09-095-094-19	Sequence 19, Appl
898	57.5	11.5	443	2	US-10-115-123-147	Sequence 147, App	971	57	11.4	181	2	US-10-094-749-1792	Sequence 1792, Ap
899	57.5	11.5	566	2	US-09-489-039A-14179	Sequence 14179, A	972	57	11.4	253	2	US-09-042-785A-4	Sequence 4, Appl
900	57.5	11.5	581	2	US-10-104-047-2804	Sequence 2804, Ap	973	57	11.4	254	2	US-09-422-680A-6	Sequence 6, Appl
901	57.5	11.5	664	3	US-10-101-018A-13	Sequence 13, Appl	974	57	11.4	259	3	US-09-940-235-4	Sequence 4, Appl
902	57.5	11.5	668	1	US-08-232-538-13	Sequence 13, Appl	975	57	11.4	259	3	US-10-631-558-4	Sequence 4, Appl

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979	57	11.4	498	1	US-08-660-963-12	Sequence 12, Appli	1052	57	11.4	2324	5	PCT-US95-09819-1	Sequence 1, Appli
980	57	11.4	523	3	US-09-792-200C-14	Sequence 14, Appli	1053	57	11.4	2327	7	US-09-492-9781B-15	Sequence 15, Appli
981	57	11.4	523	3	US-09-792-200C-11730	Sequence 11730, A	1054	57	11.4	2327	7	5455158-1	Patent No. 5455158
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983	57	11.4	605	2	US-09-042-785A-23	Sequence 7838, Ap	1056	57	11.4	2328	3	US-10-360-101-235	Sequence 235, App
984	57	11.4	625	2	US-09-949-016-8500	Sequence 8500, Ap	1057	57	11.4	2355	3	US-11-040-130-28	Sequence 28, Appli
985	57	11.4	654	2	US-08-979-847B-91	Sequence 91, Appli	1058	57	11.4	2386	1	US-09-016-366A-12	Sequence 12, Appli
986	57	11.4	655	2	US-08-959-382-2	Sequence 2, Appli	1059	57	11.4	2386	1	US-09-961-403-1	Sequence 1, Appli
987	57	11.4	655	2	US-09-527-236A-2	Sequence 2, Appli	1060	57	11.4	2446	5	US-08-551-356-2	Sequence 2, Appli
988	57	11.4	655	2	US-09-314-844F-2	Sequence 2, Appli	1061	57	11.4	2446	5	PCT-US93-12681-2	Sequence 7, Appli
989	57	11.4	655	2	US-09-756-854-2	Sequence 2, Appli	1062	57	11.4	2477	3	US-09-446-274B-7	Sequence 7, Appli
990	57	11.4	655	2	US-09-999-833A-64	Sequence 64, Appli	1063	57	11.4	4393	3	US-10-030-937-1	Sequence 7, Appli
991	57	11.4	655	2	US-10-041-574-2	Sequence 2, Appli	1064	56.5	11.3	79	2	US-10-006-011A-7	Sequence 7, Appli
992	57	11.4	655	2	US-09-095-094-2	Sequence 2, Appli	1065	56.5	11.3	80	3	US-10-000-986A-196	Sequence 196, App
993	57	11.4	655	2	US-10-020-445A-64	Sequence 64, Appli	1066	56.5	11.3	80	3	US-09-992-600B-196	Sequence 196, App
994	57	11.4	655	2	US-09-978-189-64	Sequence 64, Appli	1067	56.5	11.3	80	3	US-09-999-570A-196	Sequence 196, App
995	57	11.4	655	2	US-10-017-085A-64	Sequence 64, Appli	1068	56.5	11.3	80	3	US-10-001-142C-196	Sequence 82, Appli
996	57	11.4	655	3	US-10-145-129A-64	Sequence 64, Appli	1069	56.5	11.3	99	3	US-09-950-933A-82	Sequence 82, Appli
997	57	11.4	655	3	US-10-013-929A-64	Sequence 64, Appli	1070	56.5	11.3	99	3	US-10-976-102-82	Sequence 82, Appli
998	57	11.4	655	3	US-10-013-917A-64	Sequence 64, Appli	1071	56.5	11.3	106	2	US-09-270-767-62424	Sequence 62424, A
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1000	57	11.4	655	3	US-10-663-157-2	Sequence 64, Appli	1073	56.5	11.3	122	3	US-10-703-032-109229	Sequence 109229, A
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1002	57	11.4	655	3	US-10-145-016A-64	Sequence 64, Appli	1075	56.5	11.3	186	3	US-10-703-032-175526	Sequence 175526, A
1003	57	11.4	655	3	US-10-013-926A-64	Sequence 64, Appli	1076	56.5	11.3	240	2	US-10-006-011A-5	Sequence 5, Appli
1004	57	11.4	655	3	US-10-162-522A-64	Sequence 64, Appli	1077	56.5	11.3	264	3	US-09-973-278-151	Sequence 151, App
1005	57	11.4	655	3	US-10-183-001-418	Sequence 418, App	1078	56.5	11.3	265	2	US-09-227-357-153	Sequence 153, App
1006	57	11.4	655	3	US-10-180-998-418	Sequence 418, App	1079	56.5	11.3	265	3	US-09-983-802-153	Sequence 153, App
1007	57	11.4	655	3	US-10-201-769-418	Sequence 418, App	1080	56.5	11.3	309	2	US-09-270-767-46802	Sequence 46802, A
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1009	57	11.4	655	3	US-10-165-247A-64	Sequence 64, Appli	1082	56.5	11.3	342	2	US-09-193-562D-13	Sequence 13, Appli
1010	57	11.4	655	3	US-10-174-576-418	Sequence 418, App	1083	56.5	11.3	342	2	US-10-055-412B-13	Sequence 13, Appli
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1012	57	11.4	655	3	US-10-174-581-418	Sequence 418, App	1085	56.5	11.3	428	2	US-09-252-991A-23863	Sequence 23863, A
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1016	57	11.4	655	3	US-10-013-927A-64	Sequence 64, Appli	1089	56.5	11.3	575	2	US-10-103-295-160	Sequence 160, App
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1019	57	11.4	655	3	US-09-978-564A-64	Sequence 64, Appli	1092	56.5	11.3	638	2	US-10-103-295-248	Sequence 248, App
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1313	54.5	10.9	92	2	US-10-072-844-41	Sequence 41, Appl	1386	54.5	10.9	282	3	US-10-152-395-312	Sequence 312, App
1314	54.5	10.9	92	2	US-10-072-838-41	Sequence 41, Appl	1387	54.5	10.9	282	3	US-10-131-822A-312	Sequence 312, App
1315	54.5	10.9	92	2	US-10-072-838-41	Sequence 41, Appl	1388	54.5	10.9	282	3	US-10-123-213-312	Sequence 312, App
1316	54.5	10.9	92	2	US-10-072-838-41	Sequence 41, Appl	1389	54.5	10.9	282	3	US-10-128-694A-312	Sequence 312, App
1317	54.5	10.9	92	2	US-10-219-631A-41	Sequence 41, Appl	1390	54.5	10.9	282	3	US-10-123-909-312	Sequence 312, App
1318	54.5	10.9	103	2	US-09-489-039A-7227	Sequence 7227, Ap	1391	54.5	10.9	282	3	US-10-131-826A-312	Sequence 312, App
1319	54.5	10.9	124	3	US-09-855-604A-727	Sequence 727, App	1392	54.5	10.9	282	3	US-10-448-580-127	Sequence 127, App
1320	54.5	10.9	163	2	US-09-248-796A-26186	Sequence 26186, A	1393	54.5	10.9	282	3	US-09-903-640A-127	Sequence 127, App
1321	54.5	10.9	190	2	US-09-902-540-12077	Sequence 12077, A	1394	54.5	10.9	282	3	US-10-148-580-127	Sequence 127, App
1322	54.5	10.9	232	2	US-09-270-767-39931	Sequence 39931, A	1395	54.5	10.9	282	3	US-10-147-513-312	Sequence 312, App
1323	54.5	10.9	232	2	US-09-270-767-35148	Sequence 55148, A	1396	54.5	10.9	282	3	US-10-121-043-312	Sequence 312, App
1324	54.5	10.9	259	2	US-09-006-353A-2	Sequence 2, Appli	1397	54.5	10.9	282	3	US-10-963-467-127	Sequence 127, App
1325	54.5	10.9	259	2	US-09-573-986-2	Sequence 2, Appli	1398	54.5	10.9	282	3	US-10-448-923-312	Sequence 312, App
1326	54.5	10.9	259	2	US-10-123-292-300	Sequence 300, App	1399	54.5	10.9	282	3	US-10-139-960-312	Sequence 312, App
1327	54.5	10.9	259	3	US-09-826-212A-2	Sequence 2, Appli	1400	54.5	10.9	299	2	US-09-153-927-3	Sequence 3, Appli
1328	54.5	10.9	259	3	US-10-152-398-300	Sequence 300, App	1401	54.5	10.9	299	2	US-09-134-618-4	Sequence 4, Appli
1329	54.5	10.9	259	3	US-10-123-907-300	Sequence 300, App	1402	54.5	10.9	299	2	US-09-949-016-6422	Sequence 6422, Ap
1330	54.5	10.9	259	3	US-10-147-512-300	Sequence 300, App	1403	54.5	10.9	299	2	US-10-139-785-2	Sequence 2, Appli
1331	54.5	10.9	259	3	US-10-147-485-300	Sequence 300, App	1404	54.5	10.9	299	2	US-09-949-016-9189	Sequence 9189, Ap
1332	54.5	10.9	259	3	US-10-124-814-300	Sequence 300, App	1405	54.5	10.9	301	2	US-10-703-032-122198	Sequence 122198, A
1333	54.5	10.9	259	3	US-10-124-822-300	Sequence 300, App	1406	54.5	10.9	311	3	US-10-489-039A-8062	Sequence 8062, Ap
1334	54.5	10.9	259	3	US-10-131-833A-300	Sequence 300, App	1407	54.5	10.9	320	3	US-09-248-796A-15932	Sequence 15932, A
1335	54.5	10.9	259	3	US-10-142-419-300	Sequence 300, App	1408	54.5	10.9	322	3	US-09-703-032-109749	Sequence 109749, A
1336	54.5	10.9	259	3	US-10-152-375-300	Sequence 300, App	1409	54.5	10.9	344	2	US-10-037-417-44	Sequence 44, Appl
1337	54.5	10.9	259	3	US-10-131-818A-300	Sequence 300, App	1410	54.5	10.9	357	3	US-10-037-417-46	Sequence 46, Appl
1338	54.5	10.9	259	3	US-10-145-873-300	Sequence 300, App	1411	54.5	10.9	419	3	US-09-540-209B-6160	Sequence 6160, Ap
1339	54.5	10.9	259	3	US-10-152-395-300	Sequence 300, App	1412	54.5	10.9	435	2	US-09-252-991A-23753	Sequence 23753, A
1340	54.5	10.9	259	3	US-10-131-822A-300	Sequence 300, App	1413	54.5	10.9	442	1	US-08-208-108-2	Sequence 2, Appli


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; PRIOR APPLICATION NUMBER: 60/245,882
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 10/016,481
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-323-157A-3

Query Match      100.0%; Score 498; DB 3; Length 86;
Best Local Similarity 100.0%; Pred. No. 6.7e-51;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 CLPNLLCSRFPDGRYRCMDLKNINF 86
Db 61 CLPNLLCSRFPDGRYRCMDLKNINF 86

RESULT 3
US-10-231-411A-7
; Sequence 7, Application US/10231411A
; Patent No. 7060278
; GENERAL INFORMATION:
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Le Couter, Jennifer
; TITLE OF INVENTION: BVS NUCLEIC ACIDS AND POLYPEPTIDES WITH MITOGENIC ACTIVITY
; FILE REFERENCE: GENENT.088A
; CURRENT APPLICATION NUMBER: US/10/231,411A
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-231-411A-7

Query Match      100.0%; Score 498; DB 3; Length 86;
Best Local Similarity 100.0%; Pred. No. 6.7e-51;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGECHPGSHKVPFFRKRKHTCP 60
Db 1 AVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGECHPGSHKVPFFRKRKHTCP 60

Qy 61 CLPNLLCSRFPDGRYRCMDLKNINF 86
Db 61 CLPNLLCSRFPDGRYRCMDLKNINF 86

RESULT 4
US-10-811-328-3
; Sequence 3, Application US/10811328
; Patent No. 7115560
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; TITLE OF INVENTION: Methods For Modulating Gastric Secretion
; TITLE OF INVENTION: Using Prokineticin Receptor Antagonists
; FILE REFERENCE: 66778-365
; CURRENT APPLICATION NUMBER: US/10/811,328
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: 60/457,891
; PRIOR FILING DATE: 2003-03-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
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; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-811-328-3

Query Match      100.0%; Score 498; DB 3; Length 86;
Best Local Similarity 100.0%; Pred. No. 6.7e-51;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGECHPGSHKVPFFRKRKHTCP 60
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Qy 61 CLPNLLCSRFPDGRYRCMDLKNINF 86
Db 61 CLPNLLCSRFPDGRYRCMDLKNINF 86

RESULT 5
US-10-323-157A-18
; Sequence 18, Application US/10323157A
; Patent No. 7052674
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; APPLICANT: Ehler, Frederick
; TITLE OF INVENTION: Prokineticin Polypeptides, Related
; TITLE OF INVENTION: Compositions and Methods
; FILE REFERENCE: 66678-144 (UC 5534)
; CURRENT APPLICATION NUMBER: US/10/323,157A
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: 60/245,882
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 10/016,481
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-323-157A-18

Query Match      100.0%; Score 498; DB 3; Length 87;
Best Local Similarity 100.0%; Pred. No. 6.7e-51;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGECHPGSHKVPFFRKRKHTCP 60
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Qy 61 CLPNLLCSRFPDGRYRCMDLKNINF 86
Db 62 CLPNLLCSRFPDGRYRCMDLKNINF 87

RESULT 6
US-10-811-328-18
; Sequence 18, Application US/10811328
; Patent No. 7115560
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; TITLE OF INVENTION: Methods For Modulating Gastric Secretion
; TITLE OF INVENTION: Using Prokineticin Receptor Antagonists
; FILE REFERENCE: 66778-365
; CURRENT APPLICATION NUMBER: US/10/811,328
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: 60/457,891
; PRIOR FILING DATE: 2003-03-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
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; LENGTH: 87
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-811-328-18

Query Match      100.0%; Score 498; DB 3; Length 87;
Best Local Similarity 100.0%; Pred. No. 6.7e-51;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 CLPNLLCSRFPDGRYRCSDMLKNINF 86
Db 62 CLPNLLCSRFPDGRYRCSDMLKNINF 87

RESULT 7
US-10-323-157A-15
; Sequence 15, Application US/10323157A
; Patent No. 7052674
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; APPLICANT: Ehler, Frederick
; TITLE OF INVENTION: Prokineticin Polypeptides, Related
; TITLE OF INVENTION: Compositions and Methods
; FILE REFERENCE: 66678-144 (UC 5534)
; CURRENT APPLICATION NUMBER: US/10/323,157A
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: 60/245,882
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 10/016,481
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-323-157A-15

Query Match      100.0%; Score 498; DB 3; Length 89;
Best Local Similarity 100.0%; Pred. No. 6.9e-51;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVITGACERDVQCGAGTCCCAISLWLRLGRLMCTPLGREGECHPGSHKVPFFRKRKHTTCP 60
Db 4 AVITGACERDVQCGAGTCCCAISLWLRLGRLMCTPLGREGECHPGSHKVPFFRKRKHTTCP 63

Qy 61 CLPNLLCSRFPDGRYRCSDMLKNINF 86
Db 64 CLPNLLCSRFPDGRYRCSDMLKNINF 89

RESULT 8
US-10-811-328-15
; Sequence 15, Application US/10811328
; Patent No. 7115560
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; TITLE OF INVENTION: Methods For Modulating Gastric Secretion
; TITLE OF INVENTION: Using Prokineticin Receptor Antagonists
; FILE REFERENCE: 66778-365
; CURRENT APPLICATION NUMBER: US/10/811,328
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: 60/457,891
; PRIOR FILING DATE: 2003-03-25
; NUMBER OF SEQ ID NOS: 32
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-811-328-15

Query Match      100.0%; Score 498; DB 3; Length 89;
Best Local Similarity 100.0%; Pred. No. 6.9e-51;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVITGACERDVQCGAGTCCCAISLWLRLGRLMCTPLGREGECHPGSHKVPFFRKRKHTTCP 60
Db 4 AVITGACERDVQCGAGTCCCAISLWLRLGRLMCTPLGREGECHPGSHKVPFFRKRKHTTCP 63

Qy 61 CLPNLLCSRFPDGRYRCSDMLKNINF 86
Db 64 CLPNLLCSRFPDGRYRCSDMLKNINF 89

RESULT 9
US-09-712-529-5
; Sequence 5, Application US/09712529
; Patent No. 6485938
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Thompson, Penny P.
; TITLE OF INVENTION: Human Zven Proteins
; FILE REFERENCE: 99-81
; CURRENT APPLICATION NUMBER: US/09/712,529
; CURRENT FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-09-712-529-5

Query Match      100.0%; Score 498; DB 2; Length 105;
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Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVITGACERDVQCGAGTCCCAISLWLRLGRLMCTPLGREGECHPGSHKVPFFRKRKHTTCP 60
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Qy 61 CLPNLLCSRFPDGRYRCSDMLKNINF 86
Db 80 CLPNLLCSRFPDGRYRCSDMLKNINF 105

RESULT 10
US-10-212-201A-5
; Sequence 5, Application US/10212201A
; Patent No. 6756479
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Thompson, Penny P.
; TITLE OF INVENTION: Human Zven Proteins
; FILE REFERENCE: 99-81
; CURRENT APPLICATION NUMBER: US/10/212,201A
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US/09/712,529
; PRIOR FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
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; SEQ ID NO 5
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-212-201A-5

Query Match      100.0%; Score 498; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 8.3e-51;
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QY 1 AVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGRGEGECHPGSHKVPFPRKRKHTCP 60
Db 20 AVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGRGEGECHPGSHKVPFPRKRKHTCP 79

QY 61 CLPNLLCSRPDGRYRCSDMLKNINF 86
Db 80 CLPNLLCSRPDGRYRCSDMLKNINF 105

RESULT 11
US-10-212-355-5
; Sequence 5, Application US/10212355
; Patent No. 6828425
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Thompson, Penny P.
; TITLE OF INVENTION: Human Zven Proteins
; FILE REFERENCE: 99-81
; CURRENT APPLICATION NUMBER: US/10/212,355
; CURRENT FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-212-355-5

Query Match      100.0%; Score 498; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 8.3e-51;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGRGEGECHPGSHKVPFPRKRKHTCP 60
Db 20 AVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGRGEGECHPGSHKVPFPRKRKHTCP 79

QY 61 CLPNLLCSRPDGRYRCSDMLKNINF 86
Db 80 CLPNLLCSRPDGRYRCSDMLKNINF 105

RESULT 12
US-09-991-181-371
; Sequence 371, Application US/09991181
; Patent No. 6913919
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deanoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
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; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088810
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088824
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088826
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088858
; PRIOR FILING DATE: 1998-06-11
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; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088876
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089440
; PRIOR FILING DATE: 1998-06-16
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; PRIOR APPLICATION NUMBER: 60/089599
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089600
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089907
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; PRIOR APPLICATION NUMBER: 60/089908
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089947
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/089948
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/089952
; PRIOR FILING DATE: 1998-06-19
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; PRIOR APPLICATION NUMBER: 60/090349
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; PRIOR APPLICATION NUMBER: 60/090435
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090444
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; PRIOR APPLICATION NUMBER: 60/090445
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; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
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; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090540
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090542
; PRIOR FILING DATE: 1998-06-24

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; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090676
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090678
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090690
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090694
; PRIOR FILING DATE: 1998-06-25
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; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
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Query Match 100.0%; Score 498; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 8.3e-51;
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QY 1 AVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGECHPGSHKVPFFRKRKHTCP 60
Db 20 AVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGECHPGSHKVPFFRKRKHTCP 79
QY 61 CLPNLLCSRFDPGRYRCSMDLKNIP 86
Db 80 CLPNLLCSRFDPGRYRCSMDLKNIP 105
RESULT 13
US-09-990-444-371
; Sequence 371, Application US/09990444
; Patent No. 6930170
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C19
CURRENT APPLICATION NUMBER: US/09/990,444
CURRENT FILING DATE: 2001-11-14
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PRIOR FILING DATE: 1997-06-16
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Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 14

RESOL 14
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/ Sequence 371, Application US/09997333
/ Patent No. 6953836
/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi J.
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Botstein, David
/ APPLICANT: Desnovers, Luc
/ APPLICANT: Eaton, Dan L.
/ APPLICANT: Ferrara, Napoleone
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Kljavin, Ivar J.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James
/ APPLICANT: Paoni, Nicholas P.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Watanabe, Colin K.

Fri Nov 30 07:56:33 2007

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Best Local Similarity 100.0%; Pred. No. 8.3e-51;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Sequence 371, Application US/09992598
; Patent No. 6956108
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
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; APPLICANT: Gerritsen, Mary E.
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; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin

;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

;; FILE REFERENCE: P2730PIC20

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143.348 Million cell updates/sec

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Perfect score: 498
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Scoring table: BLOSUM62

Searched: Gapop 10.0, Gapext 0.5
2782304 seq, 489333398 residues
Total number of hits satisfying chosen parameters: 2782304
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%

Database :
Listing first 1500 summaries
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PN	WO200208417-A1.					
PD	31-JAN-2002.					
PA	(TAKE) TAKEDA CHEM IND LTD.					
Query Match	100.0%;	Score 498;	DB 5;	Length 86;		
Best Local Similarity	100.0%;	Pred. No. 9.6e-47;				
RESULT 3						
ID	ABJ05338	standard; protein; 86 AA.				
DE	Human ZAQ protein ligand.					
PN	WO200236762-A1.					
PD	10-MAY-2002.					
PA	(TAKE) TAKEDA CHEM IND LTD.					
Query Match	100.0%;	Score 498;	DB 5;	Length 86;		
Best Local Similarity	100.0%;	Pred. No. 9.6e-47;				
RESULT 4						
ID	AAO15529	standard; protein; 86 AA.				
DE	Human physiologically-active ZAQ ligand-related protein 4.					
PN	WO200257443-A1.					
PD	23-JUL-2002.					
PA	(TAKE) TAKEDA CHEM IND LTD.					
Query Match	100.0%;	Score 498;	DB 5;	Length 86;		
Best Local Similarity	100.0%;	Pred. No. 9.6e-47;				
RESULT 5						
ID	ABE06306	standard; protein; 86 AA.				
DE	Human G protein-coupled receptor ZAQ ligand protein SEQ ID NO:21.					
PN	WO200206483-A1.					
PD	24-JAN-2002.					
PA	(TAKE) TAKEDA CHEM IND LTD.					
Query Match	100.0%;	Score 498;	DB 5;	Length 86;		
Best Local Similarity	100.0%;	Pred. No. 9.6e-47;				
RESULT 6						
ID	AAE24383	standard; protein; 86 AA.				

DE Human prokineticin 1 mature protein.
PN WO200236625-A2.
PD 10-MAY-2002.
PA (REGC) UNIV CALIFORNIA.
Query Match 100.0%; Score 498; DB 5; Length 86;
Best Local Similarity 100.0%; Pred. No. 9.6e-47;
RESULT 7
ID AD69104 standard; protein; 86 AA.
DE Human ZAQ-related protein - SEQ ID 82.
PN WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 100.0%; Score 498; DB 7; Length 86;
Best Local Similarity 100.0%; Pred. No. 9.6e-47;
RESULT 8
ID ADO05360 standard; protein; 86 AA.
DE Human prokineticin 1 (PK1), SEQ ID NO:9.
PN WO2003088904-A2.
PD 30-OCT-2003.
PA (REGC) UNIV CALIFORNIA.
Query Match 100.0%; Score 498; DB 7; Length 86;
Best Local Similarity 100.0%; Pred. No. 9.6e-47;
RESULT 9
ID ADN43256 standard; protein; 86 AA.
DE Amino acid sequence of human prokineticin 1 (PK1).
PN WO2004032851-A2.
PD 22-APR-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 100.0%; Score 498; DB 8; Length 86;
Best Local Similarity 100.0%; Pred. No. 9.6e-47;
RESULT 10
ID ADR24003 standard; protein; 86 AA.
DE Human ZAQ-1 ligand protein #1.
PN WO2004065419-A1.
PD 05-AUG-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 100.0%; Score 498; DB 8; Length 86;
Best Local Similarity 100.0%; Pred. No. 9.6e-47;
RESULT 11
ID ADS86471 standard; protein; 86 AA.
DE Human ZAQ ligand protein related to eating disorders & obesity Seq 3.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 100.0%; Score 498; DB 8; Length 86;
Best Local Similarity 100.0%; Pred. No. 9.6e-47;
RESULT 12
ID ADS75494 standard; protein; 86 AA.
DE Human prokineticin 1 receptor protein.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 100.0%; Score 498; DB 8; Length 86;
Best Local Similarity 100.0%; Pred. No. 9.6e-47;
RESULT 13
ID ADW0759 standard; protein; 86 AA.
DE Amino acid sequence of human prokineticin 1 (PK1).
PN WO2004113361-A2.
PD 29-DEC-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 100.0%; Score 498; DB 9; Length 86;
Best Local Similarity 100.0%; Pred. No. 9.6e-47;
RESULT 14
ID ADZ58575 standard; protein; 86 AA.
DE Human ZAQ-1 amino acid sequence - SEQ ID 2.
PN WO2005037870-A1.
PD 28-APR-2005.
PA (TAKE) TAKEDA PHARM CO LTD.
Query Match 100.0%; Score 498; DB 9; Length 86;
Best Local Similarity 100.0%; Pred. No. 9.6e-47;
RESULT 15
ID AEB45594 standard; protein; 86 AA.
DE Human Zven2 protein fragment.

PN US2005153322-A1.
PD 14-JUL-2005.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 100.0%; Score 498; DB 9; Length 86;
Best Local Similarity 100.0%; Pred. No. 9.6e-47;
RESULT 16
ID AED00599 standard; protein; 86 AA.
DE Partial human prokineticin 1 (PK1) SEQ ID NO 11.
PN WO2005091925-A2.
PD 06-OCT-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 100.0%; Score 498; DB 9; Length 86;
Best Local Similarity 100.0%; Pred. No. 9.6e-47;
RESULT 17
ID AEA43367 standard; protein; 86 AA.
DE Human prokineticin 1 (PK1) protein, SEQ ID NO: 9.
PN US2006172935-A1.
PD 03-AUG-2006.
PA (ZHOU/) ZHOU Q.
PA (BULL/) BULLOCK C M.
PA (SIEG/) SIEGEL J.
Query Match 100.0%; Score 498; DB 10; Length 86;
Best Local Similarity 100.0%; Pred. No. 9.6e-47;
RESULT 18
ID AEK60512 standard; protein; 86 AA.
DE Human prokineticin 1.
PN WO2006102112-A2.
PD 28-SEP-2006.
PA (JANC) JANSSEN PHARM NV.
Query Match 100.0%; Score 498; DB 10; Length 86;
Best Local Similarity 100.0%; Pred. No. 9.6e-47;
RESULT 19
ID AEL00449 standard; protein; 86 AA.
DE Human human prokineticin-1 ligand #1.
PN WO2006104713-A1.
PD 05-OCT-2006.
PA (JANC) JANSSEN PHARM NV.
PA (MISK/) MISKOWSKI T A.
Query Match 100.0%; Score 498; DB 10; Length 86;
Best Local Similarity 100.0%; Pred. No. 9.6e-47;
RESULT 20
ID AAE24395 standard; protein; 87 AA.
DE Human prokineticin 1 mutant protein #4.
PN WO200236825-A2.
PD 10-MAY-2002.
PA (REGC) UNIV CALIFORNIA.
Query Match 100.0%; Score 498; DB 5; Length 87;
Best Local Similarity 100.0%; Pred. No. 9.7e-47;
RESULT 21
ID ADS75509 standard; protein; 87 AA.
DE Prokineticin receptor antagonist Met PK1.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 100.0%; Score 498; DB 8; Length 87;
Best Local Similarity 100.0%; Pred. No. 9.7e-47;
RESULT 22
ID AAE24392 standard; protein; 89 AA.
DE Human prokineticin 1 mutant protein #1.
PN WO200236825-A2.
PD 10-MAY-2002.
PA (REGC) UNIV CALIFORNIA.
Query Match 100.0%; Score 498; DB 5; Length 89;
Best Local Similarity 100.0%; Pred. No. 9.9e-47;
RESULT 23
ID ADS75506 standard; protein; 89 AA.
DE Prokineticin receptor related synthetic construct protein, SEQ ID 15.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 100.0%; Score 498; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 9.9e-47;
RESULT 24

ID AAY66745 standard; protein; 105 AA.
DE Membrane-bound protein PRO1186.
PN WO9963088-A2.
PD 09-DEC-1999.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 3; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 25
ID AAB18453 standard; protein; 105 AA.
DE A human TANGO 266 polypeptide.
PN WO2000052022-A1.
PD 08-SEP-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 100.0%; Score 498; DB 3; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 26
ID AAB70148 standard; protein; 105 AA.
DE Human G protein-coupled receptor protein-related sequence #4.
PN WO200116309-A1.
PD 08-MAR-2001.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 100.0%; Score 498; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 27
ID AAB68427 standard; protein; 105 AA.
DE Amino acid sequence of a human zven2 polypeptide.
PN WO200136465-A2.
PD 25-MAY-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 100.0%; Score 498; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 28
ID AAU12406 standard; protein; 105 AA.
DE Human PRO1186 polypeptide sequence.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 29
ID AAB53096 standard; protein; 105 AA.
DE Human angiogenesis-associated protein PRO1186, SEQ ID NO:165.
PN WO200053753-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 30
ID AAB65268 standard; protein; 105 AA.
DE Human PRO1186 (UNQ600) protein sequence SEQ ID NO:371.
PN WO200073454-A1.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 31
ID AAB48175 standard; protein; 105 AA.
DE Human PRO1186 polypeptide.
PN WO200075327-A1.
PD 14-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 32
ID AAB48067 standard; protein; 105 AA.
DE Human extracellular signaling molecule (EXCS) (ID 2006548CD1).
PN WO200070049-A2.
PD 23-NOV-2000.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 100.0%; Score 498; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 33
ID AAM50773 standard; protein; 105 AA.

DE Endocrine gland-derived vascular endothelial growth factor.
 PN WO200200711-A2.
 PD 03-JAN-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 498; DB 5; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1.2e-46;
 RESULT 34
 ID AAU83674 standard; protein; 105 AA.
 DE Human PRO protein, Seq ID No 166.
 PN WO200208288-A2.
 PD 31-JAN-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 498; DB 5; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1.2e-46;
 RESULT 35
 ID ABB84902 standard; protein; 105 AA.
 DE Human PRO1186 protein sequence SEQ ID NO:172.
 PN WO20020690-A2.
 PD 03-JAN-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 498; DB 5; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1.2e-46;
 RESULT 36
 ID AAO15527 standard; protein; 105 AA.
 DE Human physiologically-active ZAQ ligand-related protein 3.
 PN WO200257443-A1.
 PD 25-JUL-2002.
 PA (TAKE) TAKEDA CHEM IND LTD.
 Query Match 100.0%; Score 498; DB 5; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1.2e-46;
 RESULT 37
 ID ABB06308 standard; protein; 105 AA.
 DE Human G protein-coupled receptor ZAQ ligand protein SEQ ID NO:23.
 PN WO200206483-A1.
 PD 24-JAN-2002.
 PA (TAKE) TAKEDA CHEM IND LTD.
 Query Match 100.0%; Score 498; DB 5; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1.2e-46;
 RESULT 38
 ID AAE24382 standard; protein; 105 AA.
 DE Human prokineticin 1 precursor protein.
 PN WO200236625-A2.
 PD 10-MAY-2002.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 100.0%; Score 498; DB 5; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1.2e-46;
 RESULT 39
 ID ABB95508 standard; protein; 105 AA.
 DE Human angiogenesis related protein PRO1186 SEQ ID NO: 172.
 PN WO200208284-A2.
 PD 31-JAN-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 498; DB 5; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1.2e-46;
 RESULT 40
 ID ADY31906 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN WO200193983-A1.

PD 13-DEC-2001.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 498; DB 5; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1.2e-46;
 RESULT 41
 ID ABUS8083 standard; protein; 105 AA.
 DE Human PRO polypeptide #115.
 PN US2003027163-A1.
 PD 06-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 498; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1.2e-46;
 RESULT 42
 ID ABUS9161 standard; protein; 105 AA.
 DE Novel human secreted or transmembrane protein PRO1186.
 PN US2002132252-A1.
 PD 19-SEP-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 498; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1.2e-46;
 RESULT 43
 ID ABUS2673 standard; protein; 105 AA.
 DE Human secreted/transmembrane protein PRO1186.
 PN US2003032023-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 498; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1.2e-46;
 RESULT 44
 ID ABO17850 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003032156-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 498; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1.2e-46;
 RESULT 45
 ID ABUS0592 standard; protein; 105 AA.
 DE Human secreted/transmembrane protein, #151.
 PN US2002160384-A1.
 PD 31-OCT-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 498; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1.2e-46;
 RESULT 46
 ID ABUS0821 standard; protein; 105 AA.
 DE Human PRO polypeptide #83.
 PN US2003036635-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 498; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1.2e-46;
 RESULT 47
 ID ABO33787 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003045687-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 498; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1.2e-46;
 RESULT 48
 ID ABUS1974 standard; protein; 105 AA.
 DE Human PRO1186 polypeptide.
 PN US2002103125-A1.
 PD 01-AUG-2002.
 PA (GETH) GENENTECH LTD.
 Query Match 100.0%; Score 498; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1.2e-46;
 RESULT 49
 ID ABUS8800 standard; protein; 105 AA.
 DE Human endocrine gland-derived vascular endothelial growth factor.
 PN US2002192634-A1.
 PD 19-DEC-2002.
 PA (FERR) FERRARA N.
 PA (WATA) WATANABE C.

PA (WOOD/) WOOD W I.
 PA (SHEK/) SHEK T.
 Query Match 100.0%; Score 498; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1.2e-46;
 RESULT 50
 ID ABU81104 standard; protein; 105 AA.
 DE Human PRO polypeptide #235.
 PN US2003004311-A1.
 PD 02-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 498; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1.2e-46;
 RESULT 51
 ID ABU07603 standard; protein; 105 AA.
 DE Human ZVEN2.
 PN US6485938-B1.
 PD 26-NOV-2002.
 PA (ZYMO) ZYMOGENETICS INC.
 Query Match 100.0%; Score 498; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1.2e-46;
 RESULT 52
 ID ABU72559 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003003531-A1.
 PD 02-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 498; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1.2e-46;
 RESULT 53
 ID ABU66804 standard; protein; 105 AA.
 DE Human PRO polypeptide #235.
 PN US2003036180-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 498; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1.2e-46;
 RESULT 54
 ID ABU59885 standard; protein; 105 AA.
 DE Novel secreted and transmembrane protein PRO1186.
 PN US2003017563-A1.
 PD 23-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 498; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1.2e-46;
 RESULT 55
 ID ABU59308 standard; protein; 105 AA.
 DE Human secreted/transmembrane protein, #151.
 PN US2003027162-A1.
 PD 06-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 498; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1.2e-46;
 RESULT 56
 ID ABO26005 standard; protein; 105 AA.
 DE Human PRO1186 polypeptide.
 PN US2002127576-A1.
 PD 12-SEP-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 498; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1.2e-46;
 RESULT 57
 ID ABO25075 standard; protein; 105 AA.
 DE Human secreted/transmembrane protein (PRO) #235.
 PN US2003036179-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 498; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1.2e-46;
 RESULT 58
 ID ABU82130 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003088063-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 498; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1.2e-46;
 RESULT 59
 ID ABU59014 standard; protein; 105 AA.
 DE Human secreted/transmembrane protein, #151.
 PN US2002142961-A1.
 PD 03-OCT-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 498; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1.2e-46;
 RESULT 60
 ID ABU92392 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003022187-A1.
 PD 30-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 498; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1.2e-46;
 RESULT 61
 ID ABU59457 standard; protein; 105 AA.
 DE Novel human secreted or transmembrane protein PRO1198.
 PN US2003027985-A1.
 PD 06-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 498; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1.2e-46;
 RESULT 62
 ID ABU67080 standard; protein; 105 AA.
 DE Human secreted/transmembrane, PRO, protein SEQ ID 470.
 PN US2003032155-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 498; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1.2e-46;
 RESULT 63
 ID ABU92223 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003017476-A1.
 PD 23-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 498; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1.2e-46;
 RESULT 64
 ID ABU10929 standard; protein; 105 AA.
 DE Human PRO polypeptide #115.
 PN US2002123463-A1.
 PD 05-SEP-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 498; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1.2e-46;
 RESULT 65
 ID ABU81681 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2002177164-A1.
 PD 28-NOV-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 498; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1.2e-46;
 RESULT 66
 ID ABU88620 standard; protein; 105 AA.
 DE Human secreted and transmembrane polypeptide PRO1186.
 PN US2002197615-A1.
 PD 26-DEC-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 498; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1.2e-46;
 RESULT 67
 ID ABO34134 standard; protein; 105 AA.
 DE Human PRO1186 polypeptide.
 PN US2003017981-A1.
 PD 23-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 498; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1.2e-46;
 RESULT 68
 ID ADA45989 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.

PD US2003022328-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 69
ID ADA76420 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 70
ID ASB72310 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 71
ID ADA19070 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 72
ID ADA61693 standard; protein; 105 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 73
ID ADB19478 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 74
ID ADB28019 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 75
ID ADA86498 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 76
ID ADB16062 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 77
ID ADA37882 standard; protein; 105 AA.
DE Human secreted/transmembrane protein PRO1186.
PN US2003008297-A1.

PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 78
ID ADA47848 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 79
ID ADA21568 standard; protein; 105 AA.
DE Human secreted/transmembrane polypeptide PRO1186.
PN US2003054404-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 80
ID ADA10355 standard; protein; 105 AA.
DE Human secreted/transmembrane protein, PRO1186.
PN US2003059831-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 81
ID ADA67643 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 82
ID ADB30650 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 83
ID ADA85946 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 84
ID ADA17899 standard; protein; 105 AA.
DE Human PRO1186 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 85
ID ADA97158 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 86
ID ADA79462 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;

RESULT 87
ID ADA87601 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003087345-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 88
ID ADB16803 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 89
ID ADA28007 standard; protein; 105 AA.
DE Human secreted/transmembrane protein PRO1186.
PN US2003054359-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 90
ID ADA91895 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 91
ID ADB14958 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 92
ID ADB18919 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 93
ID ADA94134 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 94
ID ADB20030 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 95
ID ADB13342 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 96
ID ABO43383 standard; protein; 105 AA.

DE Novel human secreted and transmembrane protein PRO1186.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 97
ID ADA94587 standard; protein; 105 AA.
DE Human secreted/transmembrane protein PRO1186.
PN US2003059832-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 98
ID ADA74596 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 99
ID ADB24829 standard; protein; 105 AA.
DE Human PRO polypeptide SEQ ID NO 470.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 100
ID ADA82353 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 101
ID ADA75316 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 102
ID ADA85394 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 103
ID ADA84842 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 104
ID ADB30098 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 105
ID ADA80626 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082761-A1.

PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 106
ID ADA75868 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 107
ID ADA38812 standard; protein; 105 AA.
DE Human secreted/transmembrane protein PRO1186.
PN US2003059780-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 108
ID ADA47093 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 109
ID ADB25389 standard; protein; 105 AA.
DE Human PRO polypeptide SEQ ID NO 470.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 110
ID ADA93565 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 111
ID ADB26915 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 112
ID ADB31202 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 113
ID ABJ72438 standard; protein; 105 AA.
DE Human secreted/transmembrane protein PRO1186.
PN US2003027988-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 114
ID ADA92933 standard; protein; 105 AA.
DE Human secreted/transmembrane protein PRO1186.
PN US2003060407-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 115
ID ADA61130 standard; protein; 105 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 116
ID ADB24277 standard; protein; 105 AA.
DE Human PRO polypeptide SEQ ID NO 470.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 117
ID ADA96606 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 118
ID ADA81178 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 119
ID ADA96054 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 120
ID ADB26363 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 121
ID ADB21848 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 122
ID AB034333 standard; protein; 105 AA.
DE Human secreted/transmembrane polypeptide PRO 1186.
PN US2003044934-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 123
ID ADA77627 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;

RESULT 124
ID ADB18367 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 125
ID ADA87050 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 126
ID ADA8153 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 127
ID ADA6541 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 128
ID ADB28571 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 129
ID ADB29123 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 130
ID ABO53220 standard; protein; 105 AA.
DE Human secreted/transmembrane protein PRO1186.
PN US2003044806-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 131
ID ADA77075 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 132
ID ADA22494 standard; protein; 105 AA.
DE Human secreted/transmembrane polypeptide PRO1186.
PN US2003040473-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 133
ID ADA88705 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.

PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 134
ID ADA97710 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 135
ID ADB27467 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003022239-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 136
ID ADB22400 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 137
ID ABO22590 standard; protein; 105 AA.
DE Human secreted/transmembrane protein PRO1186.
PN US2003017982-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 138
ID ADA06660 standard; protein; 105 AA.
DE Human secreted/transmembrane PRO polypeptide #115.
PN US2003049638-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 139
ID ABJ72140 standard; protein; 105 AA.
DE Human membrane bound receptor/protein PRO1186 amino acid sequence.
PN US2003065147-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 140
ID ADA39353 standard; protein; 105 AA.
DE Human secreted/transmembrane protein PRO1186.
PN US2003059782-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 141
ID ADA67091 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 142
ID ADB22952 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 143
ID ADB22952 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;

ID ADB23725 standard; protein; 105 AA.
DE Human PRO polypeptide SEQ ID NO 470.
PN US2003077712-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 144
ID ADA92447 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 145
ID ADB15510 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 146
ID ADB83656 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003073814-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 147
ID ADB80762 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003088068-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 148
ID ADB73303 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003096968-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 149
ID ADB38762 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 150
ID ADB96379 standard; protein; 105 AA.
DE Human PRO polypeptide #115.
PN US2003054403-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 151
ID ADB78385 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003092889-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 152
ID ADB38210 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.

PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 153
ID ADB66682 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 154
ID ADB85033 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003073817-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 155
ID ADB89762 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 156
ID ADB90494 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 157
ID ADB39595 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 158
ID ADB78139 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003092886-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 159
ID ADB87205 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003088067-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 160
ID ADB84787 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003092890-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 161
ID ADB47218 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082687-A1.

PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 162
ID ADB83902 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003069397-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 163
ID ADB86825 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 164
ID ADB73057 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003092887-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 165
ID ADB77430 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 166
ID ADB34587 standard; protein; 105 AA.
DE Human PRO polypeptide SEQ ID NO 470.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 167
ID ADB35691 standard; protein; 105 AA.
DE Human PRO polypeptide SEQ ID NO 470.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 168
ID ADB34035 standard; protein; 105 AA.
DE Human PRO polypeptide SEQ ID NO 470.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 169
ID ADB35139 standard; protein; 105 AA.
DE Human PRO polypeptide SEQ ID NO 470.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 170
ID ADB36243 standard; protein; 105 AA.
DE Human PRO polypeptide SEQ ID NO 470.
PN US2003077720-A1.
PD 24-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 171
ID ADB46638 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 172
ID ADCS7851 standard; protein; 105 AA.
DE Human PRO polypeptide #115.
PN US2003027754-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 173
ID ADC55215 standard; protein; 105 AA.
DE Human PRO polypeptide #115.
PN US2003045463-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 174
ID ADC12082 standard; protein; 105 AA.
DE Human secreted/transmembrane protein PRO1186.
PN US2003049681-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 175
ID ADC56504 standard; protein; 105 AA.
DE Human PRO polypeptide #115.
PN US2003064375-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 176
ID ADC07559 standard; protein; 105 AA.
DE Human secreted/transmembrane protein PRO1186.
PN US2003068647-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 177
ID ADC11549 standard; protein; 105 AA.
DE Human secreted/transmembrane protein PRO1186.
PN US2003069403-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 178
ID ADC36895 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003088065-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 179
ID ADC21885 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003096969-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 180
ID ADC50511 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003092106-A1.

PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 181
ID ADC72058 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 182
ID ADC60037 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 183
ID ADC49916 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003088064-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 184
ID ADC49115 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003088070-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 185
ID ADC49632 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003088071-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 186
ID ADC47493 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003088072-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 187
ID ADC53044 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein Seq ID470.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 188
ID ADC57398 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein Seq ID470.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 189
ID ADC60589 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 190
ID ADC51064 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 191
ID ADC65591 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 192
ID ADC54689 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein Seq ID470.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 193
ID ADC53650 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein Seq ID470.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 194
ID ADC59173 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein Seq ID470.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 195
ID ADC56051 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein Seq ID470.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 196
ID ADC58621 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein Seq ID470.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 197
ID ADC14671 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003082546-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 198
ID ADC47238 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003105288-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;

Best Local Similarity 100.0%; Pred. No. 1.2e-46;
 RESULT 199
 ID ADD08203 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003068623-A1.
 PD 10-APR-2003.
 Query Match
 Best Local Similarity 100.0%; Score 498; DB 7; Length 105;
 RESULT 200
 ID ADD03295 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003092104-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 498; DB 7; Length 105;
 RESULT 201
 ID ADC90287 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003087348-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 498; DB 7; Length 105;
 RESULT 202
 ID ADC82028 standard; protein; 105 AA.
 DE Human PRO polypeptide #115.
 PN US2003083461-A1.
 PD 01-MAY-2003.
 Query Match
 Best Local Similarity 100.0%; Score 498; DB 7; Length 105;
 RESULT 203
 ID ADC69706 standard; protein; 105 AA.
 DE Human PRO polypeptide #235.
 PN US2003194770-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 498; DB 7; Length 105;
 RESULT 204
 ID ADC48595 standard; protein; 105 AA.
 DE Human PRO polypeptide #235.
 PN US2003194773-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 498; DB 7; Length 105;
 RESULT 205
 ID ADD10124 standard; protein; 105 AA.
 DE Human PRO polypeptide #235.
 PN US2003194776-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 498; DB 7; Length 105;
 RESULT 206
 ID ADD07670 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2002193299-A1.
 PD 19-DEC-2002.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 498; DB 7; Length 105;
 RESULT 207
 ID ADC78113 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003096972-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 498; DB 7; Length 105;
 RESULT 208
 ID ADD04699 standard; protein; 105 AA.

DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003087354-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 498; DB 7; Length 105;
 RESULT 209
 ID ADC82561 standard; protein; 105 AA.
 DE Human PRO polypeptide #115.
 PN US2003059833-A1.
 PD 27-MAR-2003.
 Query Match
 Best Local Similarity 100.0%; Score 498; DB 7; Length 105;
 RESULT 210
 ID ADD06348 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003073816-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 498; DB 7; Length 105;
 RESULT 211
 ID ADC89655 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003092103-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 498; DB 7; Length 105;
 RESULT 212
 ID ADD11162 standard; protein; 105 AA.
 DE Human PRO polypeptide #235.
 PN US2003194774-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 498; DB 7; Length 105;
 RESULT 213
 ID ADD10461 standard; protein; 105 AA.
 DE Human secreted/transmembrane PRO polypeptide #86.
 PN US2003105011-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 498; DB 7; Length 105;
 RESULT 214
 ID ADC48043 standard; protein; 105 AA.
 DE Human PRO polypeptide #235.
 PN US2003194771-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 498; DB 7; Length 105;
 RESULT 215
 ID ADD08741 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003073090-A1.
 PD 17-APR-2003.
 Query Match
 Best Local Similarity 100.0%; Score 498; DB 7; Length 105;
 RESULT 216
 ID ADC77867 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003088066-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 498; DB 7; Length 105;
 RESULT 217
 ID ADC80103 standard; protein; 105 AA.
 DE Novel human secreted and transmembrane protein PRO1186.
 PN US2003087358-A1.
 PD 08-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 218
ID ADD06990 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 219
ID ADD11421 standard; protein; 105 AA.
DE Human secreted/transmembrane PRO polypeptide #86.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 220
ID ADD09572 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 221
ID ADC83237 standard; protein; 105 AA.
DE Human PRO polypeptide #115.
PN US2003059783-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 222
ID ADD50830 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003105291-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 223
ID ADD41285 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 224
ID ADD52424 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 225
ID ADD51076 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003105290-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 226
ID ADD53164 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 227
ID ADD53716 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 228
ID ADD55344 standard; protein; 105 AA.
DE Human PRO polypeptide #115.
PN US2003077593-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 229
ID ADD69106 standard; protein; 105 AA.
DE Human ZAQ-related protein - SEQ ID 84.
PN WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 230
ID ADD37214 standard; protein; 105 AA.
DE Human secreted/transmembrane PRO polypeptide #86.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 231
ID ADD56302 standard; protein; 105 AA.
DE Human PRO polypeptide #115.
PN US2003077594-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 232
ID ADD51872 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 233
ID ADD02671 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 234
ID ADD50557 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003096971-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 235
ID ADD02105 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 236
ID ADD54287 standard; protein; 105 AA.

DE Novel human secreted and transmembrane protein PRO1186.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 237
ID ADD54740 standard; protein; 105 AA.
DE Human PRO polypeptide #115.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 238
ID ADD50311 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003096970-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 239
ID ADD51322 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003105289-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 240
ID ADD92604 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 241
ID ADD91500 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 242
ID ADE04114 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 243
ID ADE26894 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003087304-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 244
ID ADE32411 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 245
ID ADE22343 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199056-A1.

PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 246
ID ADD79567 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 247
ID ADE42103 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 248
ID ADE17920 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 249
ID ADD92052 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 250
ID ADE33515 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 251
ID ADE34067 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 252
ID ADE80119 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 253
ID ADD93156 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 254
ID ADE19576 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199025-A1.
PD 23-OCT-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 255
ID ADE19024 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 256
ID ADE43220 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 257
ID ADD96009 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 258
ID ADE22895 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 259
ID ADD79013 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 260
ID ADE26361 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 261
ID ADE32963 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 262
ID ADE42655 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 263
ID ADD80671 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;

Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 264
ID ADD89699 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 265
ID ADE40983 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 266
ID ADE04782 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 267
ID ADE92911 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 268
ID ADE67298 standard; protein; 105 AA.
DE Human PRO1186 amino acid sequence SEQ ID NO:371.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 269
ID ADE28070 standard; protein; 105 AA.
DE Human Zven 2.
PN US2003148317-A1.
PD 07-AUG-2003.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 270
ID ADG21620 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 271
ID ADG23261 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 272
ID ADE97596 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;

RESULT 273
ID ABG75089 standard; protein; 105 AA.
DE Prokineticin 1 (PROK1).
PN WO2003083073-A2.
PD 09-OCT-2003.
PA (FARB) BAYER PHARM CORP.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 274
ID ABG75086 standard; protein; 105 AA.
DE Human prokineticin 1 (PROK1).
PN WO2003083073-A2.
PD 09-OCT-2003.
PA (FARB) BAYER PHARM CORP.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 275
ID ADG80660 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 276
ID ADG80108 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 277
ID ADH55400 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 278
ID ADH55952 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 279
ID ADI35552 standard; protein; 105 AA.
DE Human PRO polypeptide #115.
PN US2003050457-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 280
ID ADI64171 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 281
ID ADI65120 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 282
ID ADI63619 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003087357-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 283
ID ADH82033 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 284
ID ADI00045 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003049682-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 285
ID ADH81481 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 286
ID ADJ71810 standard; protein; 105 AA.
DE Human prokineticin 1 protein.
PN WO2003040326-A2.
PD 15-MAY-2003.
PA (HYSE-) HYSEQ INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 287
ID ADM82650 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 288
ID ADN16049 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 289
ID ADN16678 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 290
ID ADN15497 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 291
ID ADN14945 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003087357-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;

PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 292
ID ADC48869 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003092888-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 293
ID ADC81207 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 294
ID ADE21040 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 295
ID ADE05884 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 296
ID ADD76655 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 297
ID ADD75113 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 298
ID ADD75859 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 299
ID ADD85091 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 300
ID ADD86917 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 301
ID ADE20794 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 302
ID ADE39091 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003096362-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 303
ID ADD88019 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 304
ID ADD86423 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 305
ID ADE05638 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 306
ID ADD73623 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003100711-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 307
ID ADE75871 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 308
ID ADD78463 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 309
ID ADE41422 standard; protein; 105 AA.
DE Human secreted/transmembrane PRO polypeptide #86.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.

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Query Match      100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 310
ID ADE23447 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 311
ID ADE21286 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 312
ID ADD77401 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 313
ID ADE20548 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 314
ID ADD75613 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003100064-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 315
ID ADD74129 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 316
ID ADD74375 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 317
ID ADD76105 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 318
ID ADH85597 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100721-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 319
ID ADE23999 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 320
ID ADE24642 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 321
ID ADD87467 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 322
ID ADE05146 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 323
ID ADD75359 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 324
ID ADD76903 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 325
ID ADD86671 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 326
ID ADE89333 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 327
ID ADD78139 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
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RESULT 328
ID ADE18472 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
FN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 498; DB 8; Length 105;
  Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 329
ID ADE88781 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
FN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 498; DB 8; Length 105;
  Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 330
ID ADD77647 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
FN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 498; DB 8; Length 105;
  Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 331
ID ADD77893 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
FN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 498; DB 8; Length 105;
  Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 332
ID ADD85351 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
FN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 498; DB 8; Length 105;
  Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 333
ID ADD73883 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
FN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 498; DB 8; Length 105;
  Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 334
ID ADD74621 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
FN US2003100713-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 498; DB 8; Length 105;
  Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 335
ID ADD77149 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
FN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 498; DB 8; Length 105;
  Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 336
ID ADD85843 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
FN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 498; DB 8; Length 105;
  Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 337
ID ADE50392 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
FN US2003100723-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 498; DB 8; Length 105;
  Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 338
ID ADD74867 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
FN US2003100724-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 498; DB 8; Length 105;
  Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 339
ID ADE94801 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
FN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 498; DB 8; Length 105;
  Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 340
ID ADE91212 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
FN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 498; DB 8; Length 105;
  Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 341
ID ADF35497 standard; protein; 105 AA.
DE Human PRO1186 polypeptide.
FN US2003194760-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 498; DB 8; Length 105;
  Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 342
ID ADE95353 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
FN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 498; DB 8; Length 105;
  Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 343
ID ADE93463 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
FN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 498; DB 8; Length 105;
  Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 344
ID ADF35044 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
FN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 498; DB 8; Length 105;
  Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 345
ID ADE92359 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
FN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 498; DB 8; Length 105;
  Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 346
ID ADE90660 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
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PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 347
ID ADE91807 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 348
ID ADG11747 standard; protein; 105 AA.
DE Human PRO1186 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 349
ID ADG05679 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003096959-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 350
ID ADG27233 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003096962-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 351
ID ADG02386 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 352
ID ADG22172 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 353
ID ADG20242 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 354
ID ADF98148 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 355
ID ADG24365 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207426-A1.

PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 356
ID ADF98719 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 357
ID ADG03550 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 358
ID ADF99271 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 359
ID ADG16856 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 360
ID ADG05315 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 361
ID ADG19582 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 362
ID ADG11296 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003096967-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 363
ID ADG13419 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 364
ID ADG08476 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207424-A1.
PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 365
ID ADG15646 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
FN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 366
ID ADG12075 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
FN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 367
ID ADF97044 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
FN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 368
ID ADG06229 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
FN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 369
ID ADG23813 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
FN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 370
ID ADG04102 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
FN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 371
ID ADG25003 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
FN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 372
ID ADF94632 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
FN US2003096964-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 373
ID ADG07300 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
FN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 374
ID ADG07852 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
FN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 375
ID ADG06728 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
FN US2003096966-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 376
ID ADG55347 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
FN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 377
ID ADG61011 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
FN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 378
ID ADG62115 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
FN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 379
ID ADG82316 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
FN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 380
ID ADG57555 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
FN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 381
ID ADG57003 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
FN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 382
ID ADG55899 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
FN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 383
ID ADG07300 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
FN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 383
ID ADG58659 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 384
ID ADG71025 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 385
ID ADH39072 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003096965-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 386
ID ADG58107 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 387
ID ADG53691 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 388
ID ADG71577 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 389
ID ADG81764 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207805-A1.
PD 06-NOV-2003.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 390
ID ADH19617 standard; protein; 105 AA.
DE Human secreted/transmembrane protein PRO1186.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 391
ID ADH30726 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 392
ID ADH28650 standard; protein; 105 AA.
DE Human PRO polypeptide #235.

ID ADH12093 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 393
ID ADG52515 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 394
ID ADG54243 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 395
ID ADG81212 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 396
ID ADG56451 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 397
ID ADH12717 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 398
ID ADH21110 standard; protein; 105 AA.
DE Human secreted/transmembrane protein PRO1186.
PN US2003224358-A1.
PD 04-DEC-2003.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 399
ID ADG61563 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 400
ID ADH20150 standard; protein; 105 AA.
DE Human secreted/transmembrane protein PRO1186.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 401
ID ADH28650 standard; protein; 105 AA.
DE Human PRO polypeptide #235.

PD US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 402
ID ADG54795 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 403
ID ADG59835 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 404
ID ADH43605 standard; protein; 105 AA.
DE Human PRO polypeptide #86.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 405
ID ADG34162 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2004006206-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 406
ID ADI81259 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 407
ID ADI33632 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 408
ID ADH69726 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 409
ID ADG10002 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 410
ID ADI15473 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207382-A1.

PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 411
ID ADG09350 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 412
ID ADI14805 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 413
ID ADI29887 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003096961-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 414
ID ADI18400 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 415
ID ADM27284 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2004044179-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 416
ID ADJ63681 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 417
ID ADJ77576 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 418
ID ADK82950 standard; protein; 105 AA.
DE Human PRO polypeptide #86.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 419
ID ADK66642 standard; protein; 105 AA.
DE Human PRO polypeptide #83.
PN US2004044180-A1.
PD 04-MAR-2004.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 420
ID ADJ65698 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 421
ID ADM27834 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 422
ID ADL68891 standard; protein; 105 AA.
DE Human extracellular signaling molecule (EXCS) -11 protein.
PN US2004048244-A1.
PD 11-MAR-2004.
PA (TANG/) TANG Y T.
PA (YUEH/) YUE H.
PA (LALP/) LAL P.
PA (BURE/) BURFORD N.
PA (BAND/) BANDMAN O.
PA (BAUG/) BAUGHN M R.
PA (AZIM/) AZIMZAI Y.
PA (LUDA/) LU D A M.
PA (ARVI/) ARVIZU C.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 423
ID ADN08155 standard; protein; 105 AA.
DE Human endocrine gland vascular endothelial growth factor.
PN DE1029379-A1.
PD 29-JAN-2004.
PA (SCHD) SCHERING AG.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 424
ID ADM42558 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 425
ID ADN41842 standard; protein; 105 AA.
DE Amino acid sequence of a human zven2 polypeptide.
PN WO2004032850-A2.
PD 22-APR-2004.
PA (ZIMO) ZYMOGENETICS INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 426
ID ADM28420 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 427
ID ADI95902 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 428
ID ADI96454 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 429
ID ADS86960 standard; protein; 105 AA.
DE Human Zven2 protein.
PN WO2004031367-A2.
PD 15-APR-2004.
PA (ZIMO) ZYMOGENETICS INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 430
ID ADS00464 standard; protein; 105 AA.
DE Human EG-VEGF, SEQ ID 8.
PN WO2004081229-A2.
PD 23-SEP-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 431
ID ADS86475 standard; protein; 105 AA.
DE Human ZAQ ligand protein related to eating disorders & obesity Seq 7.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 432
ID ADS75493 standard; protein; 105 AA.
DE Human prokineticin 2 receptor protein.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 433
ID ADS32406 standard; protein; 105 AA.
DE Novel human secreted and transmembrane protein PRO1186.
PN US2004203125-A1.
PD 14-OCT-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 434
ID ADT03390 standard; protein; 105 AA.
DE Human PRO polypeptide #235.
PN US2004214269-A1.
PD 28-OCT-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 435
ID ADY86164 standard; protein; 105 AA.
DE Human EG-VEGF, SEQ ID NO:2.
PN US2005064522-A1.
PD 24-MAR-2005.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 436
ID ADZ03441 standard; protein; 105 AA.
DE Human secreted/transmembrane PRO1186 protein.
PN US2005074837-A1.
PD 07-APR-2005.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 9; Length 105;

Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 437
ID ADZ88922 standard; protein; 105 AA.
DE Human prokineticin 1 isoform.
PN WO2005042717-A2.
PD 12-MAY-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 100.0%; Score 498; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 438
ID AEA38601 standard; protein; 105 AA.
DE Human secreted/transmembrane protein, #183.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 439
ID AEB14187 standard; protein; 105 AA.
DE Cancer cell diagnosis method-related human protein - SEQ ID 470.
PN US2005153396-A1.
PD 14-JUL-2005.
PA (BAKE/) BAKER K P.
PA (BERE/) BERESINI M.
PA (DEFO/) DEFORGE L.
PA (DESN/) DESNOYERS L.
PA (FILV/) FILVAROFF E.
PA (GAOW/) GAO W.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (SHER/) SHERWOOD S.
PA (SMIT/) SMITH V.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
PA (ZHAN/) ZHANG Z.
Query Match 100.0%; Score 498; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 440
ID AEB45588 standard; protein; 105 AA.
DE Human Zven2 protein, SEQ ID NO: 5.
PN US2005153322-A1.
PD 14-JUL-2005.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 100.0%; Score 498; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 441
ID AEC06124 standard; protein; 105 AA.
DE Human EG-VEGF protein.
PN WO2005076972-A2.
PD 23-AUG-2005.
PA (OHIS) UNIV OHIO STATE RES FOUND.
Query Match 100.0%; Score 498; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 442
ID AED08088 standard; protein; 105 AA.
DE Human Zven2 protein.
PN US2005214800-A1.
PD 29-SEP-2005.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 100.0%; Score 498; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 443
ID AED0616 standard; protein; 105 AA.
DE Rhesus monkey prokineticin 1 (PK1) SEQ ID NO 28.
PN WO2005091925-A2.
PD 06-OCT-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 100.0%; Score 498; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 444
ID AED6385 standard; protein; 105 AA.
DE Human PRO amino acid sequence, seq id 470.
PN US2005245730-A1.
PD 03-NOV-2005.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 445
ID AEG58332 standard; protein; 105 AA.
DE Human PRO1186 polypeptide SEQ ID NO: 470.
PN US2006073568-A1.
PD 06-APR-2006.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 10; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 446
ID AEA49352 standard; protein; 105 AA.
DE Human secreted polypeptide PRO1136, SEQ ID NO:166.
PN EPI659177-A2.
PD 24-MAY-2006.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 10; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 447
ID AEI43977 standard; protein; 105 AA.
DE Human cancer-related PRO protein amino acid sequence - SEQ ID 470.
PN US2006040351-A1.
PD 23-FEB-2006.
PA (BAKE/) BAKER K P.
PA (BERE/) BERESINI M.
PA (DEFO/) DEFORGE L.
PA (DESN/) DESNOYERS L.
PA (FILV/) FILVAROFF E.
PA (GAOW/) GAO W.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (SHER/) SHERWOOD S.
PA (SMIT/) SMITH V.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
PA (ZHAN/) ZHANG Z.
Query Match 100.0%; Score 498; DB 10; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 448
ID AEI24060 standard; protein; 105 AA.
DE Human secreted/transmembrane protein PRO1186, SEQ ID NO:470.
PN EPI672070-A2.
PD 21-JUN-2006.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 10; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 449
ID AEX48387 standard; protein; 105 AA.
DE Human PRO1186 amino acid sequence.
PN EPI686174-A1.
PD 02-AUG-2006.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 10; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 450
ID AEA62980 standard; protein; 105 AA.
DE Human PRO1186 polypeptide, SEQ ID NO: 166.
PN EPI700867-A2.
PD 13-SEP-2006.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 10; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 451

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ID ABL17020 standard; protein; 105 AA.
DE Human secreted polypeptide PRO1136, SEQ ID NO:166.
PN EPI702928-A2.
PD 20-SEP-2006.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 498; DB 10; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-46;
RESULT 452
ID ABL00448 standard; protein; 113 AA.
DE Recombinant N-terminal FLAG-tagged human prokineticin-1.
PN WO2006104713-A1.
PD 05-OCT-2006.
PA (JANC) JANSSEN PHARM NV.
PA (MISK/) MISKOWSKI T A.
Query Match 100.0%; Score 498; DB 10; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.3e-46;
RESULT 453
ID AEK60511 standard; protein; 114 AA.
DE Human prokineticin 1(N-terminally FLAG tagged).
PN WO2006102112-A2.
PD 28-SEP-2006.
PA (JANC) JANSSEN PHARM NV.
Query Match 100.0%; Score 498; DB 10; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.3e-46;
RESULT 454
ID ABJ05340 standard; protein; 125 AA.
DE Target fusion peptide production method-related protein #3.
PN WO200236762-A1.
PD 10-MAY-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 100.0%; Score 498; DB 5; Length 125;
Best Local Similarity 100.0%; Pred. No. 1.4e-46;
RESULT 455
ID ABJ05339 standard; protein; 130 AA.
DE Human PTH(1-34)-ZQA ligand fusion protein.
PN WO200236762-A1.
PD 10-MAY-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 100.0%; Score 498; DB 5; Length 130;
Best Local Similarity 100.0%; Pred. No. 1.5e-46;
RESULT 456
ID AAB70145 standard; protein; 86 AA.
DE Human G protein-coupled receptor protein-related sequence #1.
PN WO200116309-A1.
PD 08-MAR-2001.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 99.8%; Score 497; DB 4; Length 86;
Best Local Similarity 98.8%; Pred. No. 1.2e-46;
RESULT 457
ID AAO15528 standard; protein; 86 AA.
DE Human physiologically-active ZQA ligand-related protein 3.
PN WO200257443-A1.
PD 25-JUL-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 99.8%; Score 497; DB 5; Length 86;
Best Local Similarity 98.8%; Pred. No. 1.2e-46;
RESULT 458
ID ABR06305 standard; protein; 86 AA.
DE Human G protein-coupled receptor ZQA ligand protein SEQ ID NO:20.
PN WO200206483-A1.
PD 24-JAN-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 99.8%; Score 497; DB 5; Length 86;
Best Local Similarity 98.8%; Pred. No. 1.2e-46;
RESULT 459
ID ADD69103 standard; protein; 86 AA.
DE Human ZQA-related protein - SEQ ID 81.
PN WO200306860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 99.8%; Score 497; DB 7; Length 86;
Best Local Similarity 98.8%; Pred. No. 1.2e-46;
RESULT 460

ID ADR24004 standard; protein; 86 AA.
DE Human ZQA-1 ligand protein #2.
PN WO2004065419-A1.
PD 05-AUG-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 99.8%; Score 497; DB 8; Length 86;
Best Local Similarity 98.8%; Pred. No. 1.2e-46;
RESULT 461
ID ADS86469 standard; protein; 86 AA.
DE Human ZQA ligand protein related to eating disorders & obesity Seq 1.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 99.8%; Score 497; DB 8; Length 86;
Best Local Similarity 98.8%; Pred. No. 1.2e-46;
RESULT 462
ID ADZ58576 standard; protein; 86 AA.
DE Human ZQA-1 amino acid sequence - SEQ ID 3.
PN WO2005037870-A1.
PD 28-APR-2005.
PA (TAKE) TAKEDA PHARM CO LTD.
Query Match 99.8%; Score 497; DB 9; Length 86;
Best Local Similarity 98.8%; Pred. No. 1.2e-46;
RESULT 463
ID AAB70147 standard; protein; 105 AA.
DE Human G protein-coupled receptor protein-related sequence #3.
PN WO200116309-A1.
PD 08-MAR-2001.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 99.8%; Score 497; DB 4; Length 105;
Best Local Similarity 98.8%; Pred. No. 1.5e-46;
RESULT 464
ID AAM79066 standard; protein; 105 AA.
DE Human protein SEQ ID NO 1728.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 99.8%; Score 497; DB 4; Length 105;
Best Local Similarity 98.8%; Pred. No. 1.5e-46;
RESULT 465
ID AAG79596 standard; protein; 105 AA.
DE GSSP4 sequence.
PN WO200269689-A2.
PD 12-SEP-2002.
PA (GEST) GENSET.
Query Match 99.8%; Score 497; DB 5; Length 105;
Best Local Similarity 98.8%; Pred. No. 1.5e-46;
RESULT 466
ID AAO15526 standard; protein; 105 AA.
DE Human physiologically-active ZQA ligand-related protein 2.
PN WO200257443-A1.
PD 25-JUL-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 99.8%; Score 497; DB 5; Length 105;
Best Local Similarity 98.8%; Pred. No. 1.5e-46;
RESULT 467
ID ABR06307 standard; protein; 105 AA.
DE Human G protein-coupled receptor ZQA ligand protein SEQ ID NO:22.
PN WO200206483-A1.
PD 24-JAN-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 99.8%; Score 497; DB 5; Length 105;
Best Local Similarity 98.8%; Pred. No. 1.5e-46;
RESULT 468
ID ABP75987 standard; protein; 105 AA.
DE Human GENSET protein SEQ ID 194.
PN WO200283898-A1.
PD 24-OCT-2002.
PA (GEST) GENSET.
Query Match 99.8%; Score 497; DB 6; Length 105;
Best Local Similarity 98.8%; Pred. No. 1.5e-46;
RESULT 469
ID ADD69105 standard; protein; 105 AA.

DE Human ZAQ-related protein - SEQ ID 83.
PN WO200306860-A1.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 99.8%; Score 497; DB 7; Length 105;
Best Local Similarity 98.8%; Pred. No. 1.5e-46;
RESULT 470
ID ADS86473 standard; protein; 105 AA.
DE Human ZAQ ligand protein related to eating disorders & obesity Seq 5.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 99.8%; Score 497; DB 8; Length 105;
Best Local Similarity 98.8%; Pred. No. 1.5e-46;
RESULT 471
ID AED00619 standard; protein; 105 AA.
DE Human prokineticin 1 (PK1).
PN WO2005091925-A2.
PD 08-OCT-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 99.8%; Score 497; DB 9; Length 105;
Best Local Similarity 98.8%; Pred. No. 1.5e-46;
RESULT 472
ID AAB18475 standard; protein; 105 AA.
DE A human TANGO 266 polypeptide clone.
PN WO200502022-A1.
PD 08-SEP-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 99.4%; Score 495; DB 3; Length 105;
Best Local Similarity 98.8%; Pred. No. 2.5e-46;
RESULT 473
ID AAB18473 standard; protein; 105 AA.
DE A human TANGO 266 polypeptide clone.
PN WO200502022-A1.
PD 08-SEP-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 99.4%; Score 495; DB 3; Length 105;
Best Local Similarity 98.8%; Pred. No. 2.5e-46;
RESULT 474
ID AAB18474 standard; protein; 105 AA.
DE A human TANGO 266 polypeptide clone.
PN WO200502022-A1.
PD 08-SEP-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 99.4%; Score 495; DB 3; Length 105;
Best Local Similarity 98.8%; Pred. No. 2.5e-46;
RESULT 475
ID AAE24393 standard; protein; 85 AA.
DE Human prokineticin 1 mutant protein #2.
PN WO200236625-A2.
PD 10-MAY-2002.
PA (REGC) UNIV CALIFORNIA.
Query Match 99.2%; Score 494; DB 5; Length 85;
Best Local Similarity 100.0%; Pred. No. 2.6e-46;
RESULT 476
ID ADS75507 standard; protein; 85 AA.
DE Prokineticin receptor antagonist dela-PK1.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 99.2%; Score 494; DB 8; Length 85;
Best Local Similarity 100.0%; Pred. No. 2.6e-46;
RESULT 477
ID ADS75511 standard; protein; 86 AA.
DE Prokineticin receptor antagonist MV PK1.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 99.2%; Score 494; DB 8; Length 86;
Best Local Similarity 100.0%; Pred. No. 2.6e-46;
RESULT 478
ID ADZ88921 standard; protein; 105 AA.
DE Rhesus monkey prokineticin 2.

PN WO2005042717-A2.
PD 12-MAY-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 98.8%; Score 492; DB 9; Length 105;
Best Local Similarity 98.8%; Pred. No. 5.4e-46;
RESULT 479
ID ABE76151 standard; protein; 105 AA.
DE Human GENSET protein SEQ ID 477.
PN WO200283898-A1.
PD 24-OCT-2002.
PA (GEBST) GENSET.
Query Match 98.6%; Score 491; DB 6; Length 105;
Best Local Similarity 97.7%; Pred. No. 6.9e-46;
RESULT 480
ID ABP75986 standard; protein; 105 AA.
DE Human GENSET protein SEQ ID 193.
PN WO200283898-A1.
PD 24-OCT-2002.
PA (GEBST) GENSET.
Query Match 98.6%; Score 491; DB 6; Length 105;
Best Local Similarity 97.7%; Pred. No. 6.9e-46;
RESULT 481
ID AAE24394 standard; protein; 86 AA.
DE Human prokineticin 1 mutant protein #3.
PN WO200236625-A2.
PD 10-MAY-2002.
PA (REGC) UNIV CALIFORNIA.
Query Match 96.0%; Score 478; DB 5; Length 86;
Best Local Similarity 95.3%; Pred. No. 1.5e-44;
RESULT 482
ID ADS75508 standard; protein; 86 AA.
DE Prokineticin receptor related synthetic construct protein, SEQ ID 17.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 96.0%; Score 478; DB 8; Length 86;
Best Local Similarity 95.3%; Pred. No. 1.5e-44;
RESULT 483
ID ADZ88902 standard; protein; 82 AA.
DE Human prokineticin 1.
PN WO2005042717-A2.
PD 12-MAY-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 95.6%; Score 476; DB 9; Length 82;
Best Local Similarity 100.0%; Pred. No. 2.4e-44;
RESULT 484
ID ABE60513 standard; protein; 82 AA.
DE Human prokineticin 1 (C-terminal truncation).
PN WO2006102112-A2.
PD 28-SEP-2006.
PA (JANC) JANSSEN PHARM NV.
Query Match 95.6%; Score 476; DB 10; Length 82;
Best Local Similarity 100.0%; Pred. No. 2.4e-44;
RESULT 485
ID AEL00450 standard; protein; 82 AA.
DE Human prokineticin-1 ligand #2.
PN WO2006104713-A1.
PD 05-OCT-2006.
PA (JANC) JANSSEN PHARM NV.
PA (MISK/) MISKOWSKI T A.
Query Match 95.6%; Score 476; DB 10; Length 82;
Best Local Similarity 100.0%; Pred. No. 2.4e-44;
RESULT 486
ID ABE99154 standard; protein; 86 AA.
DE Rat ZAQ protein.
PN WO200262996-A1.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 95.0%; Score 473; DB 5; Length 86;
Best Local Similarity 91.9%; Pred. No. 5.3e-44;
RESULT 487
ID ABB06959 standard; protein; 86 AA.
DE Rat G protein-coupled receptor ZAQ ligand protein SEQ ID NO:49.

PN WO200216607-A1.
PD 28-FEB-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 95.0%; Score 473; DB 5; Length 86;
Best Local Similarity 91.9%; Pred. No. 5.3e-44;
RESULT 488
ID ADD69160 standard; protein; 86 AA.
DE Rat ZAQ-related protein - SEQ ID 138.
PN WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 95.0%; Score 473; DB 7; Length 86;
Best Local Similarity 91.9%; Pred. No. 5.3e-44;
RESULT 489
ID ADN43261 standard; protein; 86 AA.
DE Amino acid sequence of rat prokineticin 1 (PK1).
PN WO2004032851-A2.
PD 22-APR-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 95.0%; Score 473; DB 8; Length 86;
Best Local Similarity 91.9%; Pred. No. 5.3e-44;
RESULT 490
ID ADS86481 standard; protein; 86 AA.
DE Rat ZAQ ligand protein related to eating disorders & obesity Seq 13.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 95.0%; Score 473; DB 8; Length 86;
Best Local Similarity 91.9%; Pred. No. 5.3e-44;
RESULT 491
ID ADS75521 standard; protein; 86 AA.
DE Modified rat prokineticin 1 receptor, SEQ ID 30.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 95.0%; Score 473; DB 8; Length 86;
Best Local Similarity 91.9%; Pred. No. 5.3e-44;
RESULT 492
ID ABB99151 standard; protein; 105 AA.
DE Rat ZAQ protein.
PN WO200262996-A1.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 95.0%; Score 473; DB 5; Length 105;
Best Local Similarity 91.9%; Pred. No. 6.5e-44;
RESULT 493
ID ABB06956 standard; protein; 105 AA.
DE Rat G protein-coupled receptor ZAQ ligand protein SEQ ID NO:43.
PN WO200216607-A1.
PD 28-FEB-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 95.0%; Score 473; DB 5; Length 105;
Best Local Similarity 91.9%; Pred. No. 6.5e-44;
RESULT 494
ID ADD69154 standard; protein; 105 AA.
DE Rat ZAQ-related protein - SEQ ID 132.
PN WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 95.0%; Score 473; DB 7; Length 105;
Best Local Similarity 91.9%; Pred. No. 6.5e-44;
RESULT 495
ID ADS86487 standard; protein; 105 AA.
DE Rat ZAQ ligand protein related to eating disorders & obesity Seq 19.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 95.0%; Score 473; DB 8; Length 105;
Best Local Similarity 91.9%; Pred. No. 6.5e-44;
RESULT 496
ID ABB99156 standard; protein; 86 AA.
DE Rat ZAQ protein.
PN WO200262996-A1.

PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 94.2%; Score 469; DB 5; Length 86;
Best Local Similarity 90.7%; Pred. No. 1.5e-43;
RESULT 497
ID ABB06961 standard; protein; 86 AA.
DE Rat G protein-coupled receptor ZAQ ligand protein SEQ ID NO:53.
PN WO200216607-A1.
PD 28-FEB-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 94.2%; Score 469; DB 5; Length 86;
Best Local Similarity 90.7%; Pred. No. 1.5e-43;
RESULT 498
ID ADD69164 standard; protein; 86 AA.
DE Rat ZAQ-related protein - SEQ ID 142.
PN WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 94.2%; Score 469; DB 7; Length 86;
Best Local Similarity 90.7%; Pred. No. 1.5e-43;
RESULT 499
ID ADS86485 standard; protein; 86 AA.
DE Rat ZAQ ligand protein related to eating disorders & obesity Seq 17.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 94.2%; Score 469; DB 8; Length 86;
Best Local Similarity 90.7%; Pred. No. 1.5e-43;
RESULT 500
ID ABB99153 standard; protein; 105 AA.
DE Rat ZAQ protein.
PN WO200262996-A1.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 94.2%; Score 469; DB 5; Length 105;
Best Local Similarity 90.7%; Pred. No. 1.8e-43;
RESULT 501
ID ABB06958 standard; protein; 105 AA.
DE Rat G protein-coupled receptor ZAQ ligand protein SEQ ID NO:47.
PN WO200216607-A1.
PD 28-FEB-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 94.2%; Score 469; DB 5; Length 105;
Best Local Similarity 90.7%; Pred. No. 1.8e-43;
RESULT 502
ID ADD69158 standard; protein; 105 AA.
DE Rat ZAQ-related protein - SEQ ID 136.
PN WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 94.2%; Score 469; DB 7; Length 105;
Best Local Similarity 90.7%; Pred. No. 1.8e-43;
RESULT 503
ID ADS86491 standard; protein; 105 AA.
DE Rat ZAQ ligand protein related to eating disorders & obesity Seq 23.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 94.2%; Score 469; DB 8; Length 105;
Best Local Similarity 90.7%; Pred. No. 1.8e-43;
RESULT 504
ID ABB99155 standard; protein; 86 AA.
DE Rat ZAQ protein.
PN WO200262996-A1.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 93.8%; Score 467; DB 5; Length 86;
Best Local Similarity 90.7%; Pred. No. 2.4e-43;
RESULT 505
ID ABB06960 standard; protein; 86 AA.
DE Rat G protein-coupled receptor ZAQ ligand protein SEQ ID NO:51.
PN WO200216607-A1.
PD 28-FEB-2002.

PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 93.8%; Score 467; DB 5; Length 86;
Best Local Similarity 90.7%; Pred. No. 2.4e-43;
RESULT 506
ID ADD69162 standard; protein; 86 AA.
DE Rat ZAQ-related protein - SEQ ID 140.
PN WO200306860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 93.8%; Score 467; DB 7; Length 86;
Best Local Similarity 90.7%; Pred. No. 2.4e-43;
RESULT 507
ID ADS86483 standard; protein; 86 AA.
DE Rat ZAQ ligand protein related to eating disorders & obesity Seq 15.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 93.8%; Score 467; DB 8; Length 86;
Best Local Similarity 90.7%; Pred. No. 2.4e-43;
RESULT 508
ID ABB99152 standard; protein; 105 AA.
DE Rat ZAQ protein.
PN WO200262996-A1.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 93.8%; Score 467; DB 5; Length 105;
Best Local Similarity 90.7%; Pred. No. 3e-43;
RESULT 509
ID ABB6957 standard; protein; 105 AA.
DE Rat G protein-coupled receptor ZAQ ligand protein SEQ ID NO:45.
PN WO200216607-A1.
PD 28-FEB-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 93.8%; Score 467; DB 5; Length 105;
Best Local Similarity 90.7%; Pred. No. 3e-43;
RESULT 510
ID ADD69156 standard; protein; 105 AA.
DE Rat ZAQ-related protein - SEQ ID 134.
PN WO200306860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 93.8%; Score 467; DB 7; Length 105;
Best Local Similarity 90.7%; Pred. No. 3e-43;
RESULT 511
ID ADS86489 standard; protein; 105 AA.
DE Rat ZAQ ligand protein related to eating disorders & obesity Seq 21.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 93.8%; Score 467; DB 8; Length 105;
Best Local Similarity 90.7%; Pred. No. 3e-43;
RESULT 512
ID ABB99149 standard; protein; 86 AA.
DE Mouse ZAQ protein.
PN WO200262996-A1.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 91.4%; Score 455; DB 5; Length 86;
Best Local Similarity 88.4%; Pred. No. 5e-42;
RESULT 513
ID ADD69131 standard; protein; 86 AA.
DE Murine ZAQ-related protein - SEQ ID 109.
PN WO200306860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 91.4%; Score 455; DB 7; Length 86;
Best Local Similarity 88.4%; Pred. No. 5e-42;
RESULT 514
ID ADO05361 standard; protein; 86 AA.
DE Mouse prokineticin 1 (PK1), SEQ ID NO:10.
PN WO2003088904-A2.
PD 30-OCT-2003.
PA (REGC) UNIV CALIFORNIA.

Query Match 91.4%; Score 455; DB 7; Length 86;
Best Local Similarity 88.4%; Pred. No. 5e-42;
RESULT 515
ID ADN43259 standard; protein; 86 AA.
DE Amino acid sequence of murine prokineticin 1 (PK1).
PN WO2004032851-A2.
PD 22-APR-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 91.4%; Score 455; DB 8; Length 86;
Best Local Similarity 88.4%; Pred. No. 5e-42;
RESULT 516
ID ADS86477 standard; protein; 86 AA.
DE Murine ZAQ ligand protein related to eating disorders & obesity Seq 9.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 91.4%; Score 455; DB 8; Length 86;
Best Local Similarity 88.4%; Pred. No. 5e-42;
RESULT 517
ID ADS75519 standard; protein; 86 AA.
DE Modified mouse prokineticin 1 receptor, SEQ ID 28.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 91.4%; Score 455; DB 8; Length 86;
Best Local Similarity 88.4%; Pred. No. 5e-42;
RESULT 518
ID ADM00760 standard; protein; 86 AA.
DE Amino acid sequence of murine prokineticin 1 (PK1).
PN WO2004113361-A2.
PD 29-DEC-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 91.4%; Score 455; DB 9; Length 86;
Best Local Similarity 88.4%; Pred. No. 5e-42;
RESULT 519
ID ADZ88903 standard; protein; 86 AA.
DE Mouse prokineticin 1.
PN WO2005042717-A2.
PD 12-MAY-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 91.4%; Score 455; DB 9; Length 86;
Best Local Similarity 88.4%; Pred. No. 5e-42;
RESULT 520
ID AED00600 standard; protein; 86 AA.
DE Mouse prokineticin 1 (PK1) SEQ ID NO 12.
PN WO2005091925-A2.
PD 06-OCT-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 91.4%; Score 455; DB 9; Length 86;
Best Local Similarity 88.4%; Pred. No. 5e-42;
RESULT 521
ID AEJ43368 standard; protein; 86 AA.
DE Mouse prokineticin 1 (PK1) protein, SEQ ID NO: 10.
PN US2006172935-A1.
PD 03-AUG-2006.
PA (ZHOU//) ZHOU Q.
PA (BULL//) BULLOCK C M.
PA (SIEG//) SIEGEL J.
Query Match 91.4%; Score 455; DB 10; Length 86;
Best Local Similarity 88.4%; Pred. No. 5e-42;
RESULT 522
ID ABB99148 standard; protein; 105 AA.
DE Mouse ZAQ protein.
PN WO200262996-A1.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 91.4%; Score 455; DB 5; Length 105;
Best Local Similarity 88.4%; Pred. No. 6.2e-42;
RESULT 523
ID ADD69129 standard; protein; 105 AA.
DE Murine ZAQ-related protein - SEQ ID 107.
PN WO200306860-A1.
PD 14-AUG-2003.

PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 82.9%; Score 413; DB 9; Length 86;
Best Local Similarity 76.7%; Pred. No. 2e-37;
RESULT 533
ID AEJ43379 standard; protein; 86 AA.
DE Human PK1 exons 1 and 2 - PK2 exon 3 fusion protein.
PN US2006172935-A1.
PD 03-AUG-2006.
PA (ZHOU//) ZHOU Q.
PA (BULL//) BULLOCK C M.
PA (SIEG//) SIEGEL J.
Query Match 82.9%; Score 413; DB 10; Length 86;
Best Local Similarity 76.7%; Pred. No. 2e-37;
RESULT 534
ID AAE24390 standard; protein; 81 AA.
DE Human prokineticin chimera 12 protein.
PN WO200236625-A2.
PD 10-MAY-2002.
PA (REGC) UNIV CALIFORNIA.
Query Match 75.5%; Score 376; DB 5; Length 81;
Best Local Similarity 84.4%; Pred. No. 2.2e-33;
RESULT 535
ID ADO05371 standard; protein; 81 AA.
DE PK1/PK2 chimeric protein, SEQ ID NO:20.
PN WO2003088904-A2.
PD 30-OCT-2003.
PA (REGC) UNIV CALIFORNIA.
Query Match 75.5%; Score 376; DB 7; Length 81;
Best Local Similarity 84.4%; Pred. No. 2.2e-33;
RESULT 536
ID ADN43266 standard; protein; 81 AA.
DE Amino acid sequence of human prokineticin 1 (PK1)/PK2 chimera.
PN WO2004032851-A2.
PD 22-APR-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 75.5%; Score 376; DB 8; Length 81;
Best Local Similarity 84.4%; Pred. No. 2.2e-33;
RESULT 537
ID ADS75504 standard; protein; 81 AA.
DE Modified human prokineticin chimeric receptor, PK1-PK2.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 75.5%; Score 376; DB 8; Length 81;
Best Local Similarity 84.4%; Pred. No. 2.2e-33;
RESULT 538
ID ADW00764 standard; protein; 81 AA.
DE Amino acid sequence of a PK1/PK2 chimera.
PN WO2004113361-A2.
PD 29-DEC-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 75.5%; Score 376; DB 9; Length 81;
Best Local Similarity 84.4%; Pred. No. 2.2e-33;
RESULT 539
ID AD288907 standard; protein; 81 AA.
DE Human prokineticin 1/prokineticin 2 chimera.
PN WO2005042717-A2.
PD 12-MAY-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 75.5%; Score 376; DB 9; Length 81;
Best Local Similarity 84.4%; Pred. No. 2.2e-33;
RESULT 540
ID AED00604 standard; protein; 81 AA.
DE Human PK1-PK2 chimera SEQ ID NO 16.
PN WO2005091925-A2.
PD 06-OCT-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 75.5%; Score 376; DB 9; Length 81;
Best Local Similarity 84.4%; Pred. No. 2.2e-33;
RESULT 541
ID AEJ43378 standard; protein; 81 AA.
DE Human PK1 exons 1 and 2 - PK2 exon 3 fusion protein.
PN US2006172935-A1.
PD 03-AUG-2006.

PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 91.4%; Score 455; DB 7; Length 105;
Best Local Similarity 88.4%; Pred. No. 6.2e-42;
RESULT 524
ID ADS00466 standard; protein; 105 AA.
DE Murine EG-VEGF, SEQ ID 10.
PN WO2004081229-A2.
PD 23-SEP-2004.
PA (GETH) GENENTECH INC.
Query Match 91.4%; Score 455; DB 8; Length 105;
Best Local Similarity 88.4%; Pred. No. 6.2e-42;
RESULT 525
ID ADS86479 standard; protein; 105 AA.
DE Murine ZAQ ligand protein related to eating disorders & obesity Seq 11.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 91.4%; Score 455; DB 8; Length 105;
Best Local Similarity 88.4%; Pred. No. 6.2e-42;
RESULT 526
ID AAE24391 standard; protein; 86 AA.
DE Human prokineticin chimera 21 protein.
PN WO200236625-A2.
PD 10-MAY-2002.
PA (REGC) UNIV CALIFORNIA.
Query Match 82.9%; Score 413; DB 5; Length 86;
Best Local Similarity 76.7%; Pred. No. 2e-37;
RESULT 527
ID ADO05372 standard; protein; 86 AA.
DE PK2/PK1 chimeric protein, SEQ ID NO:21.
PN WO2003088904-A2.
PD 30-OCT-2003.
PA (REGC) UNIV CALIFORNIA.
Query Match 82.9%; Score 413; DB 7; Length 86;
Best Local Similarity 76.7%; Pred. No. 2e-37;
RESULT 528
ID ADN43267 standard; protein; 86 AA.
DE Amino acid sequence of human prokineticin 2 (PK2)/PK1 chimera.
PN WO2004032851-A2.
PD 22-APR-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 82.9%; Score 413; DB 8; Length 86;
Best Local Similarity 76.7%; Pred. No. 2e-37;
RESULT 529
ID ADS75505 standard; protein; 86 AA.
DE Modified human prokineticin chimeric receptor, PK2-PK1.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 82.9%; Score 413; DB 8; Length 86;
Best Local Similarity 76.7%; Pred. No. 2e-37;
RESULT 530
ID ADW00765 standard; protein; 86 AA.
DE Amino acid sequence of a PK2/PK1 chimera.
PN WO2004113361-A2.
PD 29-DEC-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 82.9%; Score 413; DB 9; Length 86;
Best Local Similarity 76.7%; Pred. No. 2e-37;
RESULT 531
ID AD288908 standard; protein; 86 AA.
DE Human prokineticin 2/prokineticin 1 chimera.
PN WO2005042717-A2.
PD 12-MAY-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 82.9%; Score 413; DB 9; Length 86;
Best Local Similarity 76.7%; Pred. No. 2e-37;
RESULT 532
ID AED00605 standard; protein; 86 AA.
DE Human PK2-PK1 chimera SEQ ID NO 17.
PN WO2005091925-A2.
PD 06-OCT-2005.
PA (REGC) UNIV CALIFORNIA.

PA (ZHOU/) ZHOU Q.
PA (BULL/) BULLOCK C M.
PA (SIEG/) SIEGEL J.
Query Match 75.5%; Score 376; DB 10; Length 81;
Best Local Similarity 84.4%; Pred. No. 2.2e-33;
RESULT 542
ID RAY11745 standard; protein; 81 AA.
DE Human 5' EST secreted protein SEQ ID NO: 345.
FN WO9906550-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 72.5%; Score 361; DB 2; Length 81;
Best Local Similarity 98.4%; Pred. No. 9.7e-32;
RESULT 543
ID AAG00617 standard; protein; 80 AA.
DE Human secreted protein, SEQ ID NO: 4698.
FN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 71.7%; Score 357; DB 3; Length 80;
Best Local Similarity 98.4%; Pred. No. 2.6e-31;
RESULT 544
ID ABG94399 standard; protein; 80 AA.
DE Dendroaspis polylepsis MIT1 protein.
FN WO200262944-A2.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 63.3%; Score 315; DB 5; Length 80;
Best Local Similarity 62.3%; Pred. No. 1.1e-26;
RESULT 545
ID ABH99160 standard; protein; 80 AA.
DE Polyileps MIT1.
FN WO200262996-A1.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 63.3%; Score 315; DB 5; Length 80;
Best Local Similarity 62.3%; Pred. No. 1.1e-26;
RESULT 546
ID ABB6310 standard; protein; 80 AA.
DE Dendroaspis polylepsis MIT1 protein sequence SEQ ID NO:34.
FN WO200206483-A1.
PD 24-JAN-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 63.3%; Score 315; DB 5; Length 80;
Best Local Similarity 62.3%; Pred. No. 1.1e-26;
RESULT 547
ID ADD69043 standard; protein; 80 AA.
DE Dendroaspis polylepsis MIT1-related protein.
FN WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 63.3%; Score 315; DB 7; Length 80;
Best Local Similarity 62.3%; Pred. No. 1.1e-26;
RESULT 548
ID ADJ71812 standard; protein; 80 AA.
DE Black mamba intestinal toxin protein.
FN WO2003040326-A2.
PD 15-MAY-2003.
PA (HYSE-) HYSE INC.
Query Match 63.3%; Score 315; DB 7; Length 80;
Best Local Similarity 62.3%; Pred. No. 1.1e-26;
RESULT 549
ID ADO05364 standard; protein; 80 AA.
DE Snake prokineticin orthologue MIT1, SEQ ID NO:13.
FN WO2003088904-A2.
PD 30-OCT-2003.
PA (REGC) UNIV CALIFORNIA.
Query Match 63.3%; Score 315; DB 7; Length 80;
Best Local Similarity 62.3%; Pred. No. 1.1e-26;
RESULT 550
ID ADS86504 standard; protein; 80 AA.
DE D polyileps MIT1 protein related to eating disorders & obesity Seq 36.
FN WO2004084945-A1.

PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 63.3%; Score 315; DB 8; Length 80;
Best Local Similarity 62.3%; Pred. No. 1.1e-26;
RESULT 551
ID ADM00763 standard; protein; 80 AA.
DE Amino acid sequence of snake MIT1.
FN WO2004113361-A2.
PD 29-DEC-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 63.3%; Score 315; DB 9; Length 80;
Best Local Similarity 62.3%; Pred. No. 1.1e-26;
RESULT 552
ID AD28906 standard; protein; 80 AA.
DE Snake prokineticin 1 homologue, MIT1.
FN WO2005042717-A2.
PD 12-MAY-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 63.3%; Score 315; DB 9; Length 80;
Best Local Similarity 62.3%; Pred. No. 1.1e-26;
RESULT 553
ID AED00603 standard; protein; 80 AA.
DE Snake MIT1 SEQ ID NO 15.
FN WO2005091925-A2.
PD 06-OCT-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 63.3%; Score 315; DB 9; Length 80;
Best Local Similarity 62.3%; Pred. No. 1.1e-26;
RESULT 554
ID AEJ43371 standard; protein; 80 AA.
DE Snake MIT1 protein, SEQ ID NO: 13.
FN US2006172935-A1.
PD 03-AUG-2006.
PA (ZHOU/) ZHOU Q.
PA (BULL/) BULLOCK C M.
PA (SIEG/) SIEGEL J.
Query Match 63.3%; Score 315; DB 10; Length 80;
Best Local Similarity 62.3%; Pred. No. 1.1e-26;
RESULT 555
ID ADV86167 standard; protein; 79 AA.
DE Black mamba venom protein A (VPRA), SEQ ID NO:5.
FN US2005064522-A1.
PD 24-MAR-2005.
PA (GETH) GENENTECH INC.
Query Match 62.6%; Score 311.5; DB 9; Length 79;
Best Local Similarity 63.6%; Pred. No. 2.6e-26;
RESULT 556
ID ADN43263 standard; protein; 81 AA.
DE Amino acid sequence of MIT1.
FN WO2004032851-A2.
PD 22-APR-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 62.3%; Score 310.5; DB 8; Length 81;
Best Local Similarity 62.8%; Pred. No. 3.4e-26;
RESULT 557
ID ADS75503 standard; protein; 81 AA.
DE Modified black mamba prokineticin receptor, MIT1.
FN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 62.3%; Score 310.5; DB 8; Length 81;
Best Local Similarity 62.8%; Pred. No. 3.4e-26;
RESULT 558
ID ABG94400 standard; protein; 80 AA.
DE C-terminal Lys truncated human GPCR ligand Bv8 protein.
FN WO200262944-A2.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 58.4%; Score 291; DB 5; Length 80;
Best Local Similarity 58.4%; Pred. No. 4.6e-24;
RESULT 559
ID ADB69044 standard; protein; 80 AA.
DE Human Bv8-related protein - SEQ ID 22.

PN WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 58.4%; Score 291; DB 7; Length 80;
Best Local Similarity 58.4%; Pred. No. 4.6e-24;
RESULT 560
ID ABB94398 standard; protein; 81 AA.
DE Human GPCR ligand Bv8 protein sequence #2.
PN WO200262944-A2.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 58.4%; Score 291; DB 5; Length 81;
Best Local Similarity 58.4%; Pred. No. 4.7e-24;
RESULT 561
ID AAO15530 standard; protein; 81 AA.
DE Human physiologically-active ZAQ ligand-related protein 5.
PN WO200257443-A1.
PD 25-JUL-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 58.4%; Score 291; DB 5; Length 81;
Best Local Similarity 58.4%; Pred. No. 4.7e-24;
RESULT 562
ID AAE24385 standard; protein; 81 AA.
DE Human prokineticin 2 mature protein.
PN WO200236625-A2.
PD 10-MAY-2002.
PA (REGC) UNIV CALIFORNIA.
Query Match 58.4%; Score 291; DB 5; Length 81;
Best Local Similarity 58.4%; Pred. No. 4.7e-24;
RESULT 563
ID ADD69041 standard; protein; 81 AA.
DE Human Bv8-related protein - SEQ ID 19.
PN WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 58.4%; Score 291; DB 7; Length 81;
Best Local Similarity 58.4%; Pred. No. 4.7e-24;
RESULT 564
ID ADO05356 standard; protein; 81 AA.
DE Human major prokineticin 2 (PK2), SEQ ID NO:5.
PN WO2003088904-A2.
PD 30-OCT-2003.
PA (REGC) UNIV CALIFORNIA.
Query Match 58.4%; Score 291; DB 7; Length 81;
Best Local Similarity 58.4%; Pred. No. 4.7e-24;
RESULT 565
ID ADN43258 standard; protein; 81 AA.
DE Amino acid sequence of human prokineticin 2 (PK2) isoform 2.
PN WO2004032851-A2.
PD 22-APR-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 58.4%; Score 291; DB 8; Length 81;
Best Local Similarity 58.4%; Pred. No. 4.7e-24;
RESULT 566
ID ADR24005 standard; protein; 81 AA.
DE Human ZAQ-1 ligand-associated protein.
PN WO2004065419-A1.
PD 05-AUG-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 58.4%; Score 291; DB 8; Length 81;
Best Local Similarity 58.4%; Pred. No. 4.7e-24;
RESULT 567
ID ADS86493 standard; protein; 81 AA.
DE Human Bv8 protein related to eating disorders & obesity Seq 25.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 58.4%; Score 291; DB 8; Length 81;
Best Local Similarity 58.4%; Pred. No. 4.7e-24;
RESULT 568
ID ADS75497 standard; protein; 81 AA.
DE Human prokineticin 1 receptor protein isoform 1.
PN WO2004087054-A2.

PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 58.4%; Score 291; DB 8; Length 81;
Best Local Similarity 58.4%; Pred. No. 4.7e-24;
RESULT 569
ID ADW00755 standard; protein; 81 AA.
DE Amino acid sequence of human prokineticin 2 (PK2).
PN WO2004113361-A2.
PD 29-DEC-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 58.4%; Score 291; DB 9; Length 81;
Best Local Similarity 58.4%; Pred. No. 4.7e-24;
RESULT 570
ID ADZ88900 standard; protein; 81 AA.
DE Human prokineticin 2.
PN WO2005042717-A2.
PD 12-MAY-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 58.4%; Score 291; DB 9; Length 81;
Best Local Similarity 58.4%; Pred. No. 4.7e-24;
RESULT 571
ID ADZ58574 standard; protein; 81 AA.
DE Human ZAQ-2 amino acid sequence - SEQ ID 1.
PN WO2005037870-A1.
PD 28-APR-2005.
PA (TAKE) TAKEDA PHARM CO LTD.
Query Match 58.4%; Score 291; DB 9; Length 81;
Best Local Similarity 58.4%; Pred. No. 4.7e-24;
RESULT 572
ID AEB45593 standard; protein; 81 AA.
DE Human Zven1 protein fragment.
PN US2005153322-A1.
PD 14-JUL-2005.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 58.4%; Score 291; DB 9; Length 81;
Best Local Similarity 58.4%; Pred. No. 4.7e-24;
RESULT 573
ID AED00597 standard; protein; 81 AA.
DE Human prokineticin receptor 2 (PKR2) SEQ ID NO 9.
PN WO2005091925-A2.
PD 06-OCT-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 58.4%; Score 291; DB 9; Length 81;
Best Local Similarity 58.4%; Pred. No. 4.7e-24;
RESULT 574
ID AEU43363 standard; protein; 81 AA.
DE Human prokineticin 2 (PK2) protein, SEQ ID NO: 5.
PN US2006172935-A1.
PD 03-AUG-2006.
PA (ZHOU/) ZHOU Q.
PA (BULL/) BULLOCK C M.
PA (SIEG/) SIEGEL J.
Query Match 58.4%; Score 291; DB 10; Length 81;
Best Local Similarity 58.4%; Pred. No. 4.7e-24;
RESULT 575
ID ADY86166 standard; protein; 100 AA.
DE Human Bv8 homolog protein, SEQ ID NO:4.
PN US2005064522-A1.
PD 24-MAR-2005.
PA (GETH) GENENTECH INC.
Query Match 58.4%; Score 291; DB 9; Length 100;
Best Local Similarity 58.4%; Pred. No. 5.8e-24;
RESULT 576
ID AAB68426 standard; protein; 108 AA.
DE Amino acid sequence of a human Zven1 polypeptide.
PN WO200136465-A2.
PD 25-MAY-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 58.4%; Score 291; DB 4; Length 108;
Best Local Similarity 58.4%; Pred. No. 6.3e-24;
RESULT 577
ID ABG94397 standard; protein; 108 AA.
DE Human GPCR ligand Bv8 protein sequence #1.

PD WO200262944-A2.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 58.4%; Score 291; DB 5; Length 108;
Best Local Similarity 58.4%; Pred. No. 6.3e-24;
RESULT 578
ID AAO15531 standard; protein; 108 AA.
DE Human physiologically-active ZAQ ligand-related protein 6.
FN WO200257443-A1.
PD 25-JUL-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 58.4%; Score 291; DB 5; Length 108;
Best Local Similarity 58.4%; Pred. No. 6.3e-24;
RESULT 579
ID AAE24384 standard; protein; 108 AA.
DE Human prokineticin 2 precursor protein.
FN WO200236625-A2.
PD 10-MAY-2002.
PA (REGC) UNIV CALIFORNIA.
Query Match 58.4%; Score 291; DB 5; Length 108;
Best Local Similarity 58.4%; Pred. No. 6.3e-24;
RESULT 580
ID ABU07602 standard; protein; 108 AA.
DE Human ZVEN1.
FN US6485938-B1.
PD 26-NOV-2002.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 58.4%; Score 291; DB 6; Length 108;
Best Local Similarity 58.4%; Pred. No. 6.3e-24;
RESULT 581
ID AAB36789 standard; protein; 108 AA.
DE Human Bv8 homologue splice variant protein.
FN WO2003020892-A2.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 58.4%; Score 291; DB 6; Length 108;
Best Local Similarity 58.4%; Pred. No. 6.3e-24;
RESULT 582
ID ADP69039 standard; protein; 108 AA.
DE Human Bv8-related protein - SEQ ID 17.
FN WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 58.4%; Score 291; DB 7; Length 108;
Best Local Similarity 58.4%; Pred. No. 6.3e-24;
RESULT 583
ID ADF28067 standard; protein; 108 AA.
DE Human Zven 1.
FN US2003148317-A1.
PD 07-AUG-2003.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 58.4%; Score 291; DB 7; Length 108;
Best Local Similarity 58.4%; Pred. No. 6.3e-24;
RESULT 584
ID ABG75087 standard; protein; 108 AA.
DE Human prokineticin 2 (PROK2).
FN WO2003083073-A2.
PD 09-OCT-2003.
PA (FARB) BAYER PHARM CORP.
Query Match 58.4%; Score 291; DB 7; Length 108;
Best Local Similarity 58.4%; Pred. No. 6.3e-24;
RESULT 585
ID ADJ71811 standard; protein; 108 AA.
DE Human prokineticin 2 protein.
FN WO2003040326-A2.
PD 15-MAY-2003.
PA (HYSE-) HYSEQ INC.
Query Match 58.4%; Score 291; DB 7; Length 108;
Best Local Similarity 58.4%; Pred. No. 6.3e-24;
RESULT 586
ID ADN41839 standard; protein; 108 AA.
DE Amino acid sequence of a human Zven1 polypeptide.
FN WO2004032850-A2.

PD 22-APR-2004.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 58.4%; Score 291; DB 8; Length 108;
Best Local Similarity 58.4%; Pred. No. 6.3e-24;
RESULT 587
ID ADO24421 standard; protein; 108 AA.
DE Human PRO28691 protein SEQ ID NO:60.
FN WO2004043397-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 58.4%; Score 291; DB 8; Length 108;
Best Local Similarity 58.4%; Pred. No. 6.3e-24;
RESULT 588
ID ADS86957 standard; protein; 108 AA.
DE Human Zven1 protein.
FN WO2004031367-A2.
PD 15-APR-2004.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 58.4%; Score 291; DB 8; Length 108;
Best Local Similarity 58.4%; Pred. No. 6.3e-24;
RESULT 589
ID ADS00460 standard; protein; 108 AA.
DE Human Bv8 homologue variant #2, SEQ ID 4.
FN WO2004081229-A2.
PD 23-SEP-2004.
PA (GETH) GENENTECH INC.
Query Match 58.4%; Score 291; DB 8; Length 108;
Best Local Similarity 58.4%; Pred. No. 6.3e-24;
RESULT 590
ID ADS86495 standard; protein; 108 AA.
DE Human Bv8 protein related to eating disorders & obesity Seq 27.
FN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 58.4%; Score 291; DB 8; Length 108;
Best Local Similarity 58.4%; Pred. No. 6.3e-24;
RESULT 591
ID ADS75496 standard; protein; 108 AA.
DE Human prokineticin 1 receptor protein isoform 2.
FN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 58.4%; Score 291; DB 8; Length 108;
Best Local Similarity 58.4%; Pred. No. 6.3e-24;
RESULT 592
ID AEA23706 standard; protein; 108 AA.
DE Human PRO polypeptide SEQ ID NO 248.
FN WO2005051988-A2.
PD 09-JUN-2005.
PA (GETH) GENENTECH INC.
Query Match 58.4%; Score 291; DB 9; Length 108;
Best Local Similarity 58.4%; Pred. No. 6.3e-24;
RESULT 593
ID AEB45585 standard; protein; 108 AA.
DE Human Zven1 protein, SEQ ID NO: 2.
FN US2005153322-A1.
PD 14-JUL-2005.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 58.4%; Score 291; DB 9; Length 108;
Best Local Similarity 58.4%; Pred. No. 6.3e-24;
RESULT 594
ID AED08085 standard; protein; 108 AA.
DE Human Zven1 protein.
FN US2005214800-A1.
PD 29-SEP-2005.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 58.4%; Score 291; DB 9; Length 108;
Best Local Similarity 58.4%; Pred. No. 6.3e-24;
RESULT 595
ID ADN41861 standard; protein; 116 AA.
DE Amino acid sequence of a human Zven1 with Glu-Glu tag and Gly linker.
FN WO2004032850-A2.
PD 22-APR-2004.

PA (ZYMO) ZYMOGENETICS INC.
Query Match 58.4%; Score 291; DB 8; Length 116;
Best Local Similarity 58.4%; Pred. No. 6.8e-24;
RESULT 596
ID ADS86981 standard; protein; 116 AA.
DE Human Zvemi protein expressed in baculovirus cell expression system.
PN WO2004031367-A2.
PD 15-APR-2004.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 58.4%; Score 291; DB 8; Length 116;
Best Local Similarity 58.4%; Pred. No. 6.8e-24;
RESULT 597
ID ARL00451 standard; protein; 116 AA.
DE Recombinant N-terminal FLAG-tagged human prokineticin-2.
PN WO2006104713-A1.
PD 05-OCT-2006.
PA (JANC) JANSSEN PHARM NV.
(MISK/) MISKOWSKI T A.
Query Match 58.4%; Score 291; DB 10; Length 116;
Best Local Similarity 58.4%; Pred. No. 6.8e-24;
RESULT 598
ID ADZ8901 standard; protein; 80 AA.
DE Mouse prokineticin 2.
PN WO2005042717-A2.
PD 12-MAY-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 57.4%; Score 286; DB 9; Length 80;
Best Local Similarity 57.1%; Pred. No. 1.6e-23;
RESULT 599
ID AED00598 standard; protein; 80 AA.
DE Mouse/rat prokineticin receptor 2 (PKR2) SEQ ID NO 10.
PN WO2005091925-A2.
PD 06-OCT-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 57.4%; Score 286; DB 9; Length 80;
Best Local Similarity 57.1%; Pred. No. 1.6e-23;
RESULT 600
ID ABG94402 standard; protein; 81 AA.
DE Rat GPCR ligand Bv8 protein sequence #2.
PN WO200262944-A2.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 57.4%; Score 286; DB 5; Length 81;
Best Local Similarity 57.1%; Pred. No. 1.7e-23;
RESULT 601
ID ABB06963 standard; protein; 81 AA.
DE Rat G protein-coupled receptor protein sequence SEQ ID NO:71.
PN WO200216607-A1.
PD 28-FEB-2002.
PA - (TAKE) TAKEDA CHEM IND LTD.
Query Match 57.4%; Score 286; DB 5; Length 81;
Best Local Similarity 57.1%; Pred. No. 1.7e-23;
RESULT 602
ID ADD69061 standard; protein; 81 AA.
DE Rat Bv8-related protein - SEQ ID 39.
PN WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 57.4%; Score 286; DB 7; Length 81;
Best Local Similarity 57.1%; Pred. No. 1.7e-23;
RESULT 603
ID ADO05358 standard; protein; 81 AA.
DE Mouse major prokineticin 2 (PK2), SEQ ID NO:7.
PN WO2003088904-A2.
PD 30-OCT-2003.
PA (REGC) UNIV CALIFORNIA.
Query Match 57.4%; Score 286; DB 7; Length 81;
Best Local Similarity 57.1%; Pred. No. 1.7e-23;
RESULT 604
ID ADN43260 standard; protein; 81 AA.
DE Amino acid sequence of murine prokineticin 2 (PK2).
PN WO2004032851-A2.
PD 22-APR-2004.

PA (REGC) UNIV CALIFORNIA.
Query Match 57.4%; Score 286; DB 8; Length 81;
Best Local Similarity 57.1%; Pred. No. 1.7e-23;
RESULT 605
ID ADN43262 standard; protein; 81 AA.
DE Amino acid sequence of rat prokineticin 2 (PK2).
PN WO2004032851-A2.
PD 22-APR-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 57.4%; Score 286; DB 8; Length 81;
Best Local Similarity 57.1%; Pred. No. 1.7e-23;
RESULT 606
ID ADS86497 standard; protein; 81 AA.
DE Rat/ murine Bv8 protein related to eating disorders & obesity Seq 29.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 57.4%; Score 286; DB 8; Length 81;
Best Local Similarity 57.1%; Pred. No. 1.7e-23;
RESULT 607
ID ADS75520 standard; protein; 81 AA.
DE Modified mouse prokineticin 2 receptor, SEQ ID 29.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 57.4%; Score 286; DB 8; Length 81;
Best Local Similarity 57.1%; Pred. No. 1.7e-23;
RESULT 608
ID ADS75522 standard; protein; 81 AA.
DE Modified rat prokineticin 2 receptor, SEQ ID 31.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 57.4%; Score 286; DB 8; Length 81;
Best Local Similarity 57.1%; Pred. No. 1.7e-23;
RESULT 609
ID ADM00757 standard; protein; 81 AA.
DE Amino acid sequence of murine prokineticin 2 (PK2).
PN WO2004113361-A2.
PD 29-DEC-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 57.4%; Score 286; DB 9; Length 81;
Best Local Similarity 57.1%; Pred. No. 1.7e-23;
RESULT 610
ID AEG43365 standard; protein; 81 AA.
DE Mouse prokineticin 2 (PK2) protein, SEQ ID NO: 7.
PN US2006172935-A1.
PD 03-AUG-2006.
PA (ZHOU/) ZHOU Q.
(BULL/) BULLOCK C M.
(STEG/) SIEGEL J.
Query Match 57.4%; Score 286; DB 10; Length 81;
Best Local Similarity 57.1%; Pred. No. 1.7e-23;
RESULT 611
ID ABG94408 standard; protein; 107 AA.
DE Mouse GPCR ligand Bv8 protein.
PN WO200262944-A2.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 57.4%; Score 286; DB 5; Length 107;
Best Local Similarity 57.1%; Pred. No. 2.2e-23;
RESULT 612
ID ABG94401 standard; protein; 107 AA.
DE Rat GPCR ligand Bv8 protein sequence #1.
PN WO200262944-A2.
PD 15-AUG-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 57.4%; Score 286; DB 5; Length 107;
Best Local Similarity 57.1%; Pred. No. 2.2e-23;
RESULT 613
ID ABB06962 standard; protein; 107 AA.
DE Rat G protein-coupled receptor protein sequence SEQ ID NO:69.
PN WO200216607-A1.

PD 28-FEB-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 57.4%; Score 286; DB 5; Length 107;
Best Local Similarity 57.1%; Pred. No. 2.2e-23;
RESULT 614
ID AAE36790 standard; protein; 107 AA.
DE Mouse Bv8 homologue protein.
PN WO2003020892-A2.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 57.4%; Score 286; DB 6; Length 107;
Best Local Similarity 57.1%; Pred. No. 2.2e-23;
RESULT 615
ID ADD69059 standard; protein; 107 AA.
DE Rat Bv8-related protein - SEQ ID 37.
PN WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 57.4%; Score 286; DB 7; Length 107;
Best Local Similarity 57.1%; Pred. No. 2.2e-23;
RESULT 616
ID ADD69077 standard; protein; 107 AA.
DE Murine Bv8-related protein - SEQ ID 55.
PN WO2003066860-A1.
PD 14-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 57.4%; Score 286; DB 7; Length 107;
Best Local Similarity 57.1%; Pred. No. 2.2e-23;
RESULT 617
ID ADS00462 standard; protein; 107 AA.
DE Murine Bv8 homologue, SEQ ID 6.
PN WO2004081229-A2.
PD 23-SEP-2004.
PA (GETH) GENENTECH INC.
Query Match 57.4%; Score 286; DB 8; Length 107;
Best Local Similarity 57.1%; Pred. No. 2.2e-23;
RESULT 618
ID ADS86500 standard; protein; 107 AA.
DE Rat Bv8 protein related to eating disorders & obesity Seq 32.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 57.4%; Score 286; DB 8; Length 107;
Best Local Similarity 57.1%; Pred. No. 2.2e-23;
RESULT 619
ID ADS86502 standard; protein; 107 AA.
DE Murine Bv8 peptide DNA related to eating disorders & obesity Seq 34.
PN WO2004084945-A1.
PD 07-OCT-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 57.4%; Score 286; DB 8; Length 107;
Best Local Similarity 57.1%; Pred. No. 2.2e-23;
RESULT 620
ID ADZ88897 standard; protein; 108 AA.
DE Rhesus monkey prokineticin receptor 2.
PN WO2005042717-A2.
PD 12-MAY-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 57.0%; Score 284; DB 9; Length 108;
Best Local Similarity 57.1%; Pred. No. 3.7e-23;
RESULT 621
ID ASD00594 standard; protein; 108 AA.
DE Rhesus monkey prokineticin receptor 2 (PKR2) SEQ ID NO 6.
PN WO2005091925-A2.
PD 06-OCT-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 57.0%; Score 284; DB 9; Length 108;
Best Local Similarity 57.1%; Pred. No. 3.7e-23;
RESULT 622
ID ADN43265 standard; protein; 77 AA.
DE Amino acid sequence of a Bv8 homologue.
PN WO2004032851-A2.
PD 22-APR-2004.

PA (REGC) UNIV CALIFORNIA.
Query Match 55.9%; Score 278.5; DB 8; Length 77;
Best Local Similarity 61.5%; Pred. No. 1e-22;
RESULT 623
ID ADS75523 standard; protein; 77 AA.
DE Modified toad prokineticin receptor.
PN WO2004087054-A2.
PD 14-OCT-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 55.9%; Score 278.5; DB 8; Length 77;
Best Local Similarity 61.5%; Pred. No. 1e-22;
RESULT 624
ID ADNA3257 standard; protein; 102 AA.
DE Amino acid sequence of human prokineticin 2 (PK2) isoform 1.
PN WO2004032851-A2.
PD 22-APR-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 54.3%; Score 270.5; DB 8; Length 102;
Best Local Similarity 45.9%; Pred. No. 1.1e-21;
RESULT 625
ID ADJ71808 standard; protein; 124 AA.
DE Human Bv8 protein.
PN WO2003040326-A2.
PD 15-MAY-2003.
PA (HYSE-) HYSEQ INC.
Query Match 54.3%; Score 270.5; DB 7; Length 124;
Best Local Similarity 45.9%; Pred. No. 1.3e-21;
RESULT 626
ID AAE36788 standard; protein; 129 AA.
DE Human Bv8 homologue protein.
PN WO2003020892-A2.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 54.3%; Score 270.5; DB 6; Length 129;
Best Local Similarity 45.9%; Pred. No. 1.4e-21;
RESULT 627
ID ADJ71815 standard; protein; 129 AA.
DE Human prokineticin 2 precursor protein.
PN WO2003040326-A2.
PD 15-MAY-2003.
PA (HYSE-) HYSEQ INC.
Query Match 54.3%; Score 270.5; DB 7; Length 129;
Best Local Similarity 45.9%; Pred. No. 1.4e-21;
RESULT 628
ID ADNA1864 standard; protein; 129 AA.
DE Amino acid sequence of a longer human Zven1 polypeptide.
PN WO2004032850-A2.
PD 22-APR-2004.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 54.3%; Score 270.5; DB 8; Length 129;
Best Local Similarity 45.9%; Pred. No. 1.4e-21;
RESULT 629
ID ADS86984 standard; protein; 129 AA.
DE Human Zven1 protein longer form.
PN WO2004031367-A2.
PD 15-APR-2004.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 54.3%; Score 270.5; DB 8; Length 129;
Best Local Similarity 45.9%; Pred. No. 1.4e-21;
RESULT 630
ID ADS00458 standard; protein; 129 AA.
DE Human Bv8 homologue variant #1, SEQ ID 2.
PN WO2004081229-A2.
PD 23-SEP-2004.
PA (GETH) GENENTECH INC.
Query Match 54.3%; Score 270.5; DB 8; Length 129;
Best Local Similarity 45.9%; Pred. No. 1.4e-21;
RESULT 631
ID ADO05362 standard; protein; 77 AA.
DE Xenopus laevis prokineticin orthologue Bv8, SEQ ID NO.11.
PN WO200308904-A2.
PD 30-OCT-2003.
PA (REGC) UNIV CALIFORNIA.

Query Match 53.7%; Score 267.5; DB 7; Length 77;
 Best Local Similarity 57.7%; Pred. No. 1.7e-21;
 RESULT 632
 ID ADN43264 standard; protein; 77 AA.
 DE Amino acid sequence of Bv8.
 PN WO2004032851-A2.
 PD 22-APR-2004.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 53.7%; Score 267.5; DB 8; Length 77;
 Best Local Similarity 57.7%; Pred. No. 1.7e-21;
 RESULT 633
 ID ADW00761 standard; protein; 77 AA.
 DE Amino acid sequence of frog Bv8.
 PN WO2004113361-A2.
 PD 29-DEC-2004.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 53.7%; Score 267.5; DB 9; Length 77;
 Best Local Similarity 57.7%; Pred. No. 1.7e-21;
 RESULT 634
 ID ADZ88905 standard; protein; 77 AA.
 DE Frog prokineticin 1 homologue, Bv8.
 PN WO2005042717-A2.
 PD 12-MAY-2005.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 53.7%; Score 267.5; DB 9; Length 77;
 Best Local Similarity 57.7%; Pred. No. 1.7e-21;
 RESULT 635
 ID AED00602 standard; protein; 77 AA.
 DE Frog Bv8 SEQ ID NO 14.
 PN WO2005091925-A2.
 PD 06-OCT-2005.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 53.7%; Score 267.5; DB 9; Length 77;
 Best Local Similarity 57.7%; Pred. No. 1.7e-21;
 RESULT 636
 ID AEJ43369 standard; protein; 77 AA.
 DE Frog Bv8 protein, SEQ ID NO: 11.
 PN US2006172935-A1.
 PD 03-AUG-2006.
 PA (ZHOU/) ZHOU Q.
 PA (BULL/) BULLOCK C M.
 PA (SIEG/) SIEGEL J.
 Query Match 53.7%; Score 267.5; DB 10; Length 77;
 Best Local Similarity 57.7%; Pred. No. 1.7e-21;
 RESULT 637
 ID ADJ71813 standard; protein; 96 AA.
 DE Toad Bv8 protein.
 PN WO2003040326-A2.
 PD 15-MAY-2003.
 PA (HYSE-) HYSEQ INC.
 Query Match 53.7%; Score 267.5; DB 7; Length 96;
 Best Local Similarity 57.7%; Pred. No. 2.1e-21;
 RESULT 638
 ID ADS75502 standard; protein; 96 AA.
 DE Modified frog prokineticin receptor, Bv8.
 PN WO2004087054-A2.
 PD 14-OCT-2004.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 53.7%; Score 267.5; DB 8; Length 96;
 Best Local Similarity 57.7%; Pred. No. 2.1e-21;
 RESULT 639
 ID ADO05359 standard; protein; 102 AA.
 DE Mouse minor prokineticin 2 (PK2), SEQ ID NO:8.
 PN WO2003088904-A2.
 PD 30-OCT-2003.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 53.3%; Score 265.5; DB 7; Length 102;
 Best Local Similarity 44.9%; Pred. No. 3.7e-21;
 RESULT 640
 ID ADW00758 standard; protein; 102 AA.
 DE Amino acid sequence of murine prokineticin 2 (PK2).
 PN WO2004113361-A2.
 PD 29-DEC-2004.

PA (REGC) UNIV CALIFORNIA.
 Query Match 53.3%; Score 265.5; DB 9; Length 102;
 Best Local Similarity 44.9%; Pred. No. 3.7e-21;
 RESULT 641
 ID AEJ43366 standard; protein; 102 AA.
 DE Mouse prokineticin 2 (PK2) protein, SEQ ID NO: 8.
 PN US2006172935-A1.
 PD 03-AUG-2006.
 PA (ZHOU/) ZHOU Q.
 PA (BULL/) BULLOCK C M.
 PA (SIEG/) SIEGEL J.
 Query Match 53.3%; Score 265.5; DB 10; Length 102;
 Best Local Similarity 44.9%; Pred. No. 3.7e-21;
 RESULT 642
 ID ADJ71809 standard; protein; 128 AA.
 DE Mouse Bv8 variant 1 protein.
 PN WO2003040326-A2.
 PD 15-MAY-2003.
 PA (HYSE-) HYSEQ INC.
 Query Match 53.3%; Score 265.5; DB 7; Length 128;
 Best Local Similarity 44.9%; Pred. No. 4.7e-21;
 RESULT 643
 ID ADF17105 standard; peptide; 77 AA.
 DE Bombina maxima neurotrophic peptide.
 PN CN1390849-A.
 PD 15-JAN-2003.
 PA (KUNM-) KUNMING ZOOLOGY INST CHINESE ACAD SCI.
 Query Match 51.1%; Score 254.5; DB 7; Length 77;
 Best Local Similarity 56.4%; Pred. No. 4.5e-20;
 RESULT 644
 ID ADO05357 standard; protein; 100 AA.
 DE Human tissue specific (testis) prokineticin 2 (PK2), SEQ ID NO:6.
 PN WO2003088904-A2.
 PD 30-OCT-2003.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 50.5%; Score 251.5; DB 7; Length 100;
 Best Local Similarity 44.9%; Pred. No. 1.3e-19;
 RESULT 645
 ID ADW00756 standard; protein; 100 AA.
 DE Amino acid sequence of human prokineticin 2 (PK2).
 PN WO2004113361-A2.
 PD 29-DEC-2004.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 50.5%; Score 251.5; DB 9; Length 100;
 Best Local Similarity 44.9%; Pred. No. 1.3e-19;
 RESULT 646
 ID AEJ43364 standard; protein; 100 AA.
 DE Human prokineticin 2 (PK2) protein, SEQ ID NO: 6.
 PN US2006172935-A1.
 PD 03-AUG-2006.
 PA (ZHOU/) ZHOU Q.
 PA (BULL/) BULLOCK C M.
 PA (SIEG/) SIEGEL J.
 Query Match 50.5%; Score 251.5; DB 10; Length 100;
 Best Local Similarity 44.9%; Pred. No. 1.3e-19;
 RESULT 647
 ID ADO05363 standard; protein; 75 AA.
 DE Toad prokineticin orthologue Bv8, SEQ ID NO:12.
 PN WO2003088904-A2.
 PD 30-OCT-2003.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 50.3%; Score 250.5; DB 7; Length 75;
 Best Local Similarity 56.4%; Pred. No. 1.2e-19;
 RESULT 648
 ID ADW00762 standard; protein; 75 AA.
 DE Amino acid sequence of toad Bv8.
 PN WO2004113361-A2.
 PD 29-DEC-2004.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 50.3%; Score 250.5; DB 9; Length 75;
 Best Local Similarity 56.4%; Pred. No. 1.2e-19;
 RESULT 649
 ID ADZ88904 standard; protein; 75 AA.

DE Toad prokineticin 1 homologue, BV8.
PN WO2005042717-A2.
PA (REGC) UNIV CALIFORNIA.
Query Match 50.3%; Score 250.5; DB 9; Length 75;
Best Local Similarity 56.4%; Pred. No. 1.2e-19;
RESULT 650
ID AED0601 standard; protein; 75 AA.
DE Toad bv8 SEQ ID NO 13.
PN WO2005091925-A2.
PD 06-OCT-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 50.3%; Score 250.5; DB 9; Length 75;
Best Local Similarity 56.4%; Pred. No. 1.2e-19;
RESULT 651
ID AEJ43370 standard; protein; 75 AA.
DE Toad bv8 protein, SEQ ID NO: 12.
PN US2006172935-A1.
PD 03-AUG-2006.
PA (ZHOU/) ZHOU Q.
PA (BULL/) BULLOCK C M.
PA (SIEG/) SIEGEL J.
Query Match 50.3%; Score 250.5; DB 10; Length 75;
Best Local Similarity 56.4%; Pred. No. 1.2e-19;
RESULT 652
ID ADI60152 standard; protein; 126 AA.
DE Secretd polypeptide #36.
PN WO2003025142-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 45.2%; Score 225; DB 7; Length 126;
Best Local Similarity 43.9%; Pred. No. 1.3e-16;
RESULT 653
ID ADJ71800 standard; protein; 126 AA.
DE Human prokineticin-like protein.
PN WO2003040326-A2.
PD 15-MAY-2003.
PA (HYSE-) HYSEQ INC.
Query Match 45.2%; Score 225; DB 7; Length 126;
Best Local Similarity 43.9%; Pred. No. 1.3e-16;
RESULT 654
ID AED53711 standard; peptide; 56 AA.
DE Amino acid sequence of human PK2beta peptide.
PN WO2005097826-A2.
PD 20-OCT-2005.
PA (JANC) JANSSEN PHARM NV.
Query Match 37.3%; Score 186; DB 9; Length 56;
Best Local Similarity 52.7%; Pred. No. 1.1e-12;
RESULT 655
ID AED53712 standard; peptide; 56 AA.
DE Amino acid sequence of human PK2beta peptide #2.
PN WO2005097826-A2.
PD 20-OCT-2005.
PA (JANC) JANSSEN PHARM NV.
Query Match 36.9%; Score 184; DB 9; Length 56;
Best Local Similarity 57.4%; Pred. No. 1.8e-12;
RESULT 656
ID AA027072 standard; peptide; 30 AA.
DE Monkey AXOR8 receptor N-terminal peptide, SEQ ID No 20.
PN GB2378183-A.
PD 05-FEB-2003.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match 31.3%; Score 156; DB 6; Length 30;
Best Local Similarity 90.0%; Pred. No. 1.1e-09;
RESULT 657
ID AEA18405 standard; peptide; 24 AA.
DE R. saharica insulin releasing peptide #1.
PN WO2005047316-A2.
PD 26-MAY-2005.
PA (UYUL-) UNIV ULSTER.
Query Match 24.1%; Score 120; DB 9; Length 24;
Best Local Similarity 91.3%; Pred. No. 7.6e-06;
RESULT 658
ID AAY44934 standard; protein; 271 AA.
DE Human dickkopf-1 homolog 3 protein.
PN WO200006714-A1.
PD 10-FEB-2000.
PA (ELIL) LILLY & CO ELI.
Query Match 22.5%; Score 112; DB 3; Length 271;
Best Local Similarity 32.9%; Pred. No. 0.00072;
RESULT 659
ID ADF28074 standard; peptide; 23 AA.
DE Human Zven polypeptide motif #2.
PN US2003148317-A1.
PD 07-AUG-2003.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 21.9%; Score 109; DB 7; Length 23;
Best Local Similarity 73.9%; Pred. No. 0.00012;
RESULT 660
ID ADN41845 standard; peptide; 23 AA.
DE Motif found in Zven1 and Zven1 polypeptides.
PN WO2004032850-A2.
PD 22-APR-2004.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 21.9%; Score 109; DB 8; Length 23;
Best Local Similarity 73.9%; Pred. No. 0.00012;
RESULT 661
ID ADS86964 standard; peptide; 23 AA.
DE Human Zven protein motif #2.
PN WO2004031367-A2.
PD 15-APR-2004.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 21.9%; Score 109; DB 8; Length 23;
Best Local Similarity 73.9%; Pred. No. 0.00012;
RESULT 662
ID AEB45592 standard; peptide; 23 AA.
DE Human Zven1 and Zven2 motif peptide, SEQ ID NO: 9.
PN US2005153322-A1.
PD 14-JUL-2005.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 21.9%; Score 109; DB 9; Length 23;
Best Local Similarity 73.9%; Pred. No. 0.00012;
RESULT 663
ID AED08092 standard; peptide; 23 AA.
DE Human Zven1/Zven2 motif peptide - SEQ ID 9.
PN US2005214800-A1.
PD 29-SEP-2005.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 21.9%; Score 109; DB 9; Length 23;
Best Local Similarity 73.9%; Pred. No. 0.00012;
RESULT 664
ID AEA16257 standard; protein; 221 AA.
DE Mouse Dickkopf-4 (Dkk-4) protein.
PN WO2005049797-A2.
PD 02-JUN-2005.
PA (MERI) MERCK & CO INC.
Query Match 21.8%; Score 108.5; DB 9; Length 221;
Best Local Similarity 35.5%; Pred. No. 0.0014;
RESULT 665
ID ASC06122 standard; peptide; 18 AA.
DE Human EG-VEGF peptide (amino acids 50-67).
PN WO2005076972-A2.
PD 25-AUG-2005.
PA (OHIS) UNIV OHIO STATE RES FOUND.
Query Match 21.7%; Score 108; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.00012;
RESULT 666
ID ADI60388 standard; protein; 40 AA.
DE Secretd polypeptide encoded by gene splice variant #24.
PN WO2003025142-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 21.7%; Score 108; DB 7; Length 40;
Best Local Similarity 58.1%; Pred. No. 0.00027;
RESULT 667

Query Match

PA (CURA-) CURAGEN CORP.
 Query Match 21.6%; Score 107.5; DB 7; Length 180;
 Best Local Similarity 35.5%; Pred. No. 0.0015;
 RESULT 673
 ID ADM93402 standard; protein; 180 AA.
 DE Human NOVX polypeptide #17.
 PN US2004067882-A1.
 PD 08-APR-2004.
 PA (ALSO/) ALSBROOK J P.
 PA (ALVA/) ALVAREZ E.
 PA (ANDE/) ANDERSON D W.
 PA (BARO/) BARON M.
 PA (BOLD/) BOLDOG F L.
 PA (BURG/) BURGESS C E.
 PA (CASM/) CASMAN S J.
 PA (CHAP/) CHAPOVAL A.
 PA (DHAN/) DHANABAL M.
 PA (EDIN/) EDINGER S R.
 PA (EISE/) EISEN A.
 PA (ELLE/) ELLERMAN K.
 PA (ETTE/) ETTENBERG S.
 PA (GANG/) GANGOLLI E A.
 PA (GERL/) GERLACH V.
 PA (GORM/) GORMAN L.
 PA (GROS/) GROSSE W M.
 PA (GUOX/) GUO X.
 PA (HACK/) HACKETT C.
 PA (JIWW/) JI W.
 PA (KEKU/) KEKUDA R.
 PA (KHRA/) KHRAMTSOV N V.
 PA (LEPL/) LEPLEY D M.
 PA (LILL/) LI L.
 PA (MACD/) MACDOUGALL J R.
 PA (MALY/) MALYANKAR U M.
 PA (MAZU/) MAZUR A.
 PA (MCQU/) MCQUEENEY K.
 PA (MEZE/) MEZES P S.
 PA (MILL/) MILLER C E.
 PA (MILL/) MILLET I.
 PA (MISH/) MISHRA V.
 PA (PADI/) PADIGARU M.
 PA (PATT/) PATTURAJAN M.
 PA (PENA/) PENA C E A.
 PA (PEYM/) PEYMAN J A.
 PA (RAST/) RASTELLI L.
 PA (RIEG/) RIEGER D K.
 PA (ROTH/) ROTHENBERG M E.
 PA (SHEN/) SHENOY S G.
 PA (SHIM/) SHIMKETS R A.
 PA (SMIT/) SMITHSON G.
 PA (SPAD/) SPADERNA S K.
 PA (STAR/) STARLING G.
 PA (SPYT/) SPYTEK K A.
 PA (STON/) STONE D J.
 PA (TCHE/) TCHERNEV V T.
 PA (TWOM/) TWOMLOW N.
 PA (VERN/) VERNET C A M.
 PA (ZERH/) ZERRHUSEN B D.
 PA (VOSS/) VOSS E Z.
 PA (ZHON/) ZHONG M.
 Query Match 21.6%; Score 107.5; DB 8; Length 180;
 Best Local Similarity 35.5%; Pred. No. 0.0015;
 RESULT 674
 ID AAW73017 standard; protein; 224 AA.
 DE Human cysteine-rich secreted protein CRSP-2.
 PN WO9846755-A1.
 PD 22-OCT-1998.
 PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
 Query Match 21.6%; Score 107.5; DB 2; Length 224;
 Best Local Similarity 35.5%; Pred. No. 0.0019;
 RESULT 675
 ID AAY92075 standard; protein; 224 AA.
 DE Human DKR-4.

PN WO200018914-A2.
 PD 06-APR-2000.
 PA (ANGE-) ANGEN INC.
 Query Match 21.6%; Score 107.5; DB 3; Length 224;
 Best Local Similarity 35.5%; Pred. No. 0.0019;
 RESULT 676
 ID AAB08875 standard; protein; 224 AA.
 DE Amino acid sequence of a human Dickkopf (Dkk)-4 protein.
 PN WO200052047-A2.
 PD 08-SEP-2000.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 21.6%; Score 107.5; DB 3; Length 224;
 Best Local Similarity 35.5%; Pred. No. 0.0019;
 RESULT 677
 ID ABUS5916 standard; protein; 224 AA.
 DE Human protein DKK4.
 PN WO200277204-A2.
 PD 03-OCT-2002.
 PA (AXOR-) AXORDIA LTD.
 Query Match 21.6%; Score 107.5; DB 6; Length 224;
 Best Local Similarity 35.5%; Pred. No. 0.0019;
 RESULT 678
 ID AAE34070 standard; protein; 224 AA.
 DE DKK 4 protein.
 PN WO200290992-A2.
 PD 14-NOV-2002.
 PA (AXOR-) AXORDIA LTD.
 Query Match 21.6%; Score 107.5; DB 6; Length 224;
 Best Local Similarity 35.5%; Pred. No. 0.0019;
 RESULT 679
 ID ADE28651 standard; protein; 224 AA.
 DE Human NOV9a protein - SEQ ID 28.
 PN WO2003040330-A2.
 PD 15-MAY-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 21.6%; Score 107.5; DB 7; Length 224;
 Best Local Similarity 35.5%; Pred. No. 0.0019;
 RESULT 680
 ID ADJ68529 standard; protein; 224 AA.
 DE Human heat mitochondrial protein as a therapeutic target SeqID335.
 PN WO2003087768-A2.
 PD 23-OCT-2003.
 PA (MITO-) MITOKOR.
 PA (BUCK-) BUCK INST AGE RES.
 Query Match 21.6%; Score 107.5; DB 7; Length 224;
 Best Local Similarity 35.5%; Pred. No. 0.0019;
 RESULT 681
 ID ADN39310 standard; protein; 224 AA.
 DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:628.
 PN WO2003042661-A2.
 PD 22-MAY-2003.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 Query Match 21.6%; Score 107.5; DB 7; Length 224;
 Best Local Similarity 35.5%; Pred. No. 0.0019;
 RESULT 682
 ID ADM93396 standard; protein; 224 AA.
 DE Human NOVX polypeptide #14.
 PN US2004067882-A1.
 PD 08-APR-2004.
 PA (ALSO/) ALSBROOK J P.
 PA (ALVA/) ALVAREZ E.
 PA (ANDE/) ANDERSON D W.
 PA (BARO/) BARON M.
 PA (BOLD/) BOLDOG F L.
 PA (BURG/) BURGESS C E.
 PA (CASM/) CASMAN S J.
 PA (CHAP/) CHAPOVAL A.
 PA (DHAN/) DHANABAL M.
 PA (EDIN/) EDINGER S R.
 PA (ELLE/) EISEN A.
 PA (ETTE/) ETTENBERG S.
 PA (GANG/) GANGOLLI E A.

PA (GERL/) GERLACH V.
 PA (GORM/) GORMAN L.
 PA (GROS/) GROSSE W M.
 PA (GUOX/) GUO X.
 PA (HACK/) HACKETT C.
 PA (JIWW/) JI W.
 PA (KEKU/) KHRAMTSOV N V.
 PA (LEPL/) KEKUDA R.
 PA (LILL/) LEPLEY D M.
 PA (LILL/) LI L.
 PA (MACD/) MACDOUGALL J R.
 PA (MALY/) MALYANKAR U M.
 PA (MAZU/) MAZUR A.
 PA (MCQU/) MCQUEENEY K.
 PA (MEZE/) MEZES P S.
 PA (MILL/) MILLER C E.
 PA (MISH/) MILLET I.
 PA (MISH/) MISHRA V.
 PA (PADI/) PADIGARU M.
 PA (PATT/) PATTURAJAN M.
 PA (PENA/) PENA C E A.
 PA (PEYM/) PEYMAN J A.
 PA (RAST/) RASTELLI L.
 PA (RIEG/) RIEGER D K.
 PA (ROTH/) ROTHENBERG M E.
 PA (SHEN/) SHENOY S G.
 PA (SHIM/) SHINKETS R A.
 PA (SMIT/) SMITHSON G.
 PA (SPAD/) SPADERNA S K.
 PA (STAR/) STARLING G.
 PA (SPYT/) SPYTEK K A.
 PA (STON/) STONE D J.
 PA (TCHE/) TCHERNEV V T.
 PA (TWOM/) TWOMLOW N.
 PA (VERN/) VERNET C A M.
 PA (ZERR/) ZERHUSEN B D.
 PA (VOSS/) VOSS E Z.
 PA (ZHON/) ZHONG M.
 Query Match 21.6%; Score 107.5; DB 8; Length 224;
 Best Local Similarity 35.5%; Pred. No. 0.0019;
 RESULT 683
 ID AEA16256 standard; protein; 224 AA.
 DE Human Dickkopf-4 (Dkk-4) protein.
 PN WO2005049797-A2.
 PD 02-JUN-2005.
 PA (MERI) MERCK & CO INC.
 Query Match 21.6%; Score 107.5; DB 9; Length 224;
 Best Local Similarity 35.5%; Pred. No. 0.0019;
 RESULT 684
 ID AEA16254 standard; protein; 224 AA.
 DE Cynomolgus monkey Dickkopf-4 (CDKK-4) protein.
 PN WO2005049797-A2.
 PD 02-JUN-2005.
 PA (MERI) MERCK & CO INC.
 Query Match 21.6%; Score 107.5; DB 9; Length 224;
 Best Local Similarity 35.5%; Pred. No. 0.0019;
 RESULT 685
 ID AEI44169 standard; protein; 224 AA.
 DE Dickkopf homolog 4, DKK4, SEQ ID 2.
 PN JP2006166789-A.
 PD 29-JUN-2006.
 PA (UYHI-) UNIV HIROSHIMA.
 Query Match 21.6%; Score 107.5; DB 10; Length 224;
 Best Local Similarity 35.5%; Pred. No. 0.0019;
 RESULT 686
 ID AAW73019 standard; protein; 179 AA.
 DE Human cysteine-rich secreted protein CRSP-4.
 PN WO9846755-A1.
 PD 22-OCT-1998.
 PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
 Query Match 20.5%; Score 102; DB 2; Length 179;
 Best Local Similarity 31.5%; Pred. No. 0.0059;
 RESULT 687
 ID AAB08877 standard; protein; 179 AA.
 DE A partial human Dickkopf (Dkk)-2 protein.
 PN WO200052047-A2.
 PD 08-SEP-2000.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 20.5%; Score 102; DB 3; Length 179;
 Best Local Similarity 31.5%; Pred. No. 0.0059;
 RESULT 688
 ID ADO35297 standard; protein; 179 AA.
 DE Human Dkk2 carboxy terminal cysteine rich region.
 PN US2004014209-A1.
 PD 22-JAN-2004.
 PA (LASS/) LASSAR A B.
 PA (MERC/) MERCOLA M.
 PA (GUPT/) GUPTA R.
 PA (MARV/) MARVIN M.
 PA (SCHN/) SCHNEIDER V.
 PA (TZA/) TZAHOOR E.
 PA (BROT/) BROTT B.
 PA (SOKO/) SOKOL S.
 Query Match 20.5%; Score 102; DB 8; Length 179;
 Best Local Similarity 31.5%; Pred. No. 0.0059;
 RESULT 689
 ID AAY92074 standard; protein; 207 AA.
 DE Human DKR-2 splice variant, DKR-2a.
 PN WO200018914-A2.
 PD 06-APR-2000.
 PA (AMGE-) AMGEN INC.
 Query Match 20.5%; Score 102; DB 3; Length 207;
 Best Local Similarity 31.5%; Pred. No. 0.0068;
 RESULT 690
 ID AAY92073 standard; protein; 259 AA.
 DE Human DKR-2.
 PN WO200018914-A2.
 PD 06-APR-2000.
 PA (AMGE-) AMGEN INC.
 Query Match 20.5%; Score 102; DB 3; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.0086;
 RESULT 691
 ID AAY99360 standard; protein; 259 AA.
 DE Human PRO1316 (UNQ682) amino acid sequence SEQ ID NO:70.
 PN WO200012708-A2.
 PD 09-MAR-2000.
 PA (GETH) GENENTECH INC.
 Query Match 20.5%; Score 102; DB 3; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.0086;
 RESULT 692
 ID AAB66109 standard; protein; 259 AA.
 DE Protein of the invention #21.
 PN WO200078961-A1.
 PD 28-DEC-2000.
 PA (GETH) GENENTECH INC.
 Query Match 20.5%; Score 102; DB 4; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.0086;
 RESULT 693
 ID AAU29148 standard; protein; 259 AA.
 DE Human PRO polypeptide sequence #125.
 PN WO200168848-A2.
 PD 20-SEP-2001.
 PA (GETH) GENENTECH INC.
 Query Match 20.5%; Score 102; DB 4; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.0086;
 RESULT 694
 ID ABU58524 standard; protein; 259 AA.
 DE Human PRO polypeptide #125.
 PN US2003027272-A1.
 PD 06-FEB-2003.
 Query Match 20.5%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.0086;
 RESULT 695
 ID ABU88072 standard; protein; 259 AA.
 DE Novel human secreted and transmembrane protein PRO1316.
 PN US2003032127-A1.

PD 13-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 696
ID ABU84387 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003032112-A1.
PD 13-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 697
ID ABR66261 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003027278-A1.
PD 06-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 698
ID ABR66261 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 699
ID ABU99591 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 700
ID ABU82830 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 701
ID ABU89951 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 702
ID ABR68200 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 703
ID ABU96253 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 704
ID ABU92684 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 705
ID ABO08761 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;

RESULT 706
ID ABO02813 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 707
ID ABR74967 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 708
ID ABR94729 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 709
ID ABU5702 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 710
ID ABU98862 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 711
ID ABU98077 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 712
ID ABU91783 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 713
ID ABU89476 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 714
ID ABU86317 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 715
ID ABU67530 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;

RESULT 716
ID ABR080558 standard; protein; 259 AA.
DE Human PRO protein #125.
PN US2003036137-A1.
PD 20-FEB-2003.

Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;

RESULT 717
ID ABR99476 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040063-A1.
PD 27-FEB-2003.

Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;

RESULT 718
ID ABR9866 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040064-A1.
PD 27-FEB-2003.

Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;

RESULT 719
ID ABO16389 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003027267-A1.
PD 06-FEB-2003.

Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;

RESULT 720
ID ABR92289 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003036160-A1.
PD 20-FEB-2003.

Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;

RESULT 721
ID ABO18930 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003044925-A1.
PD 06-MAR-2003.

Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;

RESULT 722
ID ABR78351 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054474-A1.
PD 20-MAR-2003.

Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;

RESULT 723
ID ABO19235 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003036118-A1.
PD 20-FEB-2003.

Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;

RESULT 724
ID ABO00226 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003032101-A1.
PD 13-FEB-2003.

Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;

RESULT 725
ID ABO11558 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036124-A1.
PD 20-FEB-2003.

Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;

RESULT 726
ID ABO16084 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003036148-A1.
PD 20-FEB-2003.

Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;

RESULT 727
ID ABUS5914 standard; protein; 259 AA.
DE Human protein DKK2.
PN WO200277204-A2.
PD 03-OCT-2002.

Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;

RESULT 728
ID ABU88777 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003036133-A1.
PD 20-FEB-2003.

Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;

RESULT 729
ID ABUS3472 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036134-A1.
PD 20-FEB-2003.

Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;

RESULT 730
ID ABO06273 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003022294-A1.
PD 30-JAN-2003.

Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;

RESULT 731
ID ABR59309 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003027275-A1.
PD 06-FEB-2003.

Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;

RESULT 732
ID ABO09371 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003027324-A1.
PD 06-FEB-2003.

Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;

RESULT 733
ID ABO19235 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003036118-A1.
PD 20-FEB-2003.

Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;

RESULT 734
ID ABO11253 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036123-A1.
PD 20-FEB-2003.

Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;

RESULT 735
ID ABR66871 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003036148-A1.
PD 20-FEB-2003.

Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;

RESULT 736
ID ABO16084 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003036148-A1.
PD 20-FEB-2003.

Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;

DE Human secreted/transmembrane protein (PRO) #125.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 737
ID ABO13790 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 738
ID ABU65693 standard; protein; 259 AA.
DE Human secreted/transmembrane protein, SEQ ID 250.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 739
ID ABO07541 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 740
ID ABO03728 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 741
ID ABR67176 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 742
ID ABO15779 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 743
ID AAE34068 standard; protein; 259 AA.
DE DKX 2 protein.
PN WO200209092-A2.
PD 14-NOV-2002.
PA (AXOR-) AXORDIA LTD.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 744
ID ABUS6060 standard; protein; 259 AA.
DE Human secreted/transmembrane protein, PRO1316.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 745
ID ABU65388 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 746
ID ABU95333 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003027274-A1.

PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 747
ID ABU71236 standard; protein; 259 AA.
DE Human PRO1316 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 748
ID ABO07846 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 749
ID ABR70087 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 750
ID ABR69420 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 751
ID ABO01561 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 752
ID ABU81363 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 753
ID ABR60160 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 754
ID ABR67895 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 755
ID ABR65283 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 756
ID ABR68505 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003027274-A1.

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PD 06-FEB-2003.
Query Match      20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 757
ID ABR71917 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 758
ID ABU85397 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match      20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 759
ID ABU89087 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match      20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 760
ID ABU83167 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match      20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 761
ID ABU95023 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match      20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 762
ID ABU90571 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match      20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 763
ID ABU84082 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match      20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 764
ID ABU93733 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 765
ID ABR64978 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match      20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 766
ID ABR68810 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003027271-A1.
PD 06-FEB-2003.

Query Match      20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 767
ID ABO06626 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match      20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 768
ID ABR99171 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match      20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 769
ID ABU57055 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match      20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 770
ID ABU86007 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match      20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 771
ID ABU82294 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match      20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 772
ID ABU87305 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match      20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 773
ID ABU83777 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match      20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 774
ID ABO08151 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match      20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 775
ID ABU81862 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match      20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 776
ID ABU66026 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match      20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 777
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ID ABR59855 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 778
ID ABR70392 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 779
ID ABU98557 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 780
ID ABR65666 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 781
ID ABR90984 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 782
ID ABU94411 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 783
ID ABU79293 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 784
ID ABU86622 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 785
ID ABU86927 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 786
ID ABU94716 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 787
ID ABO04643 standard; protein; 259 AA.
DE Human PRO polypeptide #125.

PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 788
ID ABR70392 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 789
ID ABU98557 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 790
ID ABR65956 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 791
ID ABR64673 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 792
ID ABU79598 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 793
ID ABU92989 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 794
ID ABU95948 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 795
ID ABU91168 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 796
ID ABU90261 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 797
ID ABO09676 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003044931-A1.
PD 06-MAR-2003.

ID ABU0634 standard; protein; 259 AA.
DE Human secreted/transmembrane protein #125.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 809
ID ABU95643 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003032115-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 810
ID ABU96852 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003032140-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 811
ID ABR70697 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 812
ID ABO05048 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 813
ID ABO08456 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003044922-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 814
ID ABO05663 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003032118-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 815
ID ABR74052 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003036135-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 816
ID ABR95644 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 817
ID ABR80941 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;

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Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 818
ID ABR81246 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 819
ID ASM00942 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 820
ID ABR88544 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 821
ID ABR77365 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 822
ID ABO28849 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 823
ID ABO31594 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 824
ID ABO08011 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 825
ID ABO40491 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 826
ID ABO35916 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 827
ID ABO40055 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 828
ID ADA78002 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 829
ID ABM24850 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104539-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 830
ID ABO03118 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036131-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 831
ID ABR90374 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040075-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 832
ID ABM17288 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 833
ID ABR95034 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003044930-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 834
ID ABR95339 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 835
ID ABO21577 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 836
ID ABR97841 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064452-A1.
PD 03-APR-2003.
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PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 837
ID ABR87629 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 838
ID ABR77670 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 839
ID ABR27900 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064440-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 840
ID ABR06181 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 841
ID ABR03687 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 842
ID ABR35138 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 843
ID ABR26375 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 844
ID ABR048157 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 845
ID ABR92899 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 846
ID ABR024660 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003085159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 847
ID ABR11671 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 848
ID ABR02772 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 849
ID ABR16068 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 850
ID ABR027629 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 851
ID ABR29120 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 852
ID ABR07096 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 853
ID ABR21190 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 854
ID ABR09536 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;

RESULT 855
ID ABO41406 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 856
ID ABO36221 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 857
ID ABO43750 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 858
ID ABO43750 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 859
ID ABO43750 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003082717-A1.
PD 01-MAY-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 860
ID ABO43750 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104542-A1.
PD 05-JUN-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 861
ID ABO43750 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104543-A1.
PD 05-JUN-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 862
ID ABO43750 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036127-A1.
PD 20-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 863
ID ABO02508 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003040061-A1.
PD 27-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 864
ID ABR90679 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003036130-A1.
PD 20-FEB-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 865
ID ABR73747 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 866
ID ABO16999 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 867
ID ABR94424 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003044917-A1.
PD 06-MAR-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 868
ID ABR75931 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003044929-A1.
PD 06-MAR-2003.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 869
ID ABR71307 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 870
ID ABR93204 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 871
ID ABR93509 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 872
ID ABR87934 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 873
ID ABO33602 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003073130-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 874
ID ABO27934 standard; protein; 259 AA.

DE Human secreted/transmembrane protein (PRO) #125.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
DB 6; Length 259;
Pred. No. 0.0086;
RESULT 875
ID ABO30069 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
DB 6; Length 259;
Pred. No. 0.0086;
RESULT 876
ID ABO33278 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
DB 6; Length 259;
Pred. No. 0.0086;
RESULT 877
ID ABO4966 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
DB 6; Length 259;
Pred. No. 0.0086;
RESULT 878
ID ABO8926 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
DB 6; Length 259;
Pred. No. 0.0086;
RESULT 879
ID ABO35611 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
DB 6; Length 259;
Pred. No. 0.0086;
RESULT 880
ID ABO35611 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
DB 6; Length 259;
Pred. No. 0.0086;
RESULT 881
ID ABO3576 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
DB 6; Length 259;
Pred. No. 0.0086;
RESULT 882
ID ABM10451 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
DB 6; Length 259;
Pred. No. 0.0086;
RESULT 883
ID ABM1976 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
DB 6; Length 259;
Pred. No. 0.0086;
RESULT 884
ID ABO52122 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
DB 6; Length 259;
Pred. No. 0.0086;
RESULT 885
ID ABO52427 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
DB 6; Length 259;
Pred. No. 0.0086;
RESULT 886
ID ABO23745 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003032134-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
DB 6; Length 259;
Pred. No. 0.0086;
RESULT 887
ID ABR97231 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
DB 6; Length 259;
Pred. No. 0.0086;
RESULT 888
ID ABR87019 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
DB 6; Length 259;
Pred. No. 0.0086;
RESULT 889
ID ABM11061 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
DB 6; Length 259;
Pred. No. 0.0086;
RESULT 890
ID ABM28205 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
DB 6; Length 259;
Pred. No. 0.0086;
RESULT 891
ID ABO32204 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
DB 6; Length 259;
Pred. No. 0.0086;
RESULT 892
ID ABM15331 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
DB 6; Length 259;
Pred. No. 0.0086;

PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 893
ID ABM06486 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 894
ID ABM04297 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 895
ID ABM22410 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 896
ID ABM07706 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 897
ID ABM040796 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 898
ID ABM35443 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 899
ID ABM33206 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003087374-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 900
ID ABM02732 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 901
ID ABO50292 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 902
ID ABO99286 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003040055-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 903
ID ABO04338 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US20030316164-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 904
ID ABO05968 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003040074-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 905
ID ABM18508 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 906
ID ABR97536 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 907
ID ABR80636 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 908
ID ABM01247 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 909
ID ABR88849 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003073169-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 910
ID ABM13501 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 911
ID ABM20885 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068711-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 912
ID ABO42016 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 913
ID ABO42626 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 914
ID ABR86714 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 915
ID ABO38661 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 916
ID ABR32901 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 917
ID ABR22715 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003087373-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 918
ID ABR74926 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003096353-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 919
ID ADA79794 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003073173-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 920
ID ABR96316 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054458-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 921
ID ABO37746 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 922
ID ABR86409 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 923
ID ABR86714 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 924
ID ABR16678 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 925
ID ABR29730 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 926
ID ABO29154 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 927
ID ABR23935 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 928
ID ABR23325 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 929
ID ABR2105 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 930
ID ABO37746 standard; protein; 259 AA.

DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 931
ID ABR28510 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003082715-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 932
ID ABR28815 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003082716-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 933
ID ABR66459 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 934
ID ABR75841 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 935
ID ABR34121 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 936
ID ABR34426 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 937
ID ABO20357 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003032125-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 938
ID ABO21272 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003054454-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 939
ID ABO22187 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 940
ID ABR9621 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 941
ID ABR85799 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 942
ID ABR99781 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 943
ID ABR00332 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 944
ID ABR00637 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 945
ID ABO29764 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 946
ID ABR23630 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 947
ID ABR29425 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 948
ID ABO38356 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 949
ID ABO45656 standard; protein; 259 AA.

DE Human PRO polypeptide #125.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 950
ID ABR89764 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 951
ID ADA81521 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 952
ID ABO16694 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003027276-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 953
ID ABO18320 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003044920-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 954
ID ABO22747 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003027265-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 955
ID ABO23052 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 956
ID ABR92594 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 957
ID ABR81551 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 958
ID ABR77975 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 959
ID ABR89764 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003073171-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 960
ID ABR26680 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003032121-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 961
ID ABR13806 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 962
ID ABO28544 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 963
ID ABO30374 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 964
ID ABO7401 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 965
ID ABO3992 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 966
ID ABO37136 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 967
ID ABO41711 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 968
ID ABO77975 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

ID ABO35306 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 969
ID ABO18015 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003044918-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 979
ID ABO20967 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003032132-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 980
ID ABR96926 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 981
ID ABM12281 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 982
ID ABM16373 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 983
ID ABM24240 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064441-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 984
ID ABM14721 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 985
ID ABM04602 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 986
ID ABM06791 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 987
ID ABM16983 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040078-A1.

ID ABO35306 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 969
ID ABO25155 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104540-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 970
ID ABO47547 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 971
ID ABO47852 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 972
ID ABO48462 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 973
ID ABO51512 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 974
ID ABO51817 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 975
ID ABO50597 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 976
ID ABR79721 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040059-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 977
ID ABM16983 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040078-A1.

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RESULT 987
ID ABM09231 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003073174-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
PN US2003073174-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 31.5%; Pred. No. 0.0086;
PD 10-APR-2003.
RESULT 988
ID ABO39271 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
PN US2003068775-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 31.5%; Pred. No. 0.0086;
PD 27-FEB-2003.
RESULT 989
ID ABM75536 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
PN US2003104545-A1.
PD 05-JUN-2003.
Query Match
Best Local Similarity 31.5%; Pred. No. 0.0086;
PD 27-FEB-2003.
RESULT 990
ID ABM25460 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104541-A1.
PD 05-JUN-2003.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
PN US2003104541-A1.
PD 05-JUN-2003.
Query Match
Best Local Similarity 31.5%; Pred. No. 0.0086;
PD 27-FEB-2003.
RESULT 991
ID ABM19970 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
PN US2003104554-A1.
PD 05-JUN-2003.
Query Match
Best Local Similarity 31.5%; Pred. No. 0.0086;
PD 27-FEB-2003.
RESULT 992
ID ABO46876 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
PN US2003049762-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 31.5%; Pred. No. 0.0086;
PD 27-FEB-2003.
RESULT 993
ID ABO47181 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
PN US2003049765-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 31.5%; Pred. No. 0.0086;
PD 27-FEB-2003.
RESULT 994
ID ADA83319 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
PN US2003049752-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 31.5%; Pred. No. 0.0086;
PD 27-FEB-2003.
RESULT 995
ID ABR71612 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003032133-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
PN US2003032133-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 31.5%; Pred. No. 0.0086;
PD 27-FEB-2003.
RESULT 996
ID ABR72222 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003032136-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
PN US2003032136-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 31.5%; Pred. No. 0.0086;
PD 27-FEB-2003.
RESULT 997
ID ABR98561 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003036129-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
PN US2003036129-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 31.5%; Pred. No. 0.0086;
PD 27-FEB-2003.
RESULT 998
ID ABO06931 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003040053-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
PN US2003040053-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 31.5%; Pred. No. 0.0086;
PD 27-FEB-2003.
RESULT 999
ID ABR84884 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040057-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
PN US2003040057-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 31.5%; Pred. No. 0.0086;
PD 27-FEB-2003.
RESULT 1000
ID ABR73442 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
PN US2003054467-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 31.5%; Pred. No. 0.0086;
PD 27-FEB-2003.
RESULT 1001
ID ABR76536 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003044932-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
PN US2003044932-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 31.5%; Pred. No. 0.0086;
PD 27-FEB-2003.
RESULT 1002
ID ABR73137 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003027270-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
PN US2003027270-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 31.5%; Pred. No. 0.0086;
PD 27-FEB-2003.
RESULT 1003
ID ABM18203 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
PN US2003054469-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 31.5%; Pred. No. 0.0086;
PD 27-FEB-2003.
RESULT 1004
ID ABO20662 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003032126-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
PN US2003032126-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 31.5%; Pred. No. 0.0086;
PD 27-FEB-2003.
RESULT 1005
ID ABO25405 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
PN US2003054463-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 31.5%; Pred. No. 0.0086;
PD 27-FEB-2003.
RESULT 1006
ID ABO25710 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 20.5%; Score 102; DB 6; Length 259;
PN US2003054466-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 31.5%; Pred. No. 0.0086;
PD 27-FEB-2003.
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PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1007
ID ABR94119 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1008
ID ABR80026 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049738-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1009
ID ABM11366 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1010
ID ABO32973 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1011
ID ABO30679 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1012
ID ABO30984 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1013
ID ABM27290 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1014
ID ABM30035 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1015
ID ABM05571 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1016
ID ABM15636 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1017
ID ABM08621 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1018
ID ABO42321 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1019
ID ABO38051 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1020
ID ABO45961 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1021
ID ABM66764 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1022
ID ADB20362 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003082767-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1023
ID ABM19665 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1024
ID ABO49377 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 6; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;

RESULT 1025
 ID ABO49682 standard; protein; 259 AA.
 DE Human secreted/transmembrane protein (PRO) #125.
 PN US2003049775-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 20.5%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.0086;
 RESULT 1026
 ID ADA78614 standard; protein; 259 AA.
 DE Human secreted/transmembrane protein (PRO) #125.
 PN US2003073181-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 20.5%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.0086;
 RESULT 1027
 ID ABR88239 standard; protein; 259 AA.
 DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
 PN US2003068720-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 20.5%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.0086;
 RESULT 1028
 ID ABR26985 standard; protein; 259 AA.
 DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
 PN US2003068739-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 20.5%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.0086;
 RESULT 1029
 ID ABO3382 standard; protein; 259 AA.
 DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
 PN US2003068763-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 20.5%; Score 102; DB 6; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.0086;
 RESULT 1030
 ID ABO3981 standard; protein; 259 AA.
 DE Human secreted/transmembrane protein (PRO) #125.
 PN US2003068689-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 20.5%; Score 102; DB 7; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.0086;
 RESULT 1031
 ID ABO49987 standard; protein; 259 AA.
 DE Human secreted/transmembrane protein (PRO) #125.
 PN US2003049776-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 20.5%; Score 102; DB 7; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.0086;
 RESULT 1032
 ID ABO50902 standard; protein; 259 AA.
 DE Human secreted/transmembrane protein (PRO) #125.
 PN US2003049780-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 20.5%; Score 102; DB 7; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.0086;
 RESULT 1033
 ID ABO5358 standard; protein; 259 AA.
 DE Human secreted/transmembrane protein (PRO) #125.
 PN US2003036126-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 20.5%; Score 102; DB 7; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.0086;
 RESULT 1034
 ID ABR74662 standard; protein; 259 AA.

DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
 PN US2003044924-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 20.5%; Score 102; DB 7; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.0086;
 RESULT 1035
 ID ABO44455 standard; protein; 259 AA.
 DE Human secreted/transmembrane protein PRO1316.
 PN US2003044841-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 20.5%; Score 102; DB 7; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.0086;
 RESULT 1036
 ID ABR77141 standard; protein; 259 AA.
 DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
 PN US2003044927-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 20.5%; Score 102; DB 7; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.0086;
 RESULT 1037
 ID ABR17898 standard; protein; 259 AA.
 DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
 PN US2003040072-A1.
 PD 27-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 20.5%; Score 102; DB 7; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.0086;
 RESULT 1038
 ID ABR95949 standard; protein; 259 AA.
 DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
 PN US2003040073-A1.
 PD 27-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 20.5%; Score 102; DB 7; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.0086;
 RESULT 1039
 ID ABO21882 standard; protein; 259 AA.
 DE Human secreted/transmembrane protein (PRO) #125.
 PN US2003054475-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 20.5%; Score 102; DB 7; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.0086;
 RESULT 1040
 ID ABO20052 standard; protein; 259 AA.
 DE Human secreted/transmembrane protein (PRO) #125.
 PN US2003032124-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 20.5%; Score 102; DB 7; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.0086;
 RESULT 1041
 ID ABO24355 standard; protein; 259 AA.
 DE Human secreted/transmembrane protein (PRO) #125.
 PN US2003064467-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 20.5%; Score 102; DB 7; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.0086;
 RESULT 1042
 ID ABR86104 standard; protein; 259 AA.
 DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
 PN US2003049759-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 20.5%; Score 102; DB 7; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.0086;
 RESULT 1043
 ID ABR10756 standard; protein; 259 AA.
 DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
 PN US2003064455-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 20.5%; Score 102; DB 7; Length 259;
 Best Local Similarity 31.5%; Pred. No. 0.0086;

RESULT 1044
ID ABM76755 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1045
ID ABR89459 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003073170-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1046
ID ABR12586 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1047
ID ABR05876 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1048
ID ABO35001 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1049
ID ABO3077 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1050
ID ABM19055 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1051
ID ABM19360 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1052
ID ABO46571 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1053
ID ABO49072 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1054
ID ABR69115 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003027273-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1055
ID ABR89154 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003036119-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1056
ID ABR72527 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003036120-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1057
ID ABR74357 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1058
ID ABO18625 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003044921-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1059
ID ABR80331 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1060
ID ABM01552 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1061
ID ABR02162 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1062
ID ABR87324 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;

Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1063
ID ABM12891 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1064
ID ABM30645 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1065
ID ABM24545 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1066
ID ABO29459 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1067
ID ABO31289 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1068
ID ABM14416 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1069
ID ABM09841 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1070
ID ABO38966 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1071
ID ABM34731 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104538-A1.
PD 05-JUN-2003.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1072

ID ABO51207 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1073
ID ABO04033 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036158-A1.
PD 20-FEB-2003.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1074
ID ABO10503 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003036151-A1.
PD 20-FEB-2003.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1075
ID ABR77746 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040067-A1.
PD 27-FEB-2003.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1076
ID ABR78956 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054456-A1.
PD 20-MAR-2003.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1077
ID ABO24050 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1078
ID ABR93814 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1079
ID ABM01857 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1080
ID ABM78280 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1081
ID ABO33479 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003073129-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1082
ID ABR90069 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003073177-A1.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1083
ID ABR27595 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1084
ID ABR13196 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1085
ID ABR031899 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1086
ID ABR14111 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068683-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1087
ID ABR08316 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1088
ID ABR040186 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068681-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1089
ID ABR74621 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1090
ID ABR33816 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1091
ID ABR20275 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1092
ID ABR048767 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1093
ID ABR72832 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003036122-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1094
ID ABR15474 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1095
ID ABR85189 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003040065-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1096
ID ABR15169 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003044919-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1097
ID ABR17304 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003040077-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1098
ID ABR17593 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003044928-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1099
ID ABR85494 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1100
ID ABR7060 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

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Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1101
ID ABO28239 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1102
ID ABM23020 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1103
ID ABM30340 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1104
ID ABM21800 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1105
ID ABM21495 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1106
ID ABM15026 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1107
ID ABO41101 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1108
ID ABO36831 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1109
ID ABO37441 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1110
ID ABM75231 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1111
ID ABM33511 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1112
ID ABO46266 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1113
ID ADA82685 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1114
ID ABM31865 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068680-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1115
ID ABM31255 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1116
ID ADB85993 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1117
ID ABM32170 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1118
ID ABM32475 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1119
ID ABM31560 standard; protein; 259 AA.
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DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1120
ID ARM30950 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1121
ID ADC1939 standard; protein; 259 AA.
DE Human PRO polypeptide #21.
PN US2003064925-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1122
ID ADD05723 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1123
ID ADD70585 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003099625-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1124
ID ADD39662 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003083462-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1125
ID ADD70108 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003054406-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1126
ID ADD38229 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003096955-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1127
ID ADD39185 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003096954-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1128
ID ADD38708 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.

PN US2003092061-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1129
ID ADD40139 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003082627-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1130
ID ADE50360 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003069179-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1131
ID ADE19972 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003092883-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1132
ID ADE49883 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003082626-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1133
ID ADE21441 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003082628-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1134
ID ADF29866 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003204053-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1135
ID ADF5759 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003204054-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1136
ID ADG02718 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1137
ID ADG01425 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003207399-A1.

PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1138
ID ADF95600 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1139
ID ADG12415 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1140
ID ADH09075 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1141
ID ADH99263 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1142
ID ADL32856 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1143
ID ADM30390 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1144
ID ADN39361 standard; protein; 259 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:B45.
PD 22-MAY-2003.
PA (BOSB-) BOS BIOTECHNOLOGY INC.
Query Match 20.5%; Score 102; DB 7; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1145
ID ADE74387 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1146
ID ADE74999 standard; protein; 259 AA.
DE Human secreted/transmembrane protein (PRO) #125.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;

RESULT 1147
ID ADE96443 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1148
ID ADF25754 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1149
ID ADF24653 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1150
ID ADF29389 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1151
ID ADE96920 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1152
ID ADF96212 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1153
ID ADG04483 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1154
ID ADG00643 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1155
ID ADG82899 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1156
ID ADH02958 standard; protein; 259 AA.

DE Human secreted/transmembrane protein PRO1316.
PN US2003216562-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1157
ID ADH03912 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003220471-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1158
ID ADH03435 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2003224478-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1159
ID ADH26180 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1160
ID ADH33149 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1161
ID ADH04389 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2004005626-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1162
ID ADH61390 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2004014130-A1.
PD 22-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1163
ID ADJ54888 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1164
ID ADJ64659 standard; protein; 259 AA.
DE Human PRO polypeptide #125.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1165
ID ADM31555 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2005163766-A1.

PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1166
ID ADM36602 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1167
ID ADM40407 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1168
ID ADL94589 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316.
PN US2004073015-A1.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1169
ID ADO35295 standard; protein; 259 AA.
DE Human Dkk family protein Dkk2.
PN US2004014209-A1.
PD 22-JAN-2004.
PA (LASS/) LASSAR A B.
PA (MERC/) MERCOLA M.
PA (GUPT/) GUPTA R.
PA (MARV/) MARVIN M.
PA (SCHN/) SCHNEIDER V.
PA (TZA/) TZAHOE E.
PA (BROT/) BROTT B.
PA (SOKO/) SOKOL S.
Query Match 20.5%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1170
ID ADN38015 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 8; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1171
ID AED44976 standard; protein; 259 AA.
DE Human secreted/transmembrane protein PRO1316, SEQ:70.
PN US2005181478-A1.
PD 18-AUG-2005.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FONG/) FONG S.
PA (GROW/) GAO W.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
Query Match 20.5%; Score 102; DB 9; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1172
ID AED50245 standard; protein; 259 AA.
DE Novel human secreted and transmembrane protein PRO1316.
PN US2005163766-A1.

PD 28-JUL-2005.
Query Match 20.5%; Score 102; DB 9; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1173
ID AEG62937 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2006073544-A1.
PD 06-APR-2006.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 10; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1174
ID AEG72760 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2006074226-A1.
PD 06-APR-2006.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 10; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1175
ID AEG62325 standard; protein; 259 AA.
DE Human secreted polypeptide PRO1316, SEQ ID NO:250.
PN US2006073545-A1.
PD 06-APR-2006.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 10; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1176
ID AEG88242 standard; protein; 259 AA.
DE Human PRO protein amino acid sequence - SEQ ID 250.
PN US2006074227-A1.
PD 06-APR-2006.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 10; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1177
ID AEG17558 standard; protein; 259 AA.
DE Human tumor overexpressed cDNA protein product PRO1316 SEQ ID NO: 250.
PN US2006094864-A1.
PD 04-MAY-2006.
PA (GETH) GENENTECH INC.
Query Match 20.5%; Score 102; DB 10; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1178
ID AEG40730 standard; protein; 259 AA.
DE Human dickkopf ligand Dkk-2.
PN WO2006061717-A2.
PD 15-JUN-2006.
PA (NEUR-) NEURO THERAPEUTICS AB.
Query Match 20.5%; Score 102; DB 10; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1179
ID AEL56587 standard; protein; 259 AA.
DE Human dickkopf related protein-2 precursor, SEQ ID NO: 1050.
PN US2006216722-A1.
PD 28-SEP-2006.
PA (BETS/) BETSHOLTZ C.
PA (TRYG/) TRYGGVASON K.
PA (TAKE/) TAKEMOTO M.
PA (HELL/) HE L.
PA (PATR/) PATRAKKAS J.
Query Match 20.5%; Score 102; DB 10; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0086;
RESULT 1180
ID AAB08880 standard; protein; 263 AA.
DE Amino acid sequence of a human Dickkopf (Dkk)-2 protein.
PN WO200052047-A2.
PD 08-SEP-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 20.5%; Score 102; DB 3; Length 263;
Best Local Similarity 31.5%; Pred. No. 0.0088;
RESULT 1181
ID AAY92072 standard; protein; 259 AA.
DE Murine DKR-2.
PN WO200018914-A2.
PD 06-APR-2000.
PA (AMGE-) AMGEN INC.
Query Match 20.3%; Score 101; DB 3; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.011;
RESULT 1182
ID AEL55689 standard; protein; 259 AA.
DE Mouse dickkopf related protein-2 precursor, SEQ ID NO: 150.
PN US2006216722-A1.
PD 28-SEP-2006.
PA (BETS/) BETSHOLTZ C.
PA (TRYG/) TRYGGVASON K.
PA (TAKE/) TAKEMOTO M.
PA (HELL/) HE L.
PA (PATR/) PATRAKKAS J.
Query Match 20.3%; Score 101; DB 10; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.011;
RESULT 1183
ID AEI40729 standard; protein; 260 AA.
DE Mouse dickkopf ligand Dkk-2.
PN WO2006061717-A2.
PD 15-JUN-2006.
PA (NEUR-) NEURO THERAPEUTICS AB.
Query Match 20.3%; Score 101; DB 10; Length 260;
Best Local Similarity 31.5%; Pred. No. 0.011;
RESULT 1184
ID AEA38732 standard; protein; 272 AA.
DE Mouse dickkopf-1 (Dkk-1) protein, SEQ ID NO: 22.
PN WO2005049640-A2.
PD 02-JUN-2005.
PA (MERI) MERCK & CO INC.
Query Match 20.3%; Score 101; DB 9; Length 272;
Best Local Similarity 33.8%; Pred. No. 0.012;
RESULT 1185
ID AEF80274 standard; protein; 272 AA.
DE Mouse dickkopf-1 (Dkk-1) protein sequence.
PN WO2006015373-A2.
PD 09-FEB-2006.
PA (AMGE-) AMGEN INC.
Query Match 20.3%; Score 101; DB 10; Length 272;
Best Local Similarity 33.8%; Pred. No. 0.012;
RESULT 1186
ID AEI40727 standard; protein; 272 AA.
DE Mouse dickkopf ligand Dkk-1.
PN WO2006061717-A2.
PD 15-JUN-2006.
PA (NEUR-) NEURO THERAPEUTICS AB.
Query Match 20.3%; Score 101; DB 10; Length 272;
Best Local Similarity 33.8%; Pred. No. 0.012;
RESULT 1187
ID ADY86168 standard; protein; 83 AA.
DE Human dickkopf-3 protein, SEQ ID NO:6.
PN US2005064522-A1.
PD 24-MAR-2005.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 9; Length 83;
Best Local Similarity 37.7%; Pred. No. 0.0038;
RESULT 1188
ID ADB64042 standard; protein; 215 AA.
DE Human protein encoded by clone BRAMY20227860.
PN EPI308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 20.2%; Score 100.5; DB 7; Length 215;
Best Local Similarity 37.7%; Pred. No. 0.01;
RESULT 1189
ID AAU73016 standard; protein; 350 AA.
DE Human cysteine-rich secreted protein CRSP-1.
PN WO9846755-A1.
PD 22-OCT-1998.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.

Query Match
Best Local Similarity 20.2%; Score 100.5; DB 2; Length 350;
RESULT 1190
ID AAW62595 standard; protein; 350 AA.
DE Homo sapiens cerebellum and embryo specific protein.
PN WO9827932-A2.
PD 02-JUL-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 20.2%; Score 100.5; DB 2; Length 350;
RESULT 1191
ID AAY13384 standard; protein; 350 AA.
DE Amino acid sequence of protein PRO295.
PN WO9914328-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.2%; Score 100.5; DB 2; Length 350;
RESULT 1192
ID AAY92070 standard; protein; 350 AA.
DE Human DKR-3.
PN WO200018914-A2.
PD 06-APR-2000.
PA (AMGE-) AMGEN INC.
Query Match
Best Local Similarity 20.2%; Score 100.5; DB 3; Length 350;
RESULT 1193
ID AAB08874 standard; protein; 350 AA.
DE Amino acid sequence of a human Dickkopf (Dkk)-3 protein.
PN WO200052047-A2.
PD 08-SEP-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 20.2%; Score 100.5; DB 3; Length 350;
RESULT 1194
ID ADC78556 standard; protein; 350 AA.
DE Human PRO295 protein.
PN WO200015796-A2.
PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.2%; Score 100.5; DB 3; Length 350;
RESULT 1195
ID AAB80252 standard; protein; 350 AA.
DE Human PRO295 protein.
PN WO200104311-A1.
PD 18-JAN-2001.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.2%; Score 100.5; DB 4; Length 350;
RESULT 1196
ID AAG80271 standard; protein; 350 AA.
DE Human DKK-3 protein.
PN WO200163295-A2.
PD 30-AUG-2001.
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
Query Match
Best Local Similarity 20.2%; Score 100.5; DB 4; Length 350;
RESULT 1197
ID AAB87529 standard; protein; 350 AA.
DE Human PRO295.
PN WO200116318-A2.
PD 08-MAR-2001.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.2%; Score 100.5; DB 4; Length 350;
RESULT 1198
ID AAG62468 standard; protein; 350 AA.
DE Human reduced expression in immortalised cells protein.
PN WO200138528-A1.
PD 31-MAY-2001.
PA (HISM) HISAMITSU PHARM CO LTD.
Query Match
Best Local Similarity 20.2%; Score 100.5; DB 4; Length 350;

Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1199
ID ABB90735 standard; protein; 350 AA.
DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 202.
PN WO200210217-A2.
PD 07-FEB-2002.
PA (UYJO) UNIV JOHNS HOPKINS.
Query Match
Best Local Similarity 20.2%; Score 100.5; DB 5; Length 350;
RESULT 1200
ID ABG95854 standard; protein; 350 AA.
DE Human secreted/transmembrane protein PRO295.
PN US2002119130-A1.
PD 29-AUG-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.2%; Score 100.5; DB 5; Length 350;
RESULT 1201
ID ABB84841 standard; protein; 350 AA.
DE Human PRO295 protein sequence SEQ ID NO:50.
PN WO200200690-A2.
PD 03-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.2%; Score 100.5; DB 5; Length 350;
RESULT 1202
ID ABB95447 standard; protein; 350 AA.
DE Human angiogenesis related protein PRO295 SEQ ID NO: 50.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1203
ID ABU71630 standard; protein; 350 AA.
DE Human PRO polypeptide #41.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.2%; Score 100.5; DB 6; Length 350;
RESULT 1204
ID ABU71485 standard; protein; 350 AA.
DE Human PRO polypeptide #41.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.2%; Score 100.5; DB 6; Length 350;
RESULT 1205
ID ABU54442 standard; protein; 350 AA.
DE Human tumour endothelial marker TEM 4.
PN WO200283874-A2.
PD 24-OCT-2002.
PA (UYJO) UNIV JOHNS HOPKINS.
Query Match
Best Local Similarity 20.2%; Score 100.5; DB 6; Length 350;
RESULT 1206
ID ABU54442 standard; protein; 350 AA.
DE Human tumour endothelial marker TEM 4.
PN WO200283874-A2.
PD 24-OCT-2002.
PA (UYJO) UNIV JOHNS HOPKINS.
Query Match
Best Local Similarity 37.7%; Pred. No. 0.017;

ID ABU71931 standard; protein; 350 AA.
DE Human secreted/transmembrane protein PRO295.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1207
ID ABO01814 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1208
ID ABU90879 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1209
ID ABO33938 standard; protein; 350 AA.
DE Human secreted/transmembrane protein PRO295.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1210
ID ABU71955 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1211
ID ABU55915 standard; protein; 350 AA.
DE Human protein DKK3.
PN WO200277204-A2.
PD 03-OCT-2002.
PA (AXOR-) AXORDIA LTD.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1212
ID ABU54387 standard; protein; 350 AA.
DE Human secreted/transmembrane protein PRO295.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1213
ID ABO47402 standard; protein; 350 AA.
DE Human secreted/transmembrane polypeptide PRO295.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1214
ID ABU71509 standard; protein; 350 AA.
DE Human secreted polypeptide PRO295.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1215
ID ABE34069 standard; protein; 350 AA.

DE DKK 3 protein.
PN WO200290992-A2.
PD 14-NOV-2002.
PA (AXOR-) AXORDIA LTD.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1216
ID ABU72290 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1217
ID ABU90963 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1218
ID ABO27284 standard; protein; 350 AA.
DE Human secreted/transmembrane polypeptide PRO295.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1219
ID ABU64539 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #43.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1220
ID ABU67385 standard; protein; 350 AA.
DE Human secreted protein PRO295.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1221
ID ABU92479 standard; protein; 350 AA.
DE Human secreted/transmembrane protein PRO295.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1222
ID ABO14905 standard; protein; 350 AA.
DE Human secreted/transmembrane polypeptide PRO295.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1223
ID ABU81149 standard; protein; 350 AA.
DE Human secreted polypeptide PRO295.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1224
ID ABO53264 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.

PD US2003027986-A1.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1225
ID ABU98266 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1226
ID ABU98271 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1227
ID ABU82478 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1228
ID ABU69662 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1229
ID ABU96442 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1230
ID ABU72112 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1231
ID ABO14844 standard; protein; 350 AA.
DE Human secreted / transmembrane polypeptide PRO295.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1232
ID ADB29441 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1233
ID ADB17065 standard; protein; 350 AA.
DE Human transmembrane PRO polypeptide (SeqID 8).
PN US2003050462-A1.

PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1234
ID ABO44242 standard; protein; 350 AA.
DE Human secreted/transmembrane polypeptide PRO 295.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1235
ID ADA18297 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1236
ID ABO32796 standard; protein; 350 AA.
DE Human secreted/transmembrane protein PRO295.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1237
ID ADA19870 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1238
ID ADB17253 standard; protein; 350 AA.
DE Human transmembrane PRO polypeptide (SeqID 8).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1239
ID ABO34856 standard; protein; 350 AA.
DE Human PRO polypeptide #41.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1240
ID ADA16272 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1241
ID ADA20042 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1242
ID ABO34170 standard; protein; 350 AA.
DE Human secreted/transmembrane polypeptide PRO 295.
PN US2003060601-A1.
PD 27-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1243
ID ADA42417 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1244
ID ABO17534 standard; protein; 350 AA.
DE Human PRO polypeptide #41.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1245
ID ADA00339 standard; protein; 350 AA.
DE Human secreted/transmembrane polypeptide PRO 295.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 6; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1246
ID ADA16696 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1247
ID ADA13125 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1248
ID ADA41993 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1249
ID ADA17340 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1250
ID ADA42843 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1251
ID ABO17595 standard; protein; 350 AA.
DE Human PRO polypeptide #41.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1252
ID ADB85581 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1253
ID ADB77762 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1254
ID ADB74898 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1255
ID ADB68260 standard; protein; 350 AA.
DE Human PRO295 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1256
ID ADB68067 standard; protein; 350 AA.
DE Human PRO295 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1257
ID ADB90884 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1258
ID ADC28544 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1259
ID ADC39744 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1260
ID ADC40258 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;

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Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1261
ID ADC19082 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1262
ID ADC34382 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1263
ID ADC29437 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1264
ID ADC28968 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1265
ID ADC40853 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1266
ID ADC19510 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1267
ID ADC06964 standard; protein; 350 AA.
DE Human PRO295 protein.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1268
ID ADC17143 standard; protein; 350 AA.
DE Mammalian PRO polypeptide (Seqid 8).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1269
ID ADC33958 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1270
ID ADC13028 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1271
ID ADC14841 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1272
ID ADC52336 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1273
ID ADC12480 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1274
ID ADD10339 standard; protein; 350 AA.
DE Human secreted/transmembrane PRO polypeptide #25.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1275
ID ADD05035 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1276
ID ADD11299 standard; protein; 350 AA.
DE Human secreted/transmembrane PRO polypeptide #25.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1277
ID ADD04041 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1278
ID ADD03617 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1279
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ID ADD37092 standard; protein; 350 AA.
DE Human secreted/transmembrane PRO polypeptide #25.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1280
ID ADD36012 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1281
ID ADE34869 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1282
ID ADG01013 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1283
ID ADG08566 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1284
ID ADF95187 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1285
ID ADH24040 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1286
ID ADH34066 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1287
ID ADH29899 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1288
ID ADH23870 standard; protein; 350 AA.

DE Novel human secreted and transmembrane protein PRO295.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1289
ID ADG85274 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1290
ID ADH24550 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1291
ID ADH37406 standard; protein; 350 AA.
DE Human secreted and transmembrane protein PRO295.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1292
ID ADH01995 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1293
ID ADH37576 standard; protein; 350 AA.
DE Human secreted and transmembrane protein PRO295.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1294
ID ADG85614 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1295
ID ADH24210 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1296
ID ADH38504 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1297
ID ADG83625 standard; protein; 350 AA.
DE Human PRO polypeptide #4.

PD US2003180794-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1298
ID ADH29433 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1299
ID ADH27549 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1300
ID ADH37746 standard; protein; 350 AA.
DE Human secreted and transmembrane protein PRO295.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1301
ID ADH37923 standard; protein; 350 AA.
DE Human secreted and transmembrane protein PRO295.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1302
ID ADH57343 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1303
ID ADH59352 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1304
ID ADH53485 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1305
ID ADH53655 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1306
ID ADH51991 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181638-A1.

PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1307
ID ADH49846 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1308
ID ADI25356 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1309
ID ADH90149 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1310
ID ADI25526 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1311
ID ADH97700 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1312
ID ADI38131 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1313
ID ADI03548 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1314
ID ADI11905 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1315
ID ADH89979 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181697-A1.
PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1316
ID ADH98380 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1317
ID ADI11055 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1318
ID ADI11565 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1319
ID ADH98210 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1320
ID ADH98550 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1321
ID ADH98040 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1322
ID ADI05028 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1323
ID ADI03378 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1324
ID ADI04773 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1325
ID ADH78227 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1326
ID ADI19571 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1327
ID ADH90319 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1328
ID ADI03038 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1329
ID ADH77887 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1330
ID ADH97870 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1331
ID ADI01255 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1332
ID ADI01950 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1333
ID ADI03208 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;

Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1334
ID ADI11395 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1335
ID ADI02297 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1336
ID ADI11735 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1337
ID ADI05372 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1338
ID ADH79444 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1339
ID ADI19401 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1340
ID ADI05202 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1341
ID ADH79614 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1342
ID ADI01440 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1343
ID ADI01610 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1344
ID ADI01780 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1345
ID ADH79784 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1346
ID ADI04602 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1347
ID ADI02738 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1348
ID ADH78057 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1349
ID ADI25696 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1350
ID ADI25866 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1351
ID ADK65378 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1352

ID ADH98720 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1353
ID ADH79961 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1354
ID ADJ26399 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1355
ID ADL93692 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1356
ID ADP65205 standard; protein; 350 AA.
DE Human dickkopf homologue 3, RIG-like 7-1, RIG-like 5-6.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 20.2%; Score 100.5; DB 7; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1357
ID ADC52146 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1358
ID ADE79314 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1359
ID ADE79738 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1360
ID ADE73414 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1361
ID ADE41300 standard; protein; 350 AA.

DE Human secreted/transmembrane PRO polypeptide #25.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1362
ID ADE73949 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1363
ID ADE99503 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1364
ID ADE98622 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1365
ID ADE99049 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1366
ID ADG40519 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1367
ID ADF73913 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1368
ID ADF73489 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1369
ID ADH06578 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180852-A1.
PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1370
ID ADH06408 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO2995.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1371
ID ADG68829 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO2995.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1372
ID ADH27719 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO2995.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1373
ID ADH25060 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO2995.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1374
ID ADH33692 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1375
ID ADG92332 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1376
ID ADH02335 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1377
ID ADH07942 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO2995.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1378
ID ADG69339 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO2995.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1379
ID ADH39160 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO2995.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1380
ID ADG92759 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003027146-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1381
ID ADG83900 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1382
ID ADG85444 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO2995.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1383
ID ADH06238 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO2995.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1384
ID ADH30068 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO2995.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1385
ID ADH24380 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO2995.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1386
ID ADG69509 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO2995.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1387
ID ADH07772 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO2995.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;

Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1388
ID ADG85784 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1389
ID ADH39330 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1390
ID ADH33522 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1391
ID ADH33862 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1392
ID ADH01072 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1393
ID ADG69679 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1394
ID ADH02165 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1395
ID ADG69169 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1396
ID ADG85954 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1397
ID ADH24890 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1398
ID ADH39507 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1399
ID ADH02505 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1400
ID ADG68999 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1401
ID ADH07602 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1402
ID ADG86124 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1403
ID ADH24720 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1404
ID ADH25768 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1405
ID ADH38334 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1406
ID ADH38334 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;

ID ADH20548 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1407
ID ADH57173 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1408
ID ADH43483 standard; protein; 350 AA.
DE Human PRO polypeptide #25.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1409
ID ADH07403 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1410
ID ADH52161 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1411
ID ADH59948 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1412
ID ADH49527 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1413
ID ADH06976 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1414
ID ADH90489 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1415
ID ADI11225 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1416
ID ADI18718 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003152999-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1417
ID ADH98890 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1418
ID ADI65438 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003148419-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1419
ID ADI02120 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1420
ID ADH90659 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1421
ID ADI37697 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1422
ID ADH97497 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003190610-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;

Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1423
ID ADI5865 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003148371-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1424
ID ADH60608 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2004023331-A1.
PD 05-FEB-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1425
ID ADJ9865 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003187238-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1426
ID ADL08858 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003186358-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1427
ID ADJ98534 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1428
ID ADJ98704 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1429
ID ADH78863 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1430
ID ADJ99097 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1431
ID ADJ99267 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1432
ID ADJ98885 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1433
ID ADH79033 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1434
ID ADK00893 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1435
ID ADK14414 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1436
ID ADM25199 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003096233-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1437
ID ADM29949 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1438
ID ADK82828 standard; protein; 350 AA.
DE Human PRO polypeptide #25.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1439
ID ADM80863 standard; protein; 350 AA.
DE Human PRO polypeptide #4.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1440
ID ADO06271 standard; protein; 350 AA.
DE Human PRO polypeptide #41.

PN US6686451-B1.
PD 03-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1441
ID ADR11123 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1442
ID ADR18032 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF B.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1443
ID ADS74671 standard; protein; 350 AA.
DE Human secreted/transmembrane protein #45.
PN US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF B.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1444
ID AET03708 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2003152922-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 8; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1445
ID ADY77703 standard; protein; 350 AA.
DE Neoplastic disease detection protein PRO295.
PN US2005059102-A1.
PD 17-MAR-2005.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
Query Match 20.2%; Score 100.5; DB 9; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1446
ID AEA37946 standard; protein; 350 AA.
DE Human secreted/transmembrane protein, #45.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 9; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1447
ID AED23980 standard; protein; 350 AA.
DE Human secreted protein PRO 295, SEQ ID 236.
PN US2005214904-A1.
PD 29-SEP-2005.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 9; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1448
ID AEE69149 standard; protein; 350 AA.
DE Integrin homologous PRO295 protein, SEQ ID 236.
PN US6974689-B1.
PD 13-DEC-2005.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 10; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1449
ID AEF12534 standard; protein; 350 AA.
DE Human PRO295 protein SEQ ID NO:8.
PN US2006008901-A1.
PD 12-JAN-2006.
PA (GETH) GENENTECH INC.
Query Match 20.2%; Score 100.5; DB 10; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1450
ID AEF74223 standard; protein; 350 AA.
DE Human PRO295 protein SEQ ID NO:8.
PN US2005260647-A1.
PD 24-NOV-2005.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
Query Match 20.2%; Score 100.5; DB 10; Length 350;

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Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1451
ID AEF68232 standard; protein; 350 AA.
DE Human Dickkopf homolog 3 (DKK-3) protein.
PN WO2006010534-A1.
PD 02-FEB-2006.
PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.
Query Match 20.2%; Score 100.5; DB 10; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1452
ID AEH43561 standard; protein; 350 AA.
DE PRO295 protein sequence, SEQ ID 8.
PN US2006099657-A1.
PD 11-MAY-2006.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GER/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
Query Match 20.2%; Score 100.5; DB 10; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1453
ID AEJ11886 standard; protein; 350 AA.
DE Novel human secreted and transmembrane protein PRO295.
PN US2006160186-A1.
PD 20-JUL-2006.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GER/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
Query Match 20.2%; Score 100.5; DB 10; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1454
ID AEJ49625 standard; protein; 350 AA.
DE Heterologous polypeptide HG1018473Pl.
PN WO2006081430-A2.
PD 03-AUG-2006.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 20.2%; Score 100.5; DB 10; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1455
ID AEJ93983 standard; protein; 350 AA.
DE Benign prostatic hyperplasia-related protein, DKK3.
PN WO2006083657-A2.
PD 10-AUG-2006.
PA (BAYU ) BAYLOR COLLEGE MEDICINE.
Query Match 20.2%; Score 100.5; DB 10; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1456
ID AEL75467 standard; protein; 350 AA.
DE Human dickkopf homolog 3, SEQ ID NO: 35.
PN KR2005092659-A.
PD 22-SEP-2005.
PA (OYKY-) UNIV KYUNGPOOK NAT IND ACADEMIC COOP.
Query Match 20.2%; Score 100.5; DB 10; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.017;
RESULT 1457
ID AAW73021 standard; protein; 349 AA.
DE Mouse cysteine-rich secreted protein-1.
PN WO9846755-A1.
PD 22-OCT-1998.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Query Match 19.8%; Score 98.5; DB 2; Length 349;
Best Local Similarity 37.7%; Pred. No. 0.029;

RESULT 1458
ID AAY92069 standard; protein; 349 AA.
DE Murine DKR-3.
PN WO200018914-A2.
PD 06-APR-2000.
PA (AMGE-) AMGEN INC.
Query Match 19.8%; Score 98.5; DB 3; Length 349;
Best Local Similarity 37.7%; Pred. No. 0.029;
RESULT 1459
ID AAB08879 standard; protein; 349 AA.
DE A murine Dickkopf (Dkk)-3 protein.
PN WO200052047-A2.
PD 08-SEP-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 19.8%; Score 98.5; DB 3; Length 349;
Best Local Similarity 37.7%; Pred. No. 0.029;
RESULT 1460
ID AEF68233 standard; protein; 349 AA.
DE Murine Dickkopf homolog 3 (DKK-3) protein.
PN WO2006010534-A1.
PD 02-FEB-2006.
PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.
Query Match 19.8%; Score 98.5; DB 10; Length 349;
Best Local Similarity 37.7%; Pred. No. 0.029;
RESULT 1461
ID ADE82539 standard; protein; 84 AA.
DE Antibody that binds to DKK #6.
PN WO200292015-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP ) WYETH.
Query Match 19.5%; Score 97; DB 7; Length 84;
Best Local Similarity 32.3%; Pred. No. 0.0094;
RESULT 1462
ID ADE82541 standard; protein; 107 AA.
DE Antibody that binds to DKK #8.
PN WO200292015-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP ) WYETH.
Query Match 19.5%; Score 97; DB 7; Length 107;
Best Local Similarity 32.3%; Pred. No. 0.012;
RESULT 1463
ID ADU66981 standard; protein; 108 AA.
DE Human DKK-1 LRP-6 binding domain.
PN US2004235166-A1.
PD 25-NOV-2004.
PA (PROC/) PROCKOP D.
PA (SEKI/) SEKIYA I.
PA (GREG/) GREGORY C.
PA (SPRE/) SPEES J.
PA (SMIT/) SMITH J.
PA (POCH/) POCHAMPALLY R.
Query Match 19.5%; Score 97; DB 8; Length 108;
Best Local Similarity 32.3%; Pred. No. 0.012;
RESULT 1464
ID ADZ51669 standard; protein; 108 AA.
DE Dickkopf-1 LDL receptor-related protein 6 binding site.
PN US2005084494-A1.
PD 21-APR-2005.
PA (PROC/) PROCKOP D.
PA (GREG/) GREGORY C.
PA (GUNN/) GUNN W.
Query Match 19.5%; Score 97; DB 9; Length 108;
Best Local Similarity 32.3%; Pred. No. 0.012;
RESULT 1465
ID ADE82538 standard; protein; 128 AA.
DE Antibody that binds to DKK #5.
PN WO200292015-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP ) WYETH.
Query Match 19.5%; Score 97; DB 7; Length 128;
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Best Local Similarity 32.3%; Pred. No. 0.015;
RESULT 1466
ID ADE82540 standard; protein; 149 AA.
DE Antibody that binds to DKK #7.
PN WO200292015-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 19.5%; Score 97; DB 7; Length 149;
Best Local Similarity 32.3%; Pred. No. 0.017;
RESULT 1467
ID ADB99065 standard; protein; 151 AA.
DE LRP5 constrained peptide OST264.
PN WO200292000-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 19.5%; Score 97; DB 7; Length 151;
Best Local Similarity 32.3%; Pred. No. 0.017;
RESULT 1468
ID ADE82633 standard; protein; 151 AA.
DE LRP5 peptide aptamer #10.
PN WO200292015-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 19.5%; Score 97; DB 7; Length 151;
Best Local Similarity 32.3%; Pred. No. 0.017;
RESULT 1469
ID ADE82537 standard; protein; 170 AA.
DE Antibody that binds to DKK #4.
PN WO200292015-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 19.5%; Score 97; DB 7; Length 170;
Best Local Similarity 32.3%; Pred. No. 0.02;
RESULT 1470
ID ADB99066 standard; protein; 172 AA.
DE LRP5 constrained peptide OST265.
PN WO200292000-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 19.5%; Score 97; DB 7; Length 172;
Best Local Similarity 32.3%; Pred. No. 0.02;
RESULT 1471
ID ADE82634 standard; protein; 172 AA.
DE LRP5 peptide aptamer #11.
PN WO200292015-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 19.5%; Score 97; DB 7; Length 172;
Best Local Similarity 32.3%; Pred. No. 0.02;
RESULT 1472
ID ADO35296 standard; protein; 180 AA.
DE Human Dkl1 carboxy terminal cysteine rich region.
PN US2004014209-A1.
PD 22-JAN-2004.
PA (LASS/) LASSAR A B.
PA (MERC/) MERCOLA M.
PA (GUPT/) GUPTA R.
PA (MARV/) MARVIN M.
PA (SCHN/) SCHNEIDER V.
PA (TZAHA/) TZAHAOR E.
PA (BROT/) BROTT B.
PA (SOKO/) SOKOL S.
Query Match 19.5%; Score 97; DB 8; Length 180;
Best Local Similarity 32.3%; Pred. No. 0.021;
RESULT 1473
ID ADE82535 standard; protein; 212 AA.
DE Antibody that binds to DKK #2.
PN WO200292015-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 19.5%; Score 97; DB 7; Length 212;
Best Local Similarity 32.3%; Pred. No. 0.025;
RESULT 1474
ID ADB82534 standard; protein; 233 AA.
DE Antibody that binds to DKK #1.
PN WO200292015-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 19.5%; Score 97; DB 7; Length 233;
Best Local Similarity 32.3%; Pred. No. 0.027;
RESULT 1475
ID AEA38731 standard; protein; 265 AA.
DE Human dickkopf-1 (Dkk-1) protein, SEQ ID NO: 21 #1.
PN WO2005049640-A2.
PD 02-JUN-2005.
PA (MERI) MERCK & CO INC.
Query Match 19.5%; Score 97; DB 9; Length 265;
Best Local Similarity 32.3%; Pred. No. 0.031;
RESULT 1476
ID AAW73018 standard; protein; 266 AA.
DE Human cyteine-rich secreted protein CRSP-3.
PN WO9846755-A1.
PD 22-OCT-1998.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Query Match 19.5%; Score 97; DB 2; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.031;
RESULT 1477
ID AAY41757 standard; protein; 266 AA.
DE Human PRO1008 protein sequence.
PN WO9946281-A2.
PD 16-SEP-1999.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 2; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.031;
RESULT 1478
ID AAY92071 standard; protein; 266 AA.
DE Human DKK-1.
PN WO200018914-A2.
PD 06-APR-2000.
PA (AMGE-) AMGEN INC.
Query Match 19.5%; Score 97; DB 3; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.031;
RESULT 1479
ID AAB44313 standard; protein; 266 AA.
DE Human PRO1008 (UNQ492) protein sequence SEQ ID NO:456.
PN WO200053756-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 3; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.031;
RESULT 1480
ID AAB08876 standard; protein; 266 AA.
DE Amino acid sequence of a human Dickkopf (Dkk)-1 protein.
PN WO200052047-A2.
PD 08-SEP-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 19.5%; Score 97; DB 3; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.031;
RESULT 1481
ID AAU12385 standard; protein; 266 AA.
DE Human PRO1008 polypeptide sequence.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 4; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.031;
RESULT 1482
ID AAM78517 standard; protein; 266 AA.

DE Human protein SEQ ID NO 1179.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 19.5%; Score 97; DB 4; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.031;
RESULT 1483
ID ABO17829 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO1008.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.031;
RESULT 1484
ID ABO25259 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO1008.
PN US2003050239-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.031;
RESULT 1485
ID ABO18083 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.031;
RESULT 1486
ID ABO72265 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO1008.
PN US2002192706-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.031;
RESULT 1487
ID ABO66783 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.031;
RESULT 1488
ID ABO55913 standard; protein; 266 AA.
DE Human protein DKK1.
PN WO200277204-A2.
PD 03-OCT-2002.
PA (AXOR-) AXORDIA LTD.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.031;
RESULT 1489
ID ABO84945 standard; protein; 266 AA.
DE Human secreted and transmembrane PRO polypeptide #21.
PN US2002177553-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.031;
RESULT 1490
ID AAE34067 standard; protein; 266 AA.
DE DKK1 protein.
PN WO200290992-A2.
PD 14-NOV-2002.
PA (AXOR-) AXORDIA LTD.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.031;
RESULT 1491
ID ABO59864 standard; protein; 266 AA.
DE Novel secreted and transmembrane protein PRO1008.
PN US2003054517-A1.

PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.031;
RESULT 1492
ID ABO61143 standard; protein; 266 AA.
DE Human PRO1008 polypeptide.
PN US2002169284-A1.
PD 14-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.031;
RESULT 1493
ID ABO57630 standard; protein; 266 AA.
DE Differentially expressed breast cancer associated protein #17.
PN US2002156263-A1.
PD 24-OCT-2002.
PA (CHEN/) CHEN H.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.031;
RESULT 1494
ID ABO25054 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #214.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.031;
RESULT 1495
ID ABO1793 standard; protein; 266 AA.
DE Human cancer-related protein, 151P1C7A.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.031;
RESULT 1496
ID ABO80412 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO1008.
PN US2003004102-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.031;
RESULT 1497
ID ABO67059 standard; protein; 266 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 428.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.031;
RESULT 1498
ID ADA45947 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO1008.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.031;
RESULT 1499
ID ADA76378 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.031;
RESULT 1500
ID ADA19028 standard; protein; 266 AA.
DE Human PRO polypeptide #214.
PN US2003054517-A1.

PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 97; DB 6; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.031;

GenCore version 6.2.1
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 OM protein - protein search, using sw model
 Run on: November 29, 2007, 17:18:54 ; Search time 163 Seconds
 (without alignments)
 564.121 Million cell updates/sec

Title: US-10-692-299-2_COPY_20_105
 Perfect score: 498
 Sequence: 1 AVITGACERDVQAGTCCA.....CSRPPDGRVRCSDMLKNINF 86

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : UniProt 8.4.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	498	100.0	105	1	PROK1 HUMAN
2	498	100.0	105	2	Q5VMD4 HUMAN
3	497	99.8	105	2	Q8TC69 HUMAN
4	473	95.0	105	1	PROK1 RAT
5	432	86.7	81	2	Q8K457 MOUSE
6	417	83.7	81	2	Q3ZF12 BOVIN
7	345	69.3	104	2	Q2XXR8 VARVA
8	340	68.3	104	2	Q2XXR7 VARVA
9	315	63.3	81	1	VPRA_DENPO
10	311	62.4	106	2	Q4RVU3 TETNG
11	304	61.0	108	2	Q863H4 BOVIN
12	291	58.4	108	2	Q6ISR0 HUMAN
13	286	57.4	107	1	PROK2 RAT
14	286	57.4	107	2	Q5OE37 9MURI
15	286	57.4	107	2	Q5OE38 9MURI
16	285	57.2	102	2	Q4SR12 TETNG
17	284	57.0	128	2	Q863H5 BOVIN
18	278.5	55.9	96	2	Q8JFQ0 BOMMX
19	273.5	54.9	96	2	Q5W280 BOMMX
20	270.5	54.3	129	1	PROK2 HUMAN
21	270.5	54.3	129	2	Q53278 HUMAN
22	267.5	53.7	96	1	BV8_BOMVA
23	265.5	53.3	128	1	PROK2 MOUSE
24	265.5	53.3	128	2	Q5V8J7 RAT
25	265.5	53.3	128	2	Q5OE33 9MURI
26	265.5	53.3	128	2	Q5OE34 9MURI
27	254.5	51.1	96	2	Q8JF86 BOMMX
28	253.5	50.9	96	2	Q8JFX8 BOMMX
29	253.5	50.9	96	2	Q8JFY1 BOMMX
30	249.5	50.1	96	2	Q8JFY0 BOMMX
31	249.5	50.1	96	2	Q8JFX9 BOMMX

32	246.5	49.5	96.	2	Q8JFY2 BOMMX
33	193	38.8	39	2	Q5OE61 9MURI
34	191	38.4	82	2	Q2TBS7 BOVIN
35	188	37.8	86	2	Q5OE35 9MURI
36	188	37.8	86	2	Q5OE36 9MURI
37	121.5	24.4	124	2	Q56R10 PENMO
38	112	22.5	96	2	Q8UUX3 CHICK
39	108.5	21.8	221	1	DKK4 MOUSE
40	107.5	21.6	224	1	DKK4 HUMAN
41	107.5	21.6	224	1	Q3KNX0 HUMAN
42	107.5	21.6	350	1	DKK3 CHICK
43	104	20.9	255	2	Q9DDA4 XENLA
44	102	20.5	180	2	Q4RJF1 TETNG
45	102	20.5	259	1	DKK2 HUMAN
46	101.5	20.4	256	2	Q5EHU6 GECJA
47	101	20.3	259	1	DKK2 MOUSE
48	101	20.3	259	2	Q8BFW0 MOUSE
49	101	20.3	272	1	DKK1 MOUSE
50	101	20.3	272	2	Q8OU55 MOUSE
51	100.5	20.2	171	2	Q43532 HUMAN
52	100.5	20.2	215	2	Q8N294 HUMAN
53	100.5	20.2	341	2	Q5R870 PONPY
54	100.5	20.2	349	2	Q2HWP5 PIG
55	100.5	20.2	350	1	DKK3 HUMAN
56	100.5	20.2	350	2	Q5R4Q2 PONPY
57	100.5	20.2	350	2	Q4R417 MACFA
58	99.5	20.0	277	2	Q9ES33 RAT
59	99.5	20.0	348	2	Q5RKL1 RAT
60	98.5	19.8	349	1	DKK3 MOUSE
61	97	19.5	266	1	DKK1 HUMAN
62	96.5	19.4	268	2	Q6FVU5 RABIT
63	95.5	19.2	259	2	Q57464 XENLA
64	95	19.1	177	2	Q4SL69 TETNG
65	94.5	19.0	350	2	Q6PQ81 HUMAN
66	94	18.9	240	2	Q3PMH3 BEARE
67	90.5	18.2	104	2	Q96R11 PACLE
68	88.5	17.8	640	2	Q96397 CHLRE
69	88	17.7	88	2	Q5D229 HADSP
70	87	17.5	88	2	Q5D228 HADSP
71	86	17.3	241	2	Q9W6D9 BEARE
72	84.5	17.0	102	2	Q3UW21 MOUSE
73	84	16.9	88	2	Q5D230 HADSP
74	83.5	16.8	110	2	Q4PML0 IXOSC
75	83.5	16.8	504	2	Q1XB78 MYTED
76	82.5	16.6	400	2	Q3U128 MOUSE
77	82.5	16.6	425	1	CN130 MOUSE
78	82.5	16.6	425	2	Q52KC0 MOUSE
79	82.5	16.6	425	2	Q642A8 RAT
80	82	16.5	1013	2	Q28CM0 XENTR
81	82	16.5	1165	2	Q5BKF5 XENTR
82	81.5	16.4	446	2	Q8NB03 HUMAN
83	81	16.3	1964	1	NOTC4 MOUSE
84	80.5	16.2	1193	2	Q4S758 TETNG
85	80	16.1	412	2	Q557F1 DICDI
86	80	16.1	412	2	Q86HY9 DICDI
87	79.5	16.0	191	2	Q6ZOW6 HUMAN
88	79.5	16.0	404	2	Q6ZOR7 HUMAN
89	79.5	16.0	418	2	Q4T860 TETNG
90	79.5	16.0	446	2	Q8N1N5 HUMAN
91	79.5	16.0	870	2	Q8IQG6 DROME
92	79.5	16.0	1233	2	Q4S163 TETNG
93	79.5	16.0	1331	2	Q4S572 TETNG
94	79.5	16.0	1353	2	Q4UG29 THEAN
95	79	15.9	107	1	COL_RABIT
96	79	15.9	224	2	Q4H3Q2 CIOIN
97	79	15.9	225	2	Q4H3Q3 CIOIN
98	79	15.9	704	1	PBLN1 CHICK
99	79	15.9	1293	2	Q16M09 AEDAE
100	79	15.9	2447	2	Q13149 FUGRU
101	78.5	15.8	162	2	Q5JH8 PYRKO
102	78	15.7	593	2	Q5H5T2 PONPY
103	77.5	15.6	350	2	Q54EN7 DICDI
104	77.5	15.6	473	1	FP2_MYTGA

Q8Jfy2	bombina max
Q5OE61	arvicanthus
Q2Tbs7	bos taurus
Q5OE35	arvicanthus
Q5OE36	arvicanthus
Q56R10	penaeus mon
Q8Uux3	gallus gall
Q8vej3	mus musculus
Q9ubt3	homo sapien
Q3knx0	homo sapien
Q90839	gallus gall
Q9ad44	xenopus lae
Q4rjf1	tetraodon n
Q9ubt2	homo sapien
Q9gyz8	gecko japon
Q8bfw0	mus musculus
Q8bfw0	m 10, 11 da
Q54908	mus musculus
Q8ou15	m dickkopf
Q43532	homo sapien
Q8n294	homo sapien
Q5r870	pongo pygma
Q2hwr5	sus scrofa
Q9ubp4	homo sapien
Q5r4q2	pongo pygma
Q4r417	macaca fasc
Q9es33	rattus norv
Q5rkl1	rattus norv
Q9run9	mus musculus
Q94907	homo sapien
Q6pvu5	oryctolagus
Q57464	xenopus lae
Q4sl69	tetraodon n
Q6pq81	homo sapien
Q9wh3	brachydanio
Q5er11	pacifastacu
Q96397	chlamydomon
Q5d229	hadronyche
Q5d228	hadronyche
Q9w6d9	brachydanio
Q3uw21	mus musculus
Q5d230	hadronyche
Q4pml0	ixodes scap
Q1xbt8	mytilus edu
Q3u128	mus musculus
Q8bu04	mus musculus
Q52kc0	m hypohetci
Q642a8	rattus norv
Q28cm0	xenopus tro
Q5bkf5	xenopus tro
Q8nb03	homo sapien
P31695	mus musculus
Q4758	tetraodon n
Q557f1	dictyosteli
Q86hy9	dictyosteli
Q6zqw6	homo sapien
Q6zqr7	homo sapien
Q4t860	tetraodon n
Q8n1n5	homo sapien
Q8iqg6	drosofila
Q4s163	tetraodon n
Q4s572	tetraodon n
Q4ug29	theileria a
P42890	oryctolagus
Q4h3q2	ciona intes
Q4h3q3	ciona intes
Q73775	gallus gall
Q16m09	aedes aegypt
Q15m09	aedes aegypt
Q5jh8	pyrococcus
Q5st52	pongo pygma
Q54en7	dictyosteli
Q25464	mytilus gal

105	77	15.5	5533	2	Q5RIP6	BRARE	Q5rip6	brachydanio	178	71	14.3	457	2	Q8TEC5	HUMAN	Q8tec5	homo sapien
106	76	15.3	113	2	Q9D2R7	MOUSE	Q9d2r7	mus musculus	179	71	14.3	587	2	Q2HJ16	BOVIN	Q2hj16	bos taurus
107	76	15.3	264	2	Q5H2W5	RAT	Q5h2w5	rattus norv	180	71	14.3	593	2	GRN	HUMAN	GRN	homo sapien
108	76	15.3	496	2	Q541I9	DICDI	Q541i9	dictyosteli	181	71	14.3	593	2	Q540U8	HUMAN	Q540u8	homo sapien
109	76	15.3	496	2	Q6TMJ0	DICDI	Q6tmj0	dictyosteli	182	71	14.3	593	2	Q53H08	HUMAN	Q53h08	homo sapien
110	75.5	15.2	1259	2	Q85C6	9TRYP	Q85c6	trypanosoma	183	70.5	14.2	172	2	Q19QV7	9CNID	Q19qv7	nematostell
111	75.5	15.2	1651	2	Q9TVQ2	CABEL	Q9tvq2	caenorhabdi	184	70.5	14.2	212	2	Q16TD8	AEDAE	Q16td8	aedes aegypt
112	75	15.1	130	2	Q4PMW2	IXOSC	Q4pmw2	ixodes scap	185	70.5	14.2	287	2	Q75Z12	BRARE	Q75z12	brachydanio
113	75	15.1	425	2	Q53RA0	HUMAN	Q53ra0	homo sapien	186	70.5	14.2	555	2	Q4RN57	TETNG	Q4rn57	tetraodon n
114	75	15.1	647	2	Q6P3V5	HUMAN	Q6p3v5	homo sapien	187	70.5	14.2	591	1	GRN	CAVPO	Q4rn57	cavia porce
115	75	15.1	762	2	Q8ML23	DROME	Q8ml23	drosophila	188	70.5	14.2	655	2	Q1WX2	DROER	Q1wx2	drosophila
116	75	15.1	918	2	Q1EC02	DROME	Q1ec02	drosophila	189	70.5	14.2	667	2	Q1WKW9	DROTE	Q1wk9	drosophila
117	75	15.1	1581	1	LAMC3	MOUSE	Q9r0b6	mus musculus	190	70.5	14.2	919	2	Q61V24	CAEBR	Q61v24	caenorhabdi
118	75	15.1	1581	2	Q4VAI3	MOUSE	Q4vai3	mus musculus	191	70.5	14.2	966	2	Q22378	CABEL	Q22378	caenorhabdi
119	75	15.1	1957	2	Q4SU28	TETNG	Q4su28	tetraodon n	192	70.5	14.2	2318	1	NOTC3	MOUSE	Q61n82	mus musculus
120	75	15.1	1961	2	Q6MG89	RAT	Q6mg89	rattus norv	193	70.5	14.2	2319	1	NOTC3	RAT	Q61n82	mus musculus
121	75	15.1	2003	1	NOTC4	HUMAN	Q99466	homo sapien	194	70	14.1	68	1	TX16	PHONI	Q99466	homo sapien
122	75	15.1	2003	2	Q5SPL1	HUMAN	Q5spl1	homo sapien	195	70	14.1	92	2	Q2MCM5	HYDMA	Q2mcm5	hydra magni
123	75	15.1	2003	2	Q5SSV7	HUMAN	Q5ssv7	homo sapien	196	70	14.1	113	1	COL	MOUSE	Q9cqc2	mus musculus
124	75	15.1	2005	2	Q5STG5	HUMAN	Q5stg5	homo sapien	197	70	14.1	251	2	Q70LQ4	ENCBU	Q70lq4	enchytraeus
125	75	15.1	2531	2	Q16004	LYTVA	Q16004	lytechinus	198	70	14.1	251	2	Q24774	ENCBU	Q24774	enchytraeus
126	75	15.1	4599	1	LRP1B	HUMAN	Q8n806	homo sapien	199	70	14.1	387	2	Q4KLX7	XENLA	Q4klx7	xenopus lae
127	74.5	15.0	190	2	Q4TBE9	TETNG	Q4tbe9	tetraodon n	200	70	14.1	392	2	Q9PVD4	XENLA	Q9pvd4	xenopus lae
128	74.5	15.0	194	2	Q4SIA7	TETNG	Q4sia7	tetraodon n	201	70	14.1	490	2	Q6NUF1	XENLA	Q6nuf1	xenopus lae
129	74.5	15.0	274	2	Q5RCC3	PONPY	Q5rc3	pongo pygma	202	70	14.1	706	2	Q4H3Q7	CIOIN	Q4h3q7	ciona intes
130	74.5	15.0	286	2	Q7R5C8	GIALA	Q7r5c8	giardia lam	203	70	14.1	729	2	Q7T3M4	BRARE	Q7t3m4	brachydanio
131	74.5	15.0	425	1	CNI130	HUMAN	Q8n806	homo sapien	204	70	14.1	729	2	Q4V9K5	BRARE	Q4v9k5	brachydanio
132	74.5	15.0	429	2	Q1XB76	MYTED	Q1xbt6	mytilus edu	205	70	14.1	729	2	Q802C1	XENLA	Q802c1	xenopus lae
133	74.5	15.0	1426	2	Q4RTA6	TETNG	Q4rta6	tetraodon n	206	70	14.1	950	2	Q802C1	XENLA	Q802c1	xenopus lae
134	74.5	15.0	5644	2	Q16KQ9	AEDAE	Q16kq9	aedes aegypt	207	69.5	14.0	111	2	Q4PN79	IXOSC	Q4pn79	ixodes scap
135	74	14.9	623	2	Q4P8A3	USTWA	Q4p8a3	ustilago ma	208	69.5	14.0	123	2	Q3XNW9	9PROT	Q3xnw9	magnetococc
136	74	14.9	693	2	Q5O5M8	XENLA	Q5o5m8	xenopus lae	209	69.5	14.0	682	2	Q1WKW8	DROYA	Q1wk8	drosophila
137	74	14.9	708	2	F87363	CHICK	Q87363	gallus gall	210	69.5	14.0	818	2	Q4V7B3	RAT	Q4v7b3	rattus norv
138	74	14.9	1171	2	Q4RLR5	TETNG	Q4rlr5	tetraodon n	211	69.5	14.0	1099	2	Q60V58	CAEBR	Q60v58	caenorhabdi
139	74	14.9	3461	2	Q16KR1	AEDAE	Q16kr1	aedes aegypt	212	69.5	14.0	1147	2	Q3TLU3	MOUSE	Q3tlu3	mus musculus
140	74	14.9	4680	2	Q7PV66	ANOGEA	Q7pv66	anopheles g	213	69	13.9	112	2	Q291D9	DROPS	Q291d9	drosophila
141	73.5	14.8	701	2	Q8AVE8	XENLA	Q8ave8	xenopus lae	214	69	13.9	413	2	Q9H8S1	HUMAN	Q9h8s1	homo sapien
142	73.5	14.8	2327	2	Q9IBG7	XENLA	Q9ibg7	xenopus lae	215	69	13.9	638	2	Q8NBH6	HUMAN	Q8nbh6	homo sapien
143	73	14.7	64	1	TX16	PHORI	Q83893	phonetria	216	69	13.9	703	1	FBLN1	HUMAN	FBLN1	homo sapien
144	73	14.7	109	2	Q5U809	HUMAN	Q5u809	homo sapien	217	69	13.9	835	2	Q69ZY6	MOUSE	Q69zy6	mus musculus
145	73	14.7	112	1	COL	HUMAN	P04118	homo sapien	218	68.5	13.8	143	2	Q330K6	TRIMU	Q330k6	trimeresuru
146	73	14.7	112	2	Q5T9G7	HUMAN	Q5t9g7	homo sapien	219	68.5	13.8	333	2	Q3HTT8	CANFA	Q3htt8	canis faml
147	73	14.7	172	2	Q8RU50	ORYSA	Q8ru50	oryza sativ	220	68.5	13.8	425	2	Q4R222	MACFA	Q4r222	macaca fasc
148	73	14.7	211	2	Q1QC1	RHOED	Q1qc1	rhodiferax	221	68.5	13.8	661	2	Q1WKX0	DROSI	Q1wkx0	drosophila
149	73	14.7	417	1	TNR16	MOUSE	Q2z0w1	mus musculus	222	68.5	13.8	708	2	Q7F803	ORYSA	Q7f803	oryza sativ
150	73	14.7	417	2	Q8BYI1	MOUSE	Q8byi1	mus musculus	223	68.5	13.8	850	2	Q44384	BRAOL	Q44384	brassica ol
151	73	14.7	427	2	Q8CFT3	MOUSE	Q8cft3	mus musculus	224	68.5	13.8	909	2	Q5ZEL8	ORYSA	Q5zel8	oryza sativ
152	73	14.7	732	2	Q9RH03	AZOIR	Q9rh03	azospirillu	225	68.5	13.8	1064	2	Q2HD56	CHAGB	Q2hd56	chaetomium
153	73	14.7	1408	2	Q4RX38	TETNG	Q4rx38	tetraodon n	226	68.5	13.8	1172	1	TSP2	MOUSE	TSP2	mouse
154	72.5	14.6	103	2	Q8Z331	ORYSA	Q8z331	oryza sativ	227	68.5	13.8	1172	2	Q7TMT3	MOUSE	Q7tmt3	mus musculus
155	72.5	14.6	457	2	Q8IVS6	HUMAN	Q8ivs6	homo sapien	228	68.5	13.8	1172	2	Q8CG21	MOUSE	Q8cg21	mus musculus
156	72.5	14.6	461	1	TNR1B	HUMAN	P20333	h tumor nec	229	68.5	13.8	1639	1	LAMC1	DROME	LAMC1	drosophila
157	72.5	14.6	461	2	Q5THJ6	HUMAN	Q5thj6	homo sapien	230	68.5	13.8	1639	2	Q5BI30	DROME	Q5bi30	drosophila
158	72.5	14.6	986	2	Q1L8S9	BRARE	Q1l8s9	brachydanio	231	68.5	13.8	1801	2	Q8WSJ2	BOMMO	Q8wsj2	bombyx mori
159	72.5	14.6	1269	2	Q1L926	BRARE	Q1l926	brachydanio	232	68.5	13.8	1838	2	Q28XF3	DROPS	Q28xf3	drosophila
160	72.5	14.6	1428	2	Q1A5L3	BRARE	Q1a5l3	brachydanio	233	68.5	13.8	1952	2	Q95SN5	DROME	Q95sn5	drosophila
161	72.5	14.6	2715	1	MLL4	HUMAN	Q9um16	homo sapien	234	68.5	13.8	2559	1	STAB2	MOUSE	STAB2	mouse
162	72.5	14.6	3277	2	Q6VU67	HUMAN	Q6vu67	homo sapien	235	68.5	13.8	4547	2	Q9W343	DROME	Q9w343	drosophila
163	72.5	14.6	3333	2	Q76E14	HUMAN	Q76e14	homo sapien	236	68	13.7	60	2	Q20A05	CRAGI	Q20a05	crassostrea
164	72.5	14.6	3333	2	Q6VU68	HUMAN	Q6vu68	homo sapien	237	68	13.7	112	1	COL	CANFA	COL	canis faml
165	72	14.5	3667	2	Q29F13	DROPS	Q29f13	drosophila	238	68	13.7	113	2	Q5T9G1	HUMAN	Q5t9g1	homo sapien
166	71.5	14.4	453	2	Q64767	ADEG1	Q64767	avian adeno	239	68	13.7	314	2	Q5XTR8	MACMU	Q5xtr8	macaca mula
167	71.5	14.4	466	2	Q1XB77	MYTED	Q1xbt7	mytilus edu	240	68	13.7	427	1	TNR16	HUMAN	TNR16	homo sapien
168	71.5	14.4	1170	1	TSP2	BOVIN	Q95116	bos taurus	241	68	13.7	489	1	MA2A1	RAT	MA2A1	rattus norv
169	71.5	14.4	1178	1	MSGF5	RAT	Q88281	rattus norv	242	68	13.7	586	2	Q6P7D7	RAT	Q6p7d7	rattus norv
170	71.5	14.4	1809	1	FTV1	DROME	Q95838	drosophila	243	68	13.7	586	2	Q6RXF3	HCNV	Q6rxf3	human cytom
171	71.5	14.4	3652	2	Q16PL9	AEDAE	Q16pl9	aedes aegypt	244	68	13.7	587	2	Q61T62	CAEBR	Q61t62	caenorhabdi
172	71.5	14.3	112	1	COL	RAT	P17084	rattus norv	245	68	13.7	587	2	Q6SW58	HCNV	Q6sw58	human cytom
173	71	14.3	286	2	Q7JMU0	MELIC	Q7jmu0	meloiodogyne	246	68	13.7	593	2	Q4R529	MACFA	Q4r529	macaca fasc
174	71	14.3	288	2	Q5RIP8	BRARE	Q5rip8	brachydanio	247	68	13.7	944	2	Q4SLY2	TETNG	Q4sly2	tetraodon n
175	71	14.3	305	2	Q25467	MELIC	Q25467	meloiodogyne	248	68	13.7	964	2	Q4STC1	TETNG	Q4stc1	tetraodon n
176	71	14.3	438	2	Q53Y88	HUMAN	Q53y88	homo sapien	249	68	13.7	1090	2	Q5SPG5	BRARE	Q5spg5	brachydanio
177	71	14.3							250	68	13.7						

251	68	13.7	1150	1	MA2A1_MOUSE	P27046	mus musculus	324	66.5	13.4	1379	2	Q59H72_HUMAN	Q59H72	homo sapien
252	68	13.7	1466	2	Q1A512_BRARE	Q1A512	brachydanio	325	66.5	13.4	1568	2	Q5VUP0_HUMAN	Q5VUP0	homo sapien
253	68	13.7	1984	1	YL_DROME	P98162	drosophila	326	66.5	13.4	1587	1	LAMC3_HUMAN	LAMC3	homo sapien
254	68	13.7	2359	2	Q59FC2_HUMAN	Q59FC2	homo sapien	327	66.5	13.4	1587	2	Q5VUP1_HUMAN	Q5VUP1	homo sapien
255	68	13.7	5147	1	FAT_DROME	P33450	drosophila	328	66.5	13.4	1945	2	Q4RQ96_TETNG	Q4RQ96	tetraodon n
256	67.5	13.6	89	2	Q5D232_HADSP	Q5D232	hadronyche	329	66.5	13.4	4545	2	Q61ZX7_MOUSE	Q61ZX7	mus musculus
257	67.5	13.6	200	2	Q7PWE6_ANOGA	Q7PWE6	anopheles g	330	66.5	13.4	4545	2	Q920Y4_MOUSE	Q920Y4	mus musculus
258	67.5	13.6	269	2	Q413B1_GIBZE	Q413B1	gibberella	331	66.5	13.4	4545	2	Q61291_MOUSE	Q61291	mus musculus
259	67.5	13.6	269	2	Q3TTU9_MOUSE	Q383F5	trypanosoma	332	66	13.3	85	1	HEPC_MORCS	HEPC	morone chry
260	67.5	13.6	303	2	Q6ZP14_HUMAN	Q6ZP14	homo sapien	333	66	13.3	149	2	Q8GA35_ECOLI	Q8GA35	escherichia
261	67.5	13.6	413	2	Q6ZP14_HUMAN	Q6ZP14	homo sapien	334	66	13.3	208	2	Q6K6H7_ORYSA	Q6K6H7	oryza sativ
262	67.5	13.6	418	2	Q5ZMNA_CHICK	Q5ZMNA	gallus gall	335	66	13.3	299	2	Q1HDL3_HUMAN	Q1HDL3	homo sapien
263	67.5	13.6	490	1	TPWSE2_MOUSE	Q9J1Q8	mus musculus	336	66	13.3	598	1	FBLN1_CERAE	FBLN1	cercopithec
264	67.5	13.6	490	2	Q3UKK3_MOUSE	Q3UKK3	mus musculus	337	66	13.3	813	2	Q1IK36_ACIBL	Q1IK36	acidobacter
265	67.5	13.6	490	2	Q7TN04_MOUSE	Q7TN04	mus musculus	338	66	13.3	1172	2	TS92_HUMAN	TS92	homo sapien
266	67.5	13.6	540	2	Q1WKX1_TRYCR	Q1WKX1	trypanosoma	339	66	13.3	1172	2	Q5RI52_HUMAN	Q5RI52	homo sapien
267	67.5	13.6	665	2	Q4CXJ4_TRYCR	Q4CXJ4	trypanosoma	340	66	13.3	1327	1	Y2006_MYCTU	Y2006	mycobacteri
268	67.5	13.6	726	2	Q8AWB7_CYNPY	Q8AWB7	cynops pyrr	341	66	13.3	1327	2	Q7TZ61_MYCBO	Q7TZ61	mycobacteri
269	67.5	13.6	729	2	Q8BNH3_MOUSE	Q8BNH3	mus musculus	342	66	13.3	1599	2	Q616G7_CAEBR	Q616G7	caenorhabdi
270	67.5	13.6	787	2	Q8K061_MOUSE	Q8K061	mus musculus	343	66	13.3	2289	2	Q4S3T6_TETNG	Q4S3T6	tetraodon n
271	67.5	13.6	896	2	Q16QQ3_AEDAE	Q16QQ3	aedes aegyp	344	66	13.3	2884	2	Q4SHN1_TETNG	Q4SHN1	tetraodon n
272	67.5	13.6	1356	2	Q4N8M7_THEPA	Q4N8M7	theileria p	345	66	13.3	3075	1	LAMAL_HUMAN	LAMAL	homo sapien
273	67.5	13.6	1637	2	Q9XSU8_BOVIN	Q9XSU8	bos taurus	346	66	13.3	3570	2	Q7Q737_ANOGA	Q7Q737	anopheles g
274	67.5	13.6	1744	2	Q8CHH1_MOUSE	Q8CHH1	mus musculus	347	66	13.3	3712	1	LAMA_DROME	LAMA	drosophila
275	67.5	13.6	2013	2	Q6PHU4_MOUSE	Q6PHU4	mus musculus	348	65.5	13.2	110	2	Q4PMX5_IXOSC	Q4PMX5	ixodes scap
276	67.5	13.6	2713	2	Q5NU09_MOUSE	Q5NU09	mus musculus	349	65.5	13.2	176	2	Q4V4J0_DROME	Q4V4J0	drosophila
277	67.5	13.6	4525	2	Q16UK9_AEDAE	Q16UK9	aedes aegyp	350	65.5	13.2	230	2	Q5VTG9_HUMAN	Q5VTG9	homo sapien
278	67.5	13.6	4699	2	Q9V383_DROME	Q9V383	drosophila	351	65.5	13.2	236	2	Q8AU09_HUMAN	Q8AU09	homo sapien
279	67.5	13.6	5146	1	SSPO_BOVIN	P98167	bos taurus	352	65.5	13.2	236	2	Q7Z3S9_HUMAN	Q7Z3S9	homo sapien
280	67	13.5	113	2	Q8MKJ5_DROME	Q8MKJ5	drosophila	353	65.5	13.2	244	2	Q7YJ99_NITMU	Q7YJ99	nitrospir
281	67	13.5	182	2	Q307E7_SHEEP	Q307E7	ovis aries	354	65.5	13.2	249	2	Q5BK78_HUMAN	Q5BK78	homo sapien
282	67	13.5	237	1	ALG14_YEAST	P38242	saccharomyc	355	65.5	13.2	269	2	Q8NC23_HUMAN	Q8NC23	homo sapien
283	67	13.5	495	2	Q54QC5_DICDI	Q54QC5	dictyosteli	356	65.5	13.2	342	2	Q6P192_HUMAN	Q6P192	homo sapien
284	67	13.5	611	2	Q4S2Z8_TETNG	Q4S2Z8	tetraodon n	357	65.5	13.2	343	2	Q5XG84_HUMAN	Q5XG84	homo sapien
285	67	13.5	749	2	Q86TP7_HUMAN	Q86TP7	homo sapien	358	65.5	13.2	356	2	Q36FY1_HUMAN	Q36FY1	homo sapien
286	67	13.5	993	1	EPHB3_MOUSE	P54754	mus musculus	359	65.5	13.2	410	2	Q171B0_AEDAE	Q171B0	aedes aegyp
287	67	13.5	993	2	Q91YS9_MOUSE	Q91YS9	mus musculus	360	65.5	13.2	589	2	Q3TW74_MOUSE	Q3TW74	mus musculus
288	67	13.5	1050	2	Q71G60_RSIV	Q71G60	red sea bre	361	65.5	13.2	722	1	DLL1_MOUSE	DLL1	mouse
289	67	13.5	1168	2	Q60XCO_CAEBR	Q60XCO	caenorhabdi	362	65.5	13.2	722	2	Q6PFV7_MOUSE	Q6PFV7	mouse
290	67	13.5	1229	1	MEGF6_HUMAN	O75095	homo sapien	363	65.5	13.2	724	2	Q4ZJ75_XENLA	Q4ZJ75	xenopus lae
291	67	13.5	1289	2	Q59FL3_HUMAN	O75095	homo sapien	364	65.5	13.2	724	2	Q32NV6_XENLA	Q32NV6	xenopus lae
292	67	13.5	1640	2	Q4AC86_HUMAN	Q4AC86	homo sapien	365	65.5	13.2	729	2	Q6GPT6_XENLA	Q6GPT6	xenopus lae
293	67	13.5	1761	2	Q86XN2_HUMAN	Q86XN2	homo sapien	366	65.5	13.2	768	2	Q36581_9RETR	Q36581	multiple sc
294	67	13.5	2321	1	NOTC3_HUMAN	Q9UM42	homo sapien	367	65.5	13.2	802	2	Q7JL02_CAEBL	Q7JL02	caenorhabdi
295	66.5	13.4	170	2	Q2BNK4_9GAMM	Q2BNK4	oceanospiri	368	65.5	13.2	804	2	Q3UK95_MOUSE	Q3UK95	mus musculus
296	66.5	13.4	287	2	Q81R11_DROME	Q81R11	drosophila	369	65.5	13.2	818	2	Q8CCS9_MOUSE	Q8CCS9	mus musculus
297	66.5	13.4	386	2	Q32NM5_XENLA	Q32NM5	xenopus lae	370	65.5	13.2	818	2	Q9DBC8_MOUSE	Q9DBC8	mus musculus
298	66.5	13.4	388	2	Q6JA22_XENLA	Q6JA22	xenopus lae	371	65.5	13.2	887	2	Q3UMW1_MOUSE	Q3UMW1	mus musculus
299	66.5	13.4	388	2	Q68Y16_XENLA	Q68Y16	xenopus lae	372	65.5	13.2	949	2	P90956_CAEBL	P90956	caenorhabdi
300	66.5	13.4	462	2	Q3UDD6_MOUSE	Q3UDD6	mus musculus	373	65.5	13.2	1114	2	Q9JKW7_MOUSE	Q9JKW7	mus musculus
301	66.5	13.4	480	2	Q34XA1_9GAMM	Q34XA1	alkalilimni	374	65.5	13.2	1114	2	Q3U2A7_MOUSE	Q3U2A7	mus musculus
302	66.5	13.4	511	2	Q6IN42_RAT	Q6IN42	rattus norv	375	65.5	13.2	1235	2	Q6IQ50_HUMAN	Q6IQ50	homo sapien
303	66.5	13.4	588	1	GRN_RAT	P23785	m granulins	376	65.5	13.2	1465	2	Q4RN50_TETNG	Q4RN50	tetraodon n
304	66.5	13.4	589	1	GRN_MOUSE	P28798	mus musculus	377	65.5	13.2	1847	2	O76952_AEDAE	O76952	aedes aegyp
305	66.5	13.4	589	2	Q3TX66_MOUSE	Q3TX66	mus musculus	378	65.5	13.2	1847	2	Q171G8_AEDAE	Q171G8	aedes aegyp
306	66.5	13.4	589	2	Q3TVQ3_MOUSE	Q3TVQ3	mus musculus	379	65.5	13.2	1847	2	Q16GV3_AEDAE	Q16GV3	aedes aegyp
307	66.5	13.4	589	2	Q3UC19_MOUSE	Q3UC19	mus musculus	380	65.5	13.2	2213	1	SORL_RABIT	SORL	o sortilin-
308	66.5	13.4	589	2	Q544Y8_MOUSE	Q544Y8	m adult mal	381	65.5	13.2	2471	1	NOTC2_HUMAN	NOTC2	homo sapien
309	66.5	13.4	593	2	Q3U9K2_MOUSE	Q3U9K2	mus musculus	382	65.5	13.2	2471	2	Q5VTD0_HUMAN	Q5VTD0	homo sapien
310	66.5	13.4	602	2	Q3U9N4_MOUSE	Q3U9N4	m bone marr	383	65.5	13.2	4532	2	Q29ID0_DROPS	Q29ID0	drosophila
311	66.5	13.4	602	2	Q3TW77_MOUSE	Q3TW77	rattus norv	384	65	13.1	111	1	COL_SPETR	COL	spetr
312	66.5	13.4	602	2	Q3U506_MOUSE	Q3U506	mus musculus	385	65	13.1	147	2	Q6QXV5_ORYSA	Q6QXV5	oryza sativ
313	66.5	13.4	602	2	Q3U8W3_MOUSE	Q3U8W3	mus musculus	386	65	13.1	400	2	Q2ZB14_TETTH	Q2ZB14	tetrahymena
314	66.5	13.4	602	2	Q9D2V3_MOUSE	Q9D2V3	mus musculus	387	65	13.1	448	2	Q8P7W2_XANCP	Q8P7W2	xanthomonas
315	66.5	13.4	674	2	Q8T4N9_STRPU	Q8T4N9	strongyloce	388	65	13.1	448	2	Q4UW87_XANCP	Q4UW87	xanthomonas
316	66.5	13.4	714	1	DLL1_RAT	P97677	rattus norv	389	65	13.1	481	2	Q2WV02_CLOBE	Q2WV02	clostridium
317	66.5	13.4	907	2	Q4R1B4_LEUMA	Q4R1B4	leucophaea	390	65	13.1	647	2	Q1M7N7_RHIL3	Q1M7N7	rhizobium 1
318	66.5	13.4	931	2	Q61FT4_CAEBR	Q61FT4	caenorhabdi	391	65	13.1	794	2	Q8T4P0_LYTVA	Q8T4P0	lytechinus
319	66.5	13.4	969	2	Q81V28_HUMAN	Q81V28	homo sapien	392	65	13.1	893	2	Q9Y1X3_9METZ	Q9Y1X3	ephydatia f
320	66.5	13.4	1180	2	Q5CZ12_HUMAN	Q5CZ12	homo sapien	393	65	13.1	1068	2	Q6QHS4_STRPU	Q6QHS4	strongyloce
321	66.5	13.4	1361	2	Q9NGV2_DROME	Q9NGV2	drosophila	394	65	13.1	1123	2	Q4H346_CIOIN	Q4H346	ciona intes
322	66.5	13.4	1361	2	Q9V714_DROME	Q9V714	drosophila	395	65	13.1	3133	1	HMCT_BOMMO	HMCT	bombyx mori
323	66.5	13.4	1375	1	NID2_HUMAN	Q14112	homo sapien	396	65	13.1	3481	2	Q4DNC0_TRYCR	Q4DNC0	trypanosoma

397	65	13.1	4599	1	LRPLB MOUSE	Q9ji18 mus musculus	470	64	12.9	1818	2	Q2YI44 BLAGE	Q2Yi44 biattella 9
398	65	13.1	23015	2	Q81Q18 DROME	Q8ig18 drosophila	471	64	12.9	1914	2	Q499U7 RAT	Q499u7 rattus norv
399	64.5	13.0	90	2	Q519G3 HUMAN	Q51g93 homo sapien	472	64	12.9	2215	1	SORL MOUSE	Q88307 m sortilin-
400	64.5	13.0	102	1	TXCA CAEX	Q8mtx1 caecrostis	473	64	12.9	2215	2	Q3UHM3 MOUSE	Q3uhm3 mus musculus
401	64.5	13.0	134	2	Q6Zr78 HUMAN	Q6zr78 homo sapien	474	64	12.9	2360	2	Q7YzP0 EIMMA	Q7yzp0 eimeria max
402	64.5	13.0	170	2	Q52VJ8 CIOIN	Q52vj8 ciona intes	475	64	12.9	2523	2	Q612I1 CAEBR	Q612i1 caenorhabdi
403	64.5	13.0	191	1	Y064 TREPA	Q83103 treponema p	476	64	12.9	2871	1	FBNI_PIG	Q83103 caenorhabdi
404	64.5	13.0	245	2	Q6Zr76 HUMAN	Q6zt76 homo sapien	477	64	12.9	3857	2	Q88840 MOUSE	Q88840 sus scrofa
405	64.5	13.0	256	1	FSTL3 MOUSE	Q9eq77 mus musculus	478	63.5	12.8	70	1	Q615U9 ORYSA	Q9u323 conus betul
406	64.5	13.0	256	2	Q542M9 MOUSE	Q542m9 mus musculus	479	63.5	12.8	92	2	Q615U9 ORYSA	Q615u9 oryza sativ
407	64.5	13.0	325	2	Q614Z3 CAEBR	Q614z3 caenorhabdi	480	63.5	12.8	208	2	Q2HJ99_9MYRI	Q2hj99 strigamia m
408	64.5	13.0	337	2	Q8NHD3 HUMAN	Q8nhd3 homo sapien	481	63.5	12.8	240	1	KCP3 RAT	Q497B3 rattus norv
409	64.5	13.0	342	2	Q8NHD5 HUMAN	Q8nhd5 homo sapien	482	63.5	12.8	320	2	Q9PUK3 CHICK	Q9puk3 gallus gall
410	64.5	13.0	375	2	Q7PR44 ANOGA	Q7pr44 anopheles g	483	63.5	12.8	349	2	Q28KF2 JANSC	Q28kf2 jannaschia
411	64.5	13.0	546	2	Q3UHW9 MOUSE	Q3uwh9 mus musculus	484	63.5	12.8	362	2	Q9PVN4 CHICK	Q9pvn4 gallus gall
412	64.5	13.0	569	2	Q8NHD4 HUMAN	Q8nhd4 homo sapien	485	63.5	12.8	395	2	Q5TV39 ANOGA	Q5tv39 anopheles g
413	64.5	13.0	656	1	MEGF6 MOUSE	Q80v70 mus musculus	486	63.5	12.8	407	2	Q3K7E8 PSEPF	Q3k7e8 pseudomonas
414	64.5	13.0	744	2	Q8NHD2 HUMAN	Q8nhd2 homo sapien	487	63.5	12.8	460	2	Q5SY22 HUMAN	Q5sy22 homo sapien
415	64.5	13.0	744	2	Q7Q8A1 ANOGA	Q7q8a1 anopheles g	488	63.5	12.8	536	2	Q5RG03 BRARE	Q5rg03 brachydanio
416	64.5	13.0	772	2	Q4QB18 LEIMA	Q4qb18 leishmania	489	63.5	12.8	542	2	Q17H65 AEDAE	Q17h65 aedes aegypt
417	64.5	13.0	804	2	Q7TPT4 MOUSE	Q7tpt4 mus musculus	490	63.5	12.8	728	2	Q90656 CHICK	Q90656 gallus gall
418	64.5	13.0	830	1	SREC HUMAN	Q4yv58 plasmodium	491	63.5	12.8	739	2	Q17AY8 AEDAE	Q17ay8 aedes aegypt
419	64.5	13.0	841	2	Q8I719 PLAF7	Q8i719 plasmodium	492	63.5	12.8	747	2	Q4DFR4 TRYCR	Q4dfr4 trypanosoma
420	64.5	13.0	853	2	Q8MW24 PLAF7	Q8mw24 plasmodium	493	63.5	12.8	747	2	Q8VHF4 MOUSE	Q8vhf4 mus musculus
421	64.5	13.0	853	2	Q8QGN9 BRARE	Q8qgn9 brachydanio	494	63.5	12.8	841	1	TS1R1 HUMAN	Q7rtx1 homo sapien
422	64.5	13.0	873	2	Q6X118 CALJA	Q6x118 callithrix	495	63.5	12.8	841	1	Q8JVB9_9VIRU	Q8jvb9 penicillium
423	64.5	13.0	987	2	Q3UGU1 MOUSE	Q3ugul mus musculus	496	63.5	12.8	871	2	Q626H3 CAEBR	Q626h3 caenorhabdi
424	64.5	13.0	1021	2	Q5U4U1 XENLA	Q5u4u1 xenopus lae	497	63.5	12.8	898	2	Q60UE2 CAEBR	Q60ue2 caenorhabdi
425	64.5	13.0	1051	2	Q3UG73 MOUSE	Q3ug73 mus musculus	498	63.5	12.8	898	2	Q3URX7 MOUSE	Q3urx7 mus musculus
426	64.5	13.0	1062	2	Q3UG73 MOUSE	Q3ug73 mus musculus	499	63.5	12.8	1004	2	Q8CGA7 MOUSE	Q8cga7 mus musculus
427	64.5	13.0	1147	2	Q6DI85 MOUSE	Q6di85 mus musculus	500	63.5	12.8	1034	2	Q8VHL7 MOUSE	Q8vhl7 mus musculus
428	64.5	13.0	1211	2	Q383K6_9TRYP	Q383k6 trypanosoma	501	63.5	12.8	1034	2	Q8VIK5 MOUSE	Q8vik5 mus musculus
429	64.5	13.0	1214	2	Q90YD2 XENLA	Q90y2d xenopus lae	502	63.5	12.8	1054	2	Q23JW8_TETTH	Q23jw8 tetrahymena
430	64.5	13.0	1216	2	Q5TZK7 BRARE	Q5tzk7 brachydanio	503	63.5	12.8	1285	1	CRUM2 HUMAN	Q5sj48 homo sapien
431	64.5	13.0	1216	2	Q90Y55 BRARE	Q90y55 brachydanio	504	63.5	12.8	1505	2	Q5S3N1 SALSA	Q5s3n1 salmo salar
432	64.5	13.0	1254	2	Q5TZK8 BRARE	Q5tzk8 brachydanio	505	63.5	12.8	1519	2	Q8WPN0_OIKOI	Q8wpn0 oikopleura
433	64.5	13.0	1254	2	Q90Y56 BRARE	Q90y56 brachydanio	506	63.5	12.8	1687	2	Q22QK0_TETTH	Q22qk0 tetrahymena
434	64.5	13.0	1254	2	Q90Y56 BRARE	Q90y56 brachydanio	507	63.5	12.8	1827	2	Q8JHV6 BRARE	Q8jhv6 brachydanio
435	64.5	13.0	1257	2	Q90Y56 BRARE	Q90y56 brachydanio	508	63.5	12.8	2672	2	Q3JUH3 MOUSE	Q3uhh3 m 14 days p
436	64.5	13.0	1557	2	Q75412 HUMAN	Q75412 homo sapien	509	63.5	12.8	3695	2	LAMAS HUMAN	Q15230 homo sapien
437	64.5	13.0	1587	2	Q00508 HUMAN	Q00508 homo sapien	510	63.5	12.8	3695	2	Q8TDF8 HUMAN	Q8tdf8 homo sapien
438	64.5	13.0	1624	2	Q75413 HUMAN	Q75413 homo sapien	511	63.5	12.8	3707	1	PGBM MOUSE	Q05793 mus musculus
439	64.5	13.0	1637	2	Q29CY8 DROPS	Q29cy8 drosophila	512	63	12.7	131	1	CHHB1_BOMMO	P05688 bombyx mori
440	64.5	13.0	1722	2	Q19350 CAEBL	Q19350 caenorhabdi	513	63	12.7	319	2	Q4T826_TETNG	Q4t826 tetraodon n
441	64.5	13.0	2214	1	SORL HUMAN	Q92673 h sortilin-	514	63	12.7	371	2	Q5U215 RAT	Q5u215 rattus norv
442	64	12.9	3718	1	LAMAS MOUSE	Q61001 mus musculus	515	63	12.7	394	2	QNGP9_POLPA	Q9ngp9 polysiphondy
443	64	12.9	81	2	Q54HF8 DICDI	Q54hf8 dictyosteli	516	63	12.7	456	2	Q54IG3 DICDI	Q54ig3 dictyosteli
444	64	12.9	84	2	Q5D231_HADSP	Q5d231 hadronyche	517	63	12.7	474	2	Q62327 MOUSE	Q62327 mus musculus
445	64	12.9	90	2	Q5D233_HADIN	Q5d233 hadronyche	518	63	12.7	474	2	Q3U2A9 MOUSE	Q3u2a9 mus musculus
446	64	12.9	116	2	Q5Q981_IXOSC	Q5q981 ixodes scap	519	63	12.7	497	2	Q4AQC1_9CHLB	Q4aqc1 chlorobium
447	64	12.9	117	2	Q9YD41_AERPE	Q9y4d41 aeropyrum p	520	63	12.7	583	2	Q3TSU5 MOUSE	Q3tsu5 mus musculus
448	64	12.9	146	1	TXVE TRIPL	P67862 trimeresuru	521	63	12.7	608	2	Q8S1M4_ORYSA	Q8s1m4 oryza sativ
449	64	12.9	163	2	Q4SFU4_TETNG	Q4sfu4 tetraodon n	522	63	12.7	626	2	Q8ND91_HUMAN	Q8nd91 homo sapien
450	64	12.9	217	2	Q7A9B9_ECO57	Q7a9b9 escherichia	523	63	12.7	648	2	Q9VJU4 DROME	Q9vjua drosophila
451	64	12.9	225	2	Q85613_ECOLI	Q85613 escherichia	524	63	12.7	669	2	Q4V526 DROME	Q4v526 drosophila
452	64	12.9	239	2	Q8XCA3_ECO57	Q8xca3 escherichia	525	63	12.7	701	2	Q86BL2_DROME	Q86bl2 drosophila
453	64	12.9	274	2	Q1FAJ6_9CHLR	Q1faj6 roseiflexus	526	63	12.7	740	2	Q5Z8V2_ORYSA	Q5z8v2 oryza sativ
454	64	12.9	286	2	Q7Q953 ANOGA	Q7q953 anopheles g	527	63	12.7	750	2	Q4RQ92_TETNG	Q4rq92 tetraodon n
455	64	12.9	315	2	Q5CAG9_ORYSA	Q5cag9 oryza sativ	528	63	12.7	782	2	Q9WU23 MOUSE	Q9wu23 mus musculus
456	64	12.9	322	2	Q616A1_CAEBR	Q616a1 caenorhabdi	529	63	12.7	827	2	Q9BRK9 MOUSE	Q9brk9 mus musculus
457	64	12.9	322	2	Q20CF5_PETMA	Q20cf5 petromyzon	530	63	12.7	909	2	Q6DIG4_XENTR	Q6dig4 xenopus tro
458	64	12.9	368	2	Q2BR21_LACRE	Q2br21 lactobacill	531	63	12.7	947	2	Q8BK77 MOUSE	Q8bk77 mus musculus
459	64	12.9	425	1	TNR16 RAT	P07174 rattus norv	532	63	12.7	969	2	Q96KG6 HUMAN	Q96kg6 homo sapien
460	64	12.9	581	2	Q5LU50_STILO	Q5lu50 silicibacte	533	63	12.7	1044	2	Q17R86 HUMAN	Q17r86 homo sapien
461	64	12.9	587	1	UJ84_HCMWT	Q51u50 human cytom	534	63	12.7	1107	2	Q4S977_TETNG	Q4s977 tetraodon n
462	64	12.9	602	2	Q3UAG3 MOUSE	Q3uag3 mus musculus	535	63	12.7	1110	2	Q614U4_CAEBR	Q614u4 caenorhabdi
463	64	12.9	602	2	Q3UD85 MOUSE	Q3ud85 mus musculus	536	63	12.7	1139	1	MA2A2_HUMAN	P49641 homo sapien
464	64	12.9	657	2	Q4PIC7_USTMA	Q4pic7 ustilago ma	537	63	12.7	1140	2	Q8OT91 MOUSE	Q8ot91 mus musculus
465	64	12.9	983	2	Q4T849_TETNG	Q4t849 tetraodon n	538	63	12.7	1150	2	Q6Q11_XENLA	Q6q11 xenopus lae
466	64	12.9	1037	2	Q3UV32 MOUSE	Q3uv32 mus musculus	539	63	12.7	1152	2	Q197W7_TETNG	Q197w7 mus musculus
467	64	12.9	1143	2	Q21010 CAEBL	Q21010 caenorhabdi	540	63	12.7	1152	2	Q4S7D3_TETNG	Q4s7d3 tetraodon n
468	64	12.9	1144	1	MAZAI_HUMAN	Q21010 caenorhabdi	541	63	12.7	1278	2	Q9U350 CAEBL	Q9u350 caenorhabdi
469	64	12.9	1145	2	Q2PJ74 CAEBL	Q2pj74 caenorhabdi	542	63	12.7	1553	2	Q29GI8_DROPS	Q29gi8 drosophila

543	63	12.7	2378	2	Q4RW31_TETNG	Q4RW31 tetraodon n	616	62	12.4	469	2	Q5BLE3_BRARE	Q5BLE3 brachydanio
544	63	12.7	2468	2	Q800E4_BRARE	Q800E4 brachydanio	617	62	12.4	476	2	Q8RIH9_MOUSE	Q8RIH9 mus musculus
545	63	12.7	2825	2	Q704E5_MOUSE	Q704E5 mus musculus	618	62	12.4	491	2	P90850_CAEL	P90850 caenorhabdi
546	63	12.7	2871	1	FEN1_BOVIN	P98133 bos taurus	619	62	12.4	493	2	Q7TNG6_MOUSE	Q7TNG6 mus musculus
547	62.5	12.6	158	1	KAB3_OLDAP	P58455 oldenlandia	620	62	12.4	583	2	Q1EG87_PIG	Q1EG87 sus scrofa
548	62.5	12.6	169	2	Q3TRB8_MOUSE	Q3trb8 m adult mal	621	62	12.4	585	2	Q17EL8_ADAE	Q17EL8 aedes aegyp
549	62.5	12.6	220	2	Q63404_RAT	Q63404 rattus norv	622	62	12.4	592	2	Q6IS34_MOUSE	Q6IS34 mus musculus
550	62.5	12.6	237	2	Q1VKN0_PFLAO	Q1vkn0 psychroflex	623	62	12.4	601	2	Q52KT2_XENLA	Q52KT2 xenopus lae
551	62.5	12.6	286	2	Q6IKY7_DROME	Q6iky7 drosophila	624	62	12.4	615	2	Q58E52_MOUSE	Q58E52 mus musculus
552	62.5	12.6	315	2	Q56JUI_CANFA	Q56jui canis famil	625	62	12.4	625	2	Q8JQF9_9VIRU	Q8JQF9 adeno-assoc
553	62.5	12.6	352	2	Q3MZ10_9DELT	Q3mzt0 syntrophoba	626	62	12.4	637	2	Q8R0K8_MOUSE	Q8R0K8 mus musculus
554	62.5	12.6	360	2	Q8YQ74_ANASP	Q8yqt4 anabaena sp	627	62	12.4	657	2	Q8JZM4_MOUSE	Q8Jzm4 mus musculus
555	62.5	12.6	360	2	Q3MCS3_ANAVT	Q3mcs3 anabaena va	628	62	12.4	737	2	Q8VD97_MOUSE	Q8vd97 mus musculus
556	62.5	12.6	369	2	Q565Y9_9BACT	Q565y9 uncultured	629	62	12.4	772	2	DLLA_BRARE	Q6di48 brachydanio
557	62.5	12.6	378	2	Q510R0_XENTR	Q510r0 xenopus tro	630	62	12.4	885	2	Q7R1C5_GIALA	Q7r1c5 giardia lam
558	62.5	12.6	426	2	Q6TMJ6_DICDI	Q6tmj6 dictyosteli	631	62	12.4	924	2	Q244S7_TETTH	Q244s7 tetrahymena
559	62.5	12.6	462	2	Q55FY2_DICDI	Q55fy2 dictyosteli	632	62	12.4	998	1	EPHB3_HUMAN	P54753 homo sapien
560	62.5	12.6	458	2	Q1S159_MEDTR	Q1s159 medicago tr	633	62	12.4	1047	2	Q566K6_MOUSE	Q566k6 mus musculus
561	62.5	12.6	558	2	Q2HCHO_CHAGB	Q2hcho chaetomium	634	62	12.4	1065	2	Q810H2_MOUSE	Q810h2 mus musculus
562	62.5	12.6	567	2	Q8WUL3_HUMAN	Q8wul3 homo sapien	635	62	12.4	1113	1	CORIN_MOUSE	Q92319 mus musculus
563	62.5	12.6	567	2	Q3GL37_9DELT	Q3gl37 peibobacter	636	62	12.4	1170	1	TSP1_HUMAN	P07996 homo sapien
564	62.5	12.6	607	2	Q1KXY5_MYXGL	Q1kxy5 myxine glut	637	62	12.4	1170	1	TSP1_MOUSE	P35441 mus musculus
565	62.5	12.6	645	2	Q02261_CAENHABDI	Q02261 caenorhabdi	638	62	12.4	1170	2	Q71SA3_RAT	Q71sa3 rattus norv
566	62.5	12.6	645	2	Q1PHR4_SACKO	Q1phr4 saccglossu	639	62	12.4	1170	2	Q3TR40_MOUSE	Q3tr40 mus musculus
567	62.5	12.6	668	2	Q4SRK6_TETNG	Q4srk6 tetraodon n	640	62	12.4	1171	2	Q8QYQ1_MOUSE	Q8qyq1 mus musculus
568	62.5	12.6	880	1	CADHF_XENLA	P33148 xenopus lae	641	62	12.4	1171	2	Q8CGB2_MOUSE	Q8cgb2 mus musculus
569	62.5	12.6	919	2	Q298B4_DROPS	Q298b4 drosophila	642	62	12.4	1174	2	Q99K58_MOUSE	Q99k58 mus musculus
570	62.5	12.6	925	2	Q9UB95_CAEL	Q9ub95 caenorhabdi	643	62	12.4	1174	2	Q3TGL4_MOUSE	Q3tgl4 mus musculus
571	62.5	12.6	996	2	Q16ZG2_ADAE	Q16zgz aedes aegyp	644	62	12.4	1205	2	Q8KOP6_MOUSE	Q8kop6 mus musculus
572	62.5	12.6	1031	2	Q42124_CHICK	Q42124 gallus gall	645	62	12.4	1221	1	FELN2_MOUSE	P37889 mus musculus
573	62.5	12.6	1140	2	Q68DE5_HUMAN	Q68des5 homo sapien	646	62	12.4	1225	2	Q59E99_HUMAN	Q59e99 homo sapien
574	62.5	12.6	1140	2	Q96KG7_HUMAN	Q96kg7 homo sapien	647	62	12.4	1308	2	Q5GPM8_CAERE	Q5gpm8 caenorhabdi
575	62.5	12.6	1245	2	Q9Y7V5_TRIHA	Q9y7v5 trichoderma	648	62	12.4	1361	2	Q6PD18_MOUSE	Q6pd18 mus musculus
576	62.5	12.6	1280	2	Q60VE8_CAERB	Q60ve8 caenorhabdi	649	62	12.4	1403	2	Q70E20_MOUSE	Q70e20 mus musculus
577	62.5	12.6	1294	2	Q8C6Z2_MOUSE	Q8c6z2 mus musculus	650	62	12.4	1595	2	Q1EHB3_RAT	Q1ehb3 rattus norv
578	62.5	12.6	1403	1	NID2_MOUSE	Q88322 mus musculus	651	62	12.4	1808	2	Q1XD63_RAT	Q1xd63 rattus norv
579	62.5	12.6	1403	2	Q3TFN0_MOUSE	Q3tpn0 mus musculus	652	62	12.4	1813	1	LTBP2_MOUSE	Q08999 mus musculus
580	62.5	12.6	1403	2	Q3US45_MOUSE	Q3us45 mus musculus	653	62	12.4	1935	2	Q6QHS3_LYTVA	Q6qhs3 lytechinus
581	62.5	12.6	1403	2	Q7TQF0_MOUSE	Q7tqf0 mus musculus	654	62	12.4	2043	2	Q4Q510_LEIMA	Q4q510 leishmania
582	62.5	12.6	1403	2	Q8CPA3_MOUSE	Q8cpa3 mus musculus	655	62	12.4	2067	2	Q59ED8_HUMAN	Q59ed8 homo sapien
583	62.5	12.6	1403	2	Q8R5G0_MOUSE	Q8r5g0 mus musculus	656	62	12.4	2282	1	ZAN_RABIT	P57999 oryctolagus
584	62.5	12.6	1514	2	Q29BH5_DROPS	Q29bh5 drosophila	657	62	12.4	2437	1	NOTC1_BRARE	P46530 brachydanio
585	62.5	12.6	1713	2	Q5RH37_BRARE	Q5rh37 brachydanio	658	62	12.4	2511	2	Q4T9V2_TETNG	Q4t9v2 tetraodon n
586	62.5	12.6	1732	2	Q1LY17_BRARE	Q1ly17 brachydanio	659	62	12.4	2555	2	Q5SXM3_HUMAN	Q5sxm3 homo sapien
587	62.5	12.6	2525	2	Q4QHT5_LEIMA	Q4qht5 leishmania	660	62	12.4	2556	1	NOTC1_HUMAN	P46531 homo sapien
588	62.5	12.6	2632	2	Q16UT3_AEDAE	Q16ut3 aedes aegyp	661	62	12.4	5141	1	SSPO_RAT	Q700k0 rattus norv
589	62.5	12.6	3224	2	Q4RVG6_TETNG	Q4rvg6 tetraodon n	662	61.5	12.3	83	2	Q9XXT6_CAEL	Q9txt6 caenorhabdi
590	62.5	12.6	5179	1	MUC2_HUMAN	Q02817 homo sapien	663	61.5	12.3	110	1	LCE2D_HUMAN	Q5ta82 homo sapien
591	62	12.4	92	2	Q2MCN6_HYDAT	Q2mcn6 hydra atten	664	61.5	12.3	128	2	Q52VH7_CIOIN	Q52vh7 ciona intes
592	62	12.4	93	2	Q31318_HYDMA	Q3i318 hydra magni	665	61.5	12.3	159	2	Q7XZ75_GRIJA	Q7xz75 griffithsia
593	62	12.4	100	1	VP52_BPAPS	Q9tlp6 bacterioph	666	61.5	12.3	166	1	ZCH13_HUMAN	Q8ww36 homo sapien
594	62	12.4	100	2	Q3LZQ0_9CAUD	Q3lqz0 acyrthosiph	667	61.5	12.3	176	2	Q87WA2_PSESMM	Q87wa2 pseudomonas
595	62	12.4	110	1	LCE2C_HUMAN	Q9sta81 homo sapien	668	61.5	12.3	190	2	Q3ZDR4_PIG	Q3zdr4 sus scrofa
596	62	12.4	174	2	Q9NZN0_BOMMO	Q9nzn0 bombyx mori	669	61.5	12.3	228	2	Q91NG9_9PARA	Q91ng9 tioman viru
597	62	12.4	178	1	CHBE2_BOMMO	P20730 bombyx mori	670	61.5	12.3	277	1	TNR4_HUMAN	P43489 homo sapien
598	62	12.4	178	2	Q8PPR1_XANAC	Q8ppr1 xanthomonas	671	61.5	12.3	277	2	Q2M3I2_HUMAN	Q2m3i2 homo sapien
599	62	12.4	211	2	Q6H8Q4_CANFA	Q6h8q4 canis famil	672	61.5	12.3	350	2	Q20CF4_PETWA	Q20cf4 petromyzon
600	62	12.4	212	2	Q45XK0_HUMAN	Q45xk0 homo sapien	673	61.5	12.3	351	2	Q2QTH8_ORYZA	Q2qth8 oryza sativ
601	62	12.4	217	2	Q7XZ34_GRIJA	Q7xz34 griffithsia	674	61.5	12.3	368	2	Q82VZ2_NITEU	Q82vz2 nitrosomona
602	62	12.4	222	2	Q3U697_MOUSE	Q3u697 m bone marr	675	61.5	12.3	373	2	Q5SNS5_BRARE	Q5sns5 brachydanio
603	62	12.4	240	2	Q219M8_RHOPE	Q219m8 rhodopseudo	676	61.5	12.3	408	2	Q29K93_DROPS	Q29k93 drosophila
604	62	12.4	243	2	Q4TDM7_TETNG	Q4tdm7 tetraodon n	677	61.5	12.3	452	2	Q5ISL2_NACFA	Q5isl2 macaca fasc
605	62	12.4	258	2	Q9ZS48_TOBAC	Q9zs48 nicotiana t	678	61.5	12.3	469	2	Q52V41_CIOIN	Q52v41 ciona intes
606	62	12.4	282	1	END4_DESVH	Q72c99 desulfovibr	679	61.5	12.3	587	2	Q5C3P1_SCHJA	Q5c3p1 schistosoma
607	62	12.4	306	2	Q2KJ78_BOVIN	Q2kj78 bos taurus	680	61.5	12.3	659	2	Q1Q4X4_9BACT	Q1q4x4 candidatus
608	62	12.4	311	2	Q8RIK8_MOUSE	Q8rik8 mus musculus	681	61.5	12.3	720	2	Q2U318_ASPOR	Q2u318 aspergillus
609	62	12.4	315	2	Q4U3E1_HUMAN	Q4u3e1 homo sapien	682	61.5	12.3	735	2	Q498M5_RAT	Q498m5 rattus norv
610	62	12.4	363	2	Q1CYN7_MYXXA	Q1cyn7 myxococcus	683	61.5	12.3	774	2	Q3SEM2_PARTE	Q3sem2 paramecium
611	62	12.4	383	2	Q969Y6_HUMAN	Q969y6 homo sapien	684	61.5	12.3	774	2	Q3SEM3_PARTE	Q3sem3 paramecium
612	62	12.4	388	2	Q66JK7_XENTR	Q66jk7 xenopus tro	685	61.5	12.3	782	2	Q7PD82_PLAYO	Q7pds2 plasmodium
613	62	12.4	389	2	Q8R226_MOUSE	Q8r226 mus musculus	686	61.5	12.3	812	2	Q77779_BOVIN	Q77779 bos taurus
614	62	12.4	402	1	GUN1_HUMIN	P56680 humicola in	687	61.5	12.3	816	2	Q5R449_PONPY	Q5r449 pongo pygma
615	62	12.4	435	1	GUN1_HUMGT	Q12622 humicola gr	688	61.5	12.3	833	2	Q5R6S4_PONPY	Q5r6s4 pongo pygma

689	61.5	12.3	932	2	Q5Y4N8_RAT	Q5Y4n8 rattus norv	762	61	12.2	1162	2	Q2Q422_CANFA	Q2q422 canis famil
690	61.5	12.3	941	2	Q54YPO_DICDI	Q54yp0 dictyosteli	763	61	12.2	1212	2	Q42347_CHICK	Q42347 gallus gall
691	61.5	12.3	1045	2	Q8T3A6_CABEL	Q8t3a6 caenorhabdi	764	61	12.2	1249	2	Q8VI66_RAT	Q8v166 rattus norv
692	61.5	12.3	1070	2	Q8T3A7_CABEL	Q8t3a7 caenorhabdi	765	61	12.2	1396	2	Q4RRY1_TETNG	Q4rpy1 tetraodon n
693	61.5	12.3	1111	2	Q9XWD6_CABEL	Q9xwd6 caenorhabdi	766	61	12.2	1418	2	Q93451_SCOMX	Q93451 scophthalmu
694	61.5	12.3	1124	2	Q23GM4_TETTH	Q23gm4 tetrahymena	767	61	12.2	1476	2	Q90285_CARAU	Q90285 carassius a
695	61.5	12.3	1179	2	Q1SIZ0_MEDTR	Q1siz0 medicago tr	768	61	12.2	1599	2	Q09983_CABEL	Q09983 caenorhabdi
696	61.5	12.3	1267	2	Q2EG68_PONPY	Q2eg68 pongo pygma	769	61	12.2	1624	2	Q17AS8_AEDAE	Q17as8 aedes aegyp
697	61.5	12.3	1316	2	Q96JU7_HUMAN	Q96ju7 homo sapien	770	61	12.2	1790	2	Q17AS8_AEDAE	Q17as8 dictyosteli
698	61.5	12.3	1394	2	Q8MST1_DROME	Q8mst1 drosophila	771	61	12.2	2476	1	Q55F41_DICDI	Q55f41 sus scrofa
699	61.5	12.3	1458	2	Q1ASL1_BRARE	Q1asl1 brachydanio	772	61	12.2	2532	2	Q629H6_CABER	Q629h6 caenorhabdi
700	61.5	12.3	1511	2	Q9VB21_DROME	Q9vb21 drosophila	773	61	12.2	2806	2	Q4DH79_TRYCR	Q4dh79 trypanosoma
701	61.5	12.3	1666	1	LTPB4_MOUSE	Q8k4g1 mus musculu	774	61	12.2	4998	1	SSFO_MOUSE	Q8cg5 mus musculu
702	61.5	12.3	1687	2	Q61204_MOUSE	Q61204 mus musculu	775	61	12.2	5429	2	Q16KQ8_AEDAE	Q16kq8 aedes aegyp
703	61.5	12.3	1721	2	Q9VXV3_DROME	Q9vxv3 caenorhabdi	776	61	12.2	92	2	Q8GXV9_ARATH	Q8gxv9 arabidopsis
704	61.5	12.3	2030	2	Q614N6_CABEL	Q614n6 caenorhabdi	777	60.5	12.1	96	2	Q9C111_LACIA	Q9c111 lactococcus
705	61.5	12.3	2224	2	Q44131_CABEL	Q44131 caenorhabdi	778	60.5	12.1	106	2	Q33AQ5_ORYSA	Q33aq5 oryza sativ
706	61.5	12.3	2277	2	Q22QJ9_TETTH	Q22qj9 tetrahymena	779	60.5	12.1	113	2	Q8H3W9_ORYSA	Q8h3w9 oryza sativ
707	61.5	12.3	2470	1	NOTC2_MOUSE	Q35516 mus musculu	780	60.5	12.1	129	2	Q9YCE5_AERPE	Q9yc5 aeropyrum p
708	61.5	12.3	2471	1	NOTC2_RAT	Q9q30 rattus norv	781	60.5	12.1	168	2	Q8T229_TRYCR	Q8t229 trypanosoma
709	61.5	12.3	2570	1	STAB1_HUMAN	Q8r4y4 mus musculu	782	60.5	12.1	181	2	Q3F736_9BURK	Q3f736 burkholderi
710	61.5	12.3	2571	1	STAB1_MOUSE	Q8r4y4 mus musculu	783	60.5	12.1	234	2	Q5C033_SCHJA	Q5c033 schistosoma
711	61.5	12.3	2966	2	Q4RMT7_TETNG	Q4rmt7 tetraodon n	784	60.5	12.1	251	2	Q2EPY6_ATEGE	Q2efy6 ateles geof
712	61.5	12.3	3145	2	Q22M95_TETTH	Q22m95 tetrahymena	785	60.5	12.1	252	2	Q2GLX9_CHAGB	Q2glx9 chaeomium
713	61.5	12.3	3333	1	LAMA3_MOUSE	Q4e0c7 trypanosoma	786	60.5	12.1	252	2	Q2EG79_LAGIA	Q2eg79 lagotherix l
714	61.5	12.3	3457	2	Q4E0C7_TRYCR	Q4e0c7 trypanosoma	787	60.5	12.1	261	2	Q39TH1_GEOMG	Q39th1 geobacter m
715	61.5	12.3	3548	2	Q5VTE4_HUMAN	Q5vte4 homo sapien	788	60.5	12.1	289	2	Q1PG16_HYDSY	Q1pg16 hydractinia
716	61.5	12.3	3574	2	Q4LDE5_HUMAN	Q4ldes homo sapien	789	60.5	12.1	296	2	Q5M8H8_XENTR	Q5m8h8 xenopus tro
717	61.5	12.3	4260	2	Q4T3Y2_TETNG	Q4t3y2 tetraodon n	790	60.5	12.1	316	1	IBP2_PIG	Q24837 sus scrofa
718	61.5	12.3	5374	2	Q99ND0_MOUSE	Q99nd0 mus musculu	791	60.5	12.1	343	2	Q17CJ7_AEDAE	Q17cj7 aedes aegyp
719	61.5	12.3	5376	1	ZAN_MOUSE	Q88799 mus musculu	792	60.5	12.1	368	2	Q86IM1_DICDI	Q86im1 dictyosteli
720	61	12.2	104	2	Q7XZ46_GRIJA	Q7xz46 griffithsia	793	60.5	12.1	383	2	Q70534_RAT	Q70534 rattus norv
721	61	12.2	111	1	COL_MYOCO	P42889 myocastor c	794	60.5	12.1	383	2	Q62779_RAT	Q62779 ratia sativ
722	61	12.2	112	1	COL_PIG	P02703 sus scrofa	795	60.5	12.1	386	2	Q53LE2_ORYSA	Q53le2 dictyosteli
723	61	12.2	115	1	MERT_SHEPU	Q54482 shewanella	796	60.5	12.1	395	2	Q55923_DICDI	Q55923 dictyosteli
724	61	12.2	116	2	Q5T6Z9_HUMAN	Q5t6z9 homo sapien	797	60.5	12.1	401	2	Q811K6_MOUSE	Q811k6 mus musculu
725	61	12.2	146	1	TXVE_BOTIN	Q90x24 bothrops in	798	60.5	12.1	407	2	Q96113_DROME	Q96113 drosophila
726	61	12.2	156	2	Q29FD2_DROPS	Q29fd2 drosophila	799	60.5	12.1	452	1	Q611L6_AEDAE	Q611l6 aedes aegyp
727	61	12.2	156	2	Q21VF9_RHOP2	Q21vf9 rhodopseudo	800	60.5	12.1	469	2	Q161L6_AEDAE	Q161l6 aedes aegyp
728	61	12.2	173	2	Q9R135_STRCO	Q9r135 streptomyce	801	60.5	12.1	515	1	NAGPA_HUMAN	Q9uk23 homo sapien
729	61	12.2	205	2	Q5T700_HUMAN	Q5t700 homo sapien	802	60.5	12.1	544	2	Q5BW73_SCHJA	Q5bw73 schistosoma
730	61	12.2	211	2	Q9RK27_STRCO	Q9rk27 streptomyce	803	60.5	12.1	556	2	Q5VXW6_HUMAN	Q5vxw6 homo sapien
731	61	12.2	307	2	Q4C965_CROWT	Q4c965 crocospaer	804	60.5	12.1	637	2	Q7PF07_ANOGA	Q7pf07 anopheles g
732	61	12.2	369	2	Q7QDZ6_ANOGA	Q7qdze anopheles g	805	60.5	12.1	723	1	DL11_HUMAN	Q00548 homo sapien
733	61	12.2	380	2	Q60214_METCA	Q60214 methylococc	806	60.5	12.1	754	2	Q1L8H4_BRARE	Q1l8h4 brachydanio
734	61	12.2	409	2	Q3TV46_MOUSE	Q3tv46 mus musculu	807	60.5	12.1	767	2	Q9DGR2_XENLA	Q9dgr2 xenopus lae
735	61	12.2	413	2	Q23015_CABEL	Q23015 caenorhabdi	808	60.5	12.1	780	2	Q3U2X9_MOUSE	Q3u2x9 mus musculu
736	61	12.2	442	2	Q55GL3_DICDI	Q55gl3 dictyosteli	809	60.5	12.1	790	2	Q4R728_MACFA	Q4r728 macaca fasc
737	61	12.2	442	2	Q569T8_XENLA	Q569t8 xenopus lae	810	60.5	12.1	871	2	Q4SCX8_TETNG	Q4scx8 tetraodon n
738	61	12.2	443	2	Q2TAU8_XENLA	Q2tau8 xenopus lae	811	60.5	12.1	905	2	Q18260_CABEL	Q18260 caenorhabdi
739	61	12.2	447	2	Q4J3W1_AZOVI	Q4j3w1 azotobacter	812	60.5	12.1	917	2	Q9VE20_DROME	Q9ve20 drosophila
740	61	12.2	456	2	Q3WTR3_9RHIZ	Q3wtr3 mesorhizobi	813	60.5	12.1	978	1	MCR_MOUSE	Q8v118 mus musculu
741	61	12.2	506	2	Q8C7W2_MOUSE	Q8c7w2 mus musculu	814	60.5	12.1	1024	2	Q9BX11_HUMAN	Q9bx11 homo sapien
742	61	12.2	525	2	P92162_BOMMO	P92162 bombyx mori	815	60.5	12.1	1030	2	Q22D69_TETTH	Q22d69 tetrahymena
743	61	12.2	538	2	Q8CC86_MOUSE	Q8cc86 m adult mal	816	60.5	12.1	1087	2	Q23H08_TETTH	Q23h08 tetrahymena
744	61	12.2	563	2	Q7TP82_RAT	Q7tp82 rattus norv	817	60.5	12.1	1101	2	Q1SA17_MEDTR	Q1sa17 medicago tr
745	61	12.2	571	2	Q8C1B3_MOUSE	Q8c1b3 mus musculu	818	60.5	12.1	1104	2	NFX1_HUMAN	Q12986 homo sapien
746	61	12.2	606	2	Q17LW1_AEDAE	Q17lw1 aedes aegyp	819	60.5	12.1	1120	2	Q96EL5_HUMAN	Q96el5 mus sapien
747	61	12.2	652	2	Q4B0K0_9BURK	Q4b0k0 polaromonas	820	60.5	12.1	1389	1	L7B1S_MOUSE	Q8eg18 mus musculu
748	61	12.2	617	2	Q4T6N0_TETNG	Q4t6n0 tetraodon n	821	60.5	12.1	1394	2	Q505C9_MOUSE	Q505c9 mus musculu
749	61	12.2	650	2	Q8C122_MOUSE	Q8c122 mus musculu	822	60.5	12.1	1622	2	Q3ZTM4_SAISC	Q3ztm4 saimiri sci
750	61	12.2	703	2	FLN1_MOUSE	Q98879 mus musculu	823	60.5	12.1	1713	1	L7B1L_MOUSE	Q8eg19 mus musculu
751	61	12.2	705	1	FLN1_MOUSE	Q3twk8 mus musculu	824	60.5	12.1	1778	2	Q45VP9_DERVA	Q45vp9 dermator
752	61	12.2	723	2	Q3TWK8_MOUSE	Q3twk8 mus musculu	825	60.5	12.1	1897	2	Q29H17_DROPS	Q29h17 drosophila
753	61	12.2	735	2	Q9QW16_9MURI	Q9qw16 rattus sp.	826	60.5	12.1	1914	2	Q4WHJ5_ASPFU	Q4whj5 aspergillus
754	61	12.2	881	2	Q9W0A0_DROME	Q9w0a0 drosophila	827	60.5	12.1	2038	2	Q7QF82_ANOGA	Q7qf82 anopheles g
755	61	12.2	903	2	Q44397_TRITR	Q44397 trichuris t	828	60.5	12.1	2653	2	Q25F82_ANOGA	Q25f82 anopheles g
756	61	12.2	987	2	Q616G9_CABER	Q616g9 caenorhabdi	829	60.5	12.1	2703	1	NOTCH_DROME	Q25253 lucilia cup
757	61	12.2	1031	2	Q1EC80_DROME	Q1ec80 drosophila	830	60.5	12.1	2771	2	Q9WTS7_MOUSE	P07207 drosophila
758	61	12.2	1037	2	Q5VY43_HUMAN	Q5vy43 homo sapien	831	60.5	12.1	2783	2	Q7M559_BRARE	Q7m559 brachydanio
759	61	12.2	1057	2	Q4N4P8_THEPA	Q4n4p8 theileria p	832	60.5	12.1	2796	2	Q3UHK6_MOUSE	Q3uhk6 mus musculu
760	61	12.2	1111	2	Q80YN4_RAT	Q80yn4 rattus norv	833	60.5	12.1	2833	2	Q3UH52_MOUSE	Q3uh52 mus musculu
761	61	12.2	1123	2	Q5RDI5_PONPY	Q5rdi5 pongo pygma	834	60.5	12.1	3486	2	Q4DGM4_TRYCR	Q4dgm4 trypanosoma

835	60.5	12.1	12269	2	Q1JSM5_TOXGO	Q1Jem5 toxoplasma	908	60	12.0	1955	1	AGRN_CHICK	P31696 gallus galli
836	60	12.0	60	2	Q20A06_CRAIG	Q20a06 crassostrea	909	60	12.0	1976	2	Q59E86_HUMAN	Q59E86 homo sapiens
837	60	12.0	125	2	Q4WZP5_ASPFU	Q4wzp5 aspergillus	910	60	12.0	2016	2	Q7PF90_ANOGA	Q7PF90 anopheles gambiae
838	60	12.0	126	2	Q8T5W4_CAERE	Q8t5w4 caenorhabditis	911	60	12.0	2030	2	Q4RHF2_TETNG	Q4RHF2 tetraodon
839	60	12.0	127	2	Q8T5X2_CAERE	Q8t5x2 caenorhabditis	912	60	12.0	2433	2	Q24F98_TETTH	Q24F98 tetrahymena
840	60	12.0	128	2	Q8T5W8_CAERE	Q8t5w8 caenorhabditis	913	60	12.0	2911	1	PBN2_HUMAN	P35556 homo sapiens
841	60	12.0	129	2	Q8T5W7_CAERE	Q8t5w7 caenorhabditis	914	60	12.0	3126	2	Q3V5L4_MOUSE	Q3V5L4 mus musculus
842	60	12.0	146	2	Q5K4F7_SCHGR	Q5k4f7 schistocerca	915	60	12.0	3493	2	Q4RJ20_TETNG	Q4RJ20 tetraodon
843	60	12.0	159	2	Q2CGN9_9RHOB	Q2cgn9 oceanicola	916	60	12.0	4006	2	Q35452_MOUSE	Q35452 mus musculus
844	60	12.0	181	2	Q4AF9A_9CHLB	Q4afa9 chlorobium	917	60	12.0	4114	2	Q54796_MOUSE	Q54796 mus musculus
845	60	12.0	184	1	ESM1_HUMAN	Q9nq30 homo sapiens	918	59.5	11.9	98	1	KRA33_HUMAN	Q9byr6 homo sapiens
846	60	12.0	185	2	Q6X1W9_DROYA	Q6x1w9 drosophila	919	59.5	11.9	98	2	Q6NTD4_HUMAN	Q6ntd4 homo sapiens
847	60	12.0	211	2	Q6TPK5_CHICK	Q6tpk5 gallus galli	920	59.5	11.9	101	2	Q6S313_GROSI	Q6s313 lavatera thymifolia
848	60	12.0	309	2	Q74ZS4_ASHGO	Q74zsa4 ashbya gossypii	921	59.5	11.9	105	2	Q5SZI7_HUMAN	Q5sz17 homo sapiens
849	60	12.0	318	2	Q6A853_PROAC	Q6a853 propionibacterium	922	59.5	11.9	112	2	Q9ZP51_URTDI	Q9zp51 urtica dioica
850	60	12.0	320	2	Q8N780_HUMAN	Q8n780 homo sapiens	923	59.5	11.9	118	2	Q21ZF4_RHOP2	Q21zf4 rhodopsin
851	60	12.0	348	2	Q54KB6_DICDI	Q54kb6 dictyostelium	924	59.5	11.9	128	1	KAPB_BACSU	Q08429 bacillus subtilis
852	60	12.0	366	2	Q46SU2_RALEJ	Q46su2 ralstonia	925	59.5	11.9	132	2	Q2Q1P4_PANTR	Q2q1p4 pan troglodytes
853	60	12.0	383	2	Q3KA04_PSEPF	Q3ka04 pseudomonas	926	59.5	11.9	151	2	Q2WAL5_MAGMM	Q2wal5 magnetospirillum
854	60	12.0	397	2	Q52VK2_CIOIN	Q52vk2 ciona	927	59.5	11.9	156	2	Q6N0U5_RHOPA	Q6n0u5 rhodospirillum rubrum
855	60	12.0	398	2	Q52VK3_CIOIN	Q52vk3 ciona	928	59.5	11.9	159	2	Q5LKG8_SILPO	Q5lkg8 silicibacter
856	60	12.0	403	2	Q1EC01_DROME	Q1ec01 drosophila	929	59.5	11.9	170	2	Q1Q792_9BACT	Q1q792 candidatus
857	60	12.0	403	2	Q4R3X4_MACFA	Q4r3x4 macaca fascicularis	930	59.5	11.9	177	2	Q7RYN5_NEUCR	Q7ryn5 neurospora
858	60	12.0	415	2	Q2GRW5_CHAGB	Q2grw5 chaetomium	931	59.5	11.9	182	2	Q4AT93_9BURK	Q4at93 polaromonas
859	60	12.0	416	2	Q4KFP7_PSEFS	Q4kfp7 pseudomonas	932	59.5	11.9	182	2	Q5P9V7_ANAMM	Q5p9v7 anaplasma
860	60	12.0	433	2	Q91ZM6_RAT	Q91zm6 rattus norvegicus	933	59.5	11.9	232	2	Q2JWS8_SYNJA	Q2jws8 synechococcus
861	60	12.0	451	2	Q98173_MCV1	Q98173 molluscum contagiosum	934	59.5	11.9	248	2	Q2EG38_SAGLB	Q2eg38 saginulus laevis
862	60	12.0	454	2	Q8AXB6_BRARE	Q8axb6 brachydanio	935	59.5	11.9	289	2	Q1PG03_HYDSY	Q1pg03 hydractinia
863	60	12.0	461	2	Q6VAU8_RAT	Q6vau8 rattus norvegicus	936	59.5	11.9	289	2	Q1PG01_HYDSY	Q1pg01 hydractinia
864	60	12.0	463	2	Q6PHH5_BRARE	Q6phh5 brachydanio	937	59.5	11.9	289	2	Q1PFZ9_HYDSY	Q1pfz9 hydractinia
865	60	12.0	468	1	ZN672_RAT	Q842b2 rattus norvegicus	938	59.5	11.9	289	2	Q1PG00_HYDSY	Q1pg00 hydractinia
866	60	12.0	474	1	TNR1B_RAT	Q80wy6 rattus norvegicus	939	59.5	11.9	289	2	Q1PG02_HYDSY	Q1pg02 hydractinia
867	60	12.0	474	2	Q5YLP0_RAT	Q5y1p0 rattus norvegicus	940	59.5	11.9	289	2	Q1PG10_HYDSY	Q1pg10 hydractinia
868	60	12.0	485	2	Q4H306_CIOIN	Q4h3g6 ciona	941	59.5	11.9	289	2	Q1PG05_HYDSY	Q1pg05 hydractinia
869	60	12.0	541	2	Q1WKY1_DROYA	Q1wkyl1 drosophila	942	59.5	11.9	294	2	Q61HT4_CAEBR	Q61ht4 caenorhabditis
870	60	12.0	541	2	Q1WKY4_DROOR	Q1wkyl4 drosophila	943	59.5	11.9	300	2	Q3V1I2_MOUSE	Q3v1i2 mus musculus
871	60	12.0	542	2	Q1WKY2_DROTE	Q1wkyl2 drosophila	944	59.5	11.9	307	2	Q31YR3_RHOS4	Q31yr3 rhodobacter
872	60	12.0	542	2	Q1WKY3_DROSI	Q1wkyl3 drosophila	945	59.5	11.9	320	2	Q5Y079_COWPX	Q5y079 cowpox virus
873	60	12.0	545	2	Q1WKY5_DROER	Q1wkyl5 drosophila	946	59.5	11.9	323	2	Q4Q266_LEIMA	Q4q266 leishmania
874	60	12.0	566	2	Q617P3_CAEBR	Q617p3 caenorhabditis	947	59.5	11.9	340	2	Q54KK1_DICDI	Q54kk1 dictyostelium
875	60	12.0	569	2	Q6J2K6_ORYSA	Q6j2k6 oryza sativa	948	59.5	11.9	394	2	Q6Z434_ORYSA	Q6z434 oryza sativa
876	60	12.0	579	2	Q6P2G0_HUMAN	Q6p2g0 homo sapiens	949	59.5	11.9	402	2	Q64WV1_BACFR	Q64wv1 bacteroides
877	60	12.0	622	2	Q5Y9B3_9VIRU	Q5y9b3 adeno-associatus	950	59.5	11.9	402	2	Q5LG05_BACFN	Q5lg05 bacteroides
878	60	12.0	622	2	Q5Y9B5_9VIRU	Q5y9b5 adeno-associatus	951	59.5	11.9	411	2	Q89YQ3_BACTN	Q89yq3 bacteroides
879	60	12.0	623	2	Q9WB7_9VIRU	Q9wbp7 adeno-associatus	952	59.5	11.9	421	2	Q9DEY1_CVPCL	Q9dev1 cyprinus carpio
880	60	12.0	623	2	Q56136_9VIRU	Q56136 adeno-associatus	953	59.5	11.9	433	2	Q7ZX39_XENLA	Q7zx39 xenopus laevis
881	60	12.0	623	2	Q1I031_9VIRU	Q1i031 adeno-associatus	954	59.5	11.9	438	2	Q6INJ1_XENLA	Q6inj1 xenopus laevis
882	60	12.0	623	2	Q1I033_9VIRU	Q1i033 adeno-associatus	955	59.5	11.9	448	2	Q2GPN1_CHAGB	Q2gpn1 chaetomium
883	60	12.0	644	2	Q4REW4_TETNG	Q4rew4 tetraodon	956	59.5	11.9	448	2	Q9VJ08_DROME	Q9vj08 drosophila
884	60	12.0	654	2	Q8IPP3_DROME	Q8ipp3 drosophila	957	59.5	11.9	484	2	Q5CZ68_HUMAN	Q5cz68 homo sapiens
885	60	12.0	657	2	Q17Q48_AEDAE	Q17q48 aedes aegypti	958	59.5	11.9	488	2	Q29GV6_DROPS	Q29gv6 drosophila
886	60	12.0	699	2	Q3W1K0_9ACTO	Q3wk0 frankia	959	59.5	11.9	491	2	Q8TEK2_HUMAN	Q8tek2 homo sapiens
887	60	12.0	701	2	Q4T4W9_TETNG	Q4t4w9 tetraodon	960	59.5	11.9	507	2	Q1ESX6_COCIM	Q1esx6 coccidioides
888	60	12.0	710	2	Q3IBD5_ANGUA	Q3ibd5 anguilla	961	59.5	11.9	507	2	Q1TDJ8_9MYCO	Q1tdj8 mycobacterium
889	60	12.0	735	1	ADAM2_HUMAN	Q99965 homo sapiens	962	59.5	11.9	507	2	Q1TWM6_9MYCO	Q1twm6 mycobacterium
890	60	12.0	735	1	ADAM2_MACFA	Q28478 macaca fascicularis	963	59.5	11.9	507	2	Q1BEM7_9MYCO	Q1bem7 mycobacterium
891	60	12.0	735	2	Q4R6R6_MACFA	Q4r6r6 macaca fascicularis	964	59.5	11.9	533	2	Q6HB8_RAT	Q6hb8 rattus norvegicus
892	60	12.0	755	1	COMP_MOUSE	Q9r0g6 mus musculus	965	59.5	11.9	564	2	Q9TTS4_BOVIN	Q9tts4 bos taurus
893	60	12.0	755	2	Q8V154_MOUSE	Q8v154 mus musculus	966	59.5	11.9	587	2	Q3VQV5_PROAE	Q3qv5 prosthecococcus
894	60	12.0	797	2	Q89PY0_BRAJA	Q89py0 bradyrhizobium	967	59.5	11.9	658	2	Q4RLS7_TETNG	Q4rls7 tetraodon
895	60	12.0	893	2	Q8MJ0K_CERAE	Q8mj0k cercopithecus	968	59.5	11.9	712	2	Q50JF9_CAEEL	Q50jf9 caenorhabditis
896	60	12.0	988	2	Q22685_CAEEL	Q22685 caenorhabditis	969	59.5	11.9	765	2	Q4SMJ3_TETNG	Q4smj3 tetraodon
897	60	12.0	990	2	Q6BTQ2_DEBHA	Q6btq2 debaryomyces	970	59.5	11.9	808	2	Q23DN8_TETTH	Q23dn8 tetrahymena
898	60	12.0	1061	2	Q5B110_DROME	Q5b110 drosophila	971	59.5	11.9	836	2	Q49H10_CANFA	Q49h10 canis familiaris
899	60	12.0	1170	1	TSPI_BOVIN	Q28178 bos taurus	972	59.5	11.9	856	2	Q1J3V8_DEIGD	Q1j3v8 deinococcus
900	60	12.0	1295	1	GLPI_CAEEL	P13508 caenorhabditis	973	59.5	11.9	886	1	EMR1_HUMAN	Q14246 homo sapiens
901	60	12.0	1302	1	LTBP3_HUMAN	Q9ns15 homo sapiens	974	59.5	11.9	886	2	Q217G5_HUMAN	Q217g5 homo sapiens
902	60	12.0	1512	1	USH2A_RAT	Q9k3k1 rattus norvegicus	975	59.5	11.9	917	1	LRP8_CHICK	Q98931 gallus gallus
903	60	12.0	1547	1	RDRP_EMV	P20951 papaya mosaic virus	976	59.5	11.9	917	2	Q65XH7_ORYSA	Q65xh7 oryza sativa
904	60	12.0	1587	2	Q1LK66_CAEER	Q1lk66 caenorhabditis	977	59.5	11.9	925	2	Q9UB94_CAEEL	Q9ub94 caenorhabditis
905	60	12.0	1629	2	Q1L8K6_BRARE	Q1lk86 brachydanio	978	59.5	11.9	1070	2	Q4RJT4_TETNG	Q4rjt4 tetraodon
906	60	12.0	1679	1	FUR2_DROME	P30432 drosophila	979	59.5	11.9	1117	2	Q6E0K3_DIDMA	Q6e0k3 didelphis marsupialis
907	60	12.0	1811	2	Q1JSY5_TOXGO	Q1jsy5 toxoplasma	980	59.5	11.9	1144	2	Q4WGE0_ASPFU	Q4wge0 aspergillus

981	59.5	11.9	1191	2	Q7QH41 ANOGA	Q7qh41 anopheles g	1054	59	11.8	712	2	Q5S3M5_9AGAR	Q5s3m5 grifola sor
982	59.5	11.9	1620	2	Q3ZTN2 SAGOE	Q3ztn2 saguinus oe	1055	59	11.8	719	2	Q5S3M6 GRIFR	Q5s3m6 grifola fro
983	59.5	11.9	1621	2	Q3ZTN8 MACMU	Q3ztn8 macaca mula	1056	59	11.8	719	2	Q1CX64 MYXXA	Q1cx64 myxococcus
984	59.5	11.9	2386	2	Q22ZT9 TETTH	Q22zt9 tetrahymena	1057	59	11.8	740	2	Q6PIA2 HUMAN	Q6pia2 homo sapien
985	59.5	11.9	3102	2	Q45614 CAEBL	Q45614 caenorhabdi	1058	59	11.8	801	2	Q87J38_9HOMO	Q87j38 stereum hir
986	59.5	11.9	3108	2	Q60JW4 CAEBL	Q60jw4 caenorhabdi	1059	59	11.8	803	2	Q87J38_9HOMO	Q87j38 coltricia p
987	59.5	11.9	4135	2	Q18977 BOVIN	Q18977 bos taurus	1060	59	11.8	806	1	ADMIB MOUSE	Q8r595 mus musculus
988	59.5	11.9	4544	1	LRPI HUMAN	Q07954 homo sapien	1061	59	11.8	809	2	Q3V095 MOUSE	Q3v095 mus musculus
989	59	11.8	88	2	Q5UAZ1 PAGNA	Q5uaz1 pagrus majo	1062	59	11.8	836	2	Q61GU3 CAEBR	Q61gu3 caenorhabdi
990	59	11.8	88	2	Q6PW54 PAGNA	Q6pw54 pagrus majo	1063	59	11.8	836	2	Q61CH1 HUMAN	Q61ch1 homo sapien
991	59	11.8	96	2	Q99199 CHLRE	Q99199 chlamydomon	1064	59	11.8	859	2	Q7ZZR6 ORYLA	Q7zzr6 oryzias lat
992	59	11.8	107	2	Q8RKW5 PRORE	Q8rkws providencia	1065	59	11.8	859	2	Q98UH9 ORYLA	Q98uh9 oryzias lat
993	59	11.8	109	2	Q95987 HUMAN	Q95987 homo sapien	1066	59	11.8	871	2	Q87J3V3_9AGAR	Q87j3v3 echinodoni
994	59	11.8	115	2	Q36GZ6_9GAMM	Q36gz6 shewanella	1067	59	11.8	883	2	Q207H1 GANTS	Q207h1 ganoderma t
995	59	11.8	116	2	Q3BY18 CHLAU	Q3ely8 chloroflexu	1068	59	11.8	886	2	Q5U7W2_9HOMO	Q5u7w2 climacodon
996	59	11.8	130	2	Q61E42 RAT	Q6ie42 rattus norv	1069	59	11.8	887	2	Q207G8_9HOMO	Q207g8 phaeolus sc
997	59	11.8	150	2	Q443U5 SOLUS	Q443u5 solibacter	1070	59	11.8	891	2	Q9ULT6 HUMAN	Q9ult6 homo sapien
998	59	11.8	159	1	KRA98 HUMAN	Q9byq0 homo sapien	1071	59	11.8	896	2	Q207G6_9APHY	Q207g6 pycnoporus
999	59	11.8	186	1	AGI3 WHEAT	Q10969 triticum ae	1072	59	11.8	897	2	Q207G9_9APHY	Q207g9 laetiporus
1000	59	11.8	209	2	P93029 ARATH	P93029 arabidopsis	1073	59	11.8	898	2	Q207G7_9APHY	Q207g7 polyporus s
1001	59	11.8	215	2	Q80W51 MOUSE	Q80w51 mus musculus	1074	59	11.8	900	2	Q207G5_9APHY	Q207g5 spangis c
1002	59	11.8	218	1	YR661 MIMIV	Q5uq61 mimivirus	1075	59	11.8	901	2	Q207G4_9APHY	Q207g4 spangipelli
1003	59	11.8	220	2	Q4TF08 TETNG	Q4tf08 tetraodon n	1076	59	11.8	907	2	Q9XTS9 CAEBL	Q9xts9 caenorhabdi
1004	59	11.8	225	2	Q7XZ30 GRIJA	Q7xz30 griffithsia	1077	59	11.8	913	2	Q5U7W8_9HOMO	Q5u7w8 albatrellus
1005	59	11.8	234	2	Q7QGZ2 ANOGA	Q7qgz2 anopheles g	1078	59	11.8	932	2	Q5SSZ7 MOUSE	Q5ssz7 mus musculus
1006	59	11.8	240	2	Q16FD0 AEDAE	Q16fd0 aedes aegyp	1079	59	11.8	937	1	Q29RU4 BOVIN	Q29ru4 bos taurus
1007	59	11.8	261	2	Q1JXX7 DESAC	Q1jxx7 desulfurosm	1080	59	11.8	949	2	Q4S2B5 TETNG	Q4s2b5 tetraodon n
1008	59	11.8	269	2	Q9UZB8 CAEBL	Q9uzb8 caenorhabdi	1081	59	11.8	990	2	Q4RMV7 TETNG	Q4rmv7 tetraodon n
1009	59	11.8	272	2	Q61BN9 CAEBR	Q61bn9 caenorhabdi	1082	59	11.8	1102	2	Q23NT8 TETTH	Q23nt8 tetrahymena
1010	59	11.8	300	2	Q84BD4 MYXXA	Q84bd4 myxococcus	1083	59	11.8	1119	2	Q18034 CAEBL	Q18034 caenorhabdi
1011	59	11.8	306	2	Q3WRH0_9RHIZ	Q3wrh0 mesorhizobi	1084	59	11.8	1123	2	Q75QY0 HUMAN	Q75qy0 homo sapien
1012	59	11.8	315	2	Q8LA97 ARATH	Q8la97 arabidopsis	1085	59	11.8	1146	2	Q60M26 CAEBR	Q60m26 caenorhabdi
1013	59	11.8	315	2	Q82307 ARATH	Q82307 arabidopsis	1086	59	11.8	1154	2	Q3UIW7 MOUSE	Q3uiw7 m b6-derive
1014	59	11.8	322	2	Q4TF09 TETNG	Q4tf09 tetraodon n	1087	59	11.8	1167	2	Q6KAT1 MOUSE	Q6kat1 mus musculus
1015	59	11.8	322	2	Q1D2V4 MYXXA	Q1d2v4 myxococcus	1088	59	11.8	1175	2	Q50TW3_ENTHI	Q50tw3 entamoeba h
1016	59	11.8	332	2	Q8C3D8 MOUSE	Q8c3d8 mus musculus	1089	59	11.8	1268	1	LTBP3 MOUSE	Q61810 mus musculus
1017	59	11.8	343	2	Q6PAL1 MOUSE	Q6pal1 mus musculus	1090	59	11.8	1270	2	Q9GPN0 CAEBR	Q9gpn0 caenorhabdi
1018	59	11.8	348	2	Q6UNK8 HUMAN	Q6unk8 homo sapien	1091	59	11.8	1314	2	Q8UZJ7_9GAMA	Q8uzj7 cercopithec
1019	59	11.8	349	1	XRCQ3 MOUSE	Q9cxee mus musculus	1092	59	11.8	1674	2	Q2R3L7_ORYSA	Q2r3l7 oryza sativ
1020	59	11.8	349	2	Q1KLA5_9AGAR	Q1kla5 physalacia	1093	59	11.8	1675	2	Q23L27_COCIM	Q23l27 coccidioid
1021	59	11.8	349	2	Q8NB13 HUMAN	Q8nb13 homo sapien	1094	59	11.8	1682	2	Q1DW27_TETTH	Q1dw27 tetrahymena
1022	59	11.8	349	2	Q5SNX0 HUMAN	Q5snx0 homo sapien	1095	59	11.8	1725	2	Q23X28_TETTH	Q23x28 tetrahymena
1023	59	11.8	386	1	AMPM1 MOUSE	Q8bp48 mus musculus	1096	59	11.8	1764	1	Q22M94_TETTH	Q22m94 tetrahymena
1024	59	11.8	386	2	Q4VAA5 MOUSE	Q4vaa5 m methionyl	1097	59	11.8	1827	2	LTBP2 RAT	Q4q444 tryocr
1025	59	11.8	414	2	Q618N4 CAEBR	Q618n4 caenorhabdi	1098	59	11.8	2370	2	Q4UCQ4_TRYCR	Q4ucq4 trypanosoma
1026	59	11.8	419	2	Q92043 CROAT	Q92043 croatalus at	1099	59	11.8	2428	2	Q4UJ22_THEAN	Q4uj22 theileria a
1027	59	11.8	434	2	Q207F7_9APHY	Q207f7 scytinostro	1100	59	11.8	2549	2	Q816X6_BOOMI	Q816x6 boophilus m
1028	59	11.8	435	2	Q616G8 CAEBR	Q616g8 caenorhabdi	1101	59	11.8	2602	2	Q2L697_CIOIN	Q2l697 ciona intes
1029	59	11.8	454	2	Q7F8X9_ORYSA	Q7f8x9 oryza sativ	1102	59	11.8	2871	1	Q242T8_TETTH	Q242t8 tetrahymena
1030	59	11.8	459	1	PROC_PIG	Q9glp2 s vitamin k	1103	59	11.8	2872	2	PBN1 MOUSE	Q61554 mus musculus
1031	59	11.8	474	1	TNR1B MOUSE	P25119 mus musculus	1104	59	11.8	3843	2	Q9WUH8 RAT	Q9wuh8 rattus norv
1032	59	11.8	474	2	Q545P4 MOUSE	Q545p4 m adult mal	1105	59	11.8	3843	2	Q9U5D0_DROME	Q9u5d0 drosophila
1033	59	11.8	518	2	Q207G2_TRAVE	Q207g2 trametes ve	1106	59	11.8	3843	2	Q9VU94_DROME	Q9vu94 drosophila
1034	59	11.8	524	2	Q6QJD5_9APHY	Q6qjds cylindrobac	1107	59	11.8	4181	2	Q29IE2_DROPS	Q29ie2 drosophila
1035	59	11.8	548	2	Q207H0_TRELA	Q207h0 irpep lacte	1108	59	11.8	4349	1	FAT2 HUMAN	Q9nyq8 homo sapien
1036	59	11.8	550	2	Q4QAS0_LEIMA	Q4qae0 leishmania	1109	58.5	11.7	50	2	Q64DV8_9ARCH	Q64dv8 uncultured
1037	59	11.8	551	2	Q61MD2 CAEBR	Q61md2 caenorhabdi	1110	58.5	11.7	76	2	Q64AE9_9ARCH	Q64ae9 uncultured
1038	59	11.8	570	2	Q2UNP0 ASPOR	Q2unp0 aspergillus	1111	58.5	11.7	99	2	Q9D7P0_MOUSE	Q9d7p0 mus musculus
1039	59	11.8	573	2	Q5W9G8 HUMAN	Q5w9g8 homo sapien	1112	58.5	11.7	99	2	Q9D638_MOUSE	Q9d638 mus musculus
1040	59	11.8	576	2	Q4RG87_TETNG	Q4rg87 tetraodon n	1113	58.5	11.7	99	2	Q9CPW1_MOUSE	Q9cpw1 m adult mal
1041	59	11.8	579	2	Q5GYT3_XANOR	Q5gyt3 xanthomonas	1114	58.5	11.7	128	2	Q6ZWD3_HUMAN	Q6zwd3 homo sapien
1042	59	11.8	579	2	Q3BUC0_XANCS	Q3buc0 xanthomonas	1115	58.5	11.7	139	2	Q6UTY0_BOVIN	Q6uty0 bos taurus
1043	59	11.8	579	2	Q2P1T6_XANOM	Q2pit6 xanthomonas	1116	58.5	11.7	139	2	Q70PB6_9GEMI	Q70pb6 sida micran
1044	59	11.8	579	2	Q8P9L1_XANCP	Q8p9l1 xanthomonas	1117	58.5	11.7	181	2	Q399Z3_BURS3	Q399z3 burkholderi
1045	59	11.8	582	2	Q9L4D5_XANCA	Q9l4d5 xanthomonas	1118	58.5	11.7	200	2	Q5TUV6_ANOGA	Q5tuv6 anopheles g
1046	59	11.8	582	2	Q4UW77_XANC8	Q4uw77 xanthomonas	1119	58.5	11.7	214	2	Q58FV5_ARATH	Q58fv5 arabidopsis
1047	59	11.8	616	2	Q20852_CAEBL	Q20852 caenorhabdi	1120	58.5	11.7	214	2	Q84RKO_ARATH	Q84rko arabidopsis
1048	59	11.8	660	2	Q1KLA4_9AGAR	Q1klk4 lachnella v	1121	58.5	11.7	252	2	Q4ARR1_9ACTN	Q4arr1 rubrobacter
1049	59	11.8	674	2	Q873U0_PHLRA	Q873u0 phlebia rad	1122	58.5	11.7	254	2	Q4DN16_TYCR	Q4dn16 trypanosoma
1050	59	11.8	677	2	Q2ERY7_9HOMO	Q2ery7 botryobasid	1123	58.5	11.7	276	2	Q4PL95_ARATH	Q4pl95 arabidopsis
1051	59	11.8	690	2	Q1KLM3_FISTULINA	Q1klm3 fistulina a	1124	58.5	11.7	291	2	Q3B3V5_PELLO	Q3b3v5 petiodictyon
1052	59	11.8	701	2	Q27T05_9APHY	Q27t05 punctularia	1125	58.5	11.7	308	2	Q46370_BOVIN	Q46370 bos taurus
1053	59	11.8	704	2	Q5S3M7_9APHY	Q5s3m7 fomitopsis	1126	58.5	11.7	318	2	Q4A672_MYCS5	Q4a672 mycoplasma

1127	58.5	11.7	325	1	VT2 SPVKA	P25943 shope fibro	1200	58.5	11.7	3689	2	Q7PPF9 ANOGA	Q7ppf9 anopheles g
1128	58.5	11.7	325	2	Q77PB3_P9OXV	Q77pb3 rabbit fibr	1201	58.5	11.7	4391	1	PGBM_HUMAN	P98160 homo sapien
1129	58.5	11.7	328	2	Q8MQG3_XENLA	Q8mqg3 caenorhabdi	1202	58.5	11.7	4391	2	Q5VU27 HUMAN	Q5vu27 homo sapien
1130	58.5	11.7	358	2	Q18392_CAEEL	Q18392 caenorhabdi	1203	58.5	11.7	4981	2	Q2PZL6 MOUSE	Q2pzl6 mus musculus
1131	58.5	11.7	359	2	Q1JPB5_BOVIN	Q1jpb5 bos taurus	1204	58.5	11.7	5255	1	SSPO_CHICK	Q2pc93 gallus gall
1132	58.5	11.7	361	2	Q4V7M2_XENLA	Q4v7m2 xenopus lae	1205	58	11.6	46	1	ENAL_HORSE	P80930 equus caball
1133	58.5	11.7	375	2	Q4TCS2_TETNG	Q4tc52 tetraodon n	1206	58	11.6	98	2	Q2J8I9_FRASC	Q2j8i9 frankia sp.
1134	58.5	11.7	407	2	Q4WAJ6_ASPFU	Q4waj6 aspergillus	1207	58	11.6	116	2	Q1JVJ3_DESAC	Q1jvj3 desulfuromo
1135	58.5	11.7	429	2	Q8UZP9_GAMMA	Q8uzp9 cercopithec	1208	58	11.6	125	2	Q6ZT15_HUMAN	Q6zt15 homo sapien
1136	58.5	11.7	463	2	Q68QF3_LITFO	Q68qf3 lithobius f	1209	58	11.6	126	2	Q6F4F7_TRISC	Q6f4f7 triakis scy
1137	58.5	11.7	492	1	FSCN2_BOVIN	Q18728 bos taurus	1210	58	11.6	127	2	Q8T5W9_CAEER	Q8t5w9 caenorhabdi
1138	58.5	11.7	513	2	Q9VJW7_DROME	Q9vjw7 drosophila	1211	58	11.6	128	2	Q8T5X1_CAEER	Q8t5x1 caenorhabdi
1139	58.5	11.7	539	2	Q91VM8_MOUSE	Q91vm8 mus musculus	1212	58	11.6	129	2	Q8T5X4_CAEER	Q8t5x4 caenorhabdi
1140	58.5	11.7	554	2	Q3HBQ2_HUMAN	Q3hbq2 homo sapien	1213	58	11.6	168	2	Q2LZN5_DROPS	Q2lzn5 drosophila
1141	58.5	11.7	565	2	Q5RBP1_PONPY	Q5rbp1 pongo pygma	1214	58	11.6	170	2	Q12IH3_PSEAE	Q12ih3 pseudomonas
1142	58.5	11.7	575	2	Q729Y7_DESVH	Q729y7 desulfovibr	1215	58	11.6	187	2	Q1WNB2_9AGAR	Q1wnb2 coprinellus
1143	58.5	11.7	581	2	Q40Y44_KINRA	Q40y44 kineococcus	1216	58	11.6	190	2	Q93518_AGKHB	Q93518 agkistrodon
1144	58.5	11.7	583	2	Q6A008_MOUSE	Q6a008 mus musculus	1217	58	11.6	199	2	Q9H557_HUMAN	Q9h557 homo sapien
1145	58.5	11.7	591	2	Q5AKX6_CANAL	Q5akx6 candida alb	1218	58	11.6	210	2	Q8WSM7_PLACH	Q8wsm7 plasmodium
1146	58.5	11.7	654	2	Q4RYU0_TETNG	Q4ryu0 tetraodon n	1219	58	11.6	212	2	Q90Y44_AGKHP	Q90y44 agkistrodon
1147	58.5	11.7	671	2	Q6BET7_CABEL	Q6bet7 caenorhabdi	1220	58	11.6	227	2	Q1AVJ4_9ACTN	Q1avj4 rubrobacter
1148	58.5	11.7	675	2	Q4RYT9_TETNG	Q4ryt9 tetraodon n	1221	58	11.6	228	2	Q39X70_GROMG	Q39x70 geobacter m
1149	58.5	11.7	678	2	Q6NX58_HUMAN	Q6nx58 homo sapien	1222	58	11.6	229	2	Q4PN05_IXOSC	Q4pn05 ixodes scap
1150	58.5	11.7	684	2	Q9BIM7_TOXGO	Q9bim7 toxoplasma	1223	58	11.6	238	2	Q3V1G0_MOUSE	Q3v1g0 mus musculus
1151	58.5	11.7	701	1	TRFE_XENLA	P20233 xenopus lae	1224	58	11.6	275	2	Q7TGA5_EAV	Q7tga5 equine arte
1152	58.5	11.7	712	2	Q9VG15_DROME	Q9vg15 drosophila	1225	58	11.6	277	2	Q3IZR9_RHOS4	Q3izr9 rhodobacter
1153	58.5	11.7	712	2	Q8IGX5_DROME	Q8igx5 drosophila	1226	58	11.6	287	2	Q207F3_9HOMO	Q207f3 polyozellus
1154	58.5	11.7	721	2	Q3JGI0_BURP1	Q3jgi0 burkholderi	1227	58	11.6	288	2	Q9XYV5_TOXCA	Q9xyv5 toxocara ca
1155	58.5	11.7	721	2	Q91902_XENLA	Q91902 xenopus lae	1228	58	11.6	288	2	Q3HJX3_TRIER	Q3hjx3 trichodesmi
1156	58.5	11.7	731	2	Q47Z54_COLP3	Q47z54 colwellia p	1229	58	11.6	296	2	Q2QJDI_9CYAN	Q2qjdi symploca at
1157	58.5	11.7	739	2	Q177S7_AEDAE	Q177s7 aedes aegyp	1230	58	11.6	296	2	Q2QJC9_9CYAN	Q2qjc9 symploca at
1158	58.5	11.7	762	2	Q4V6V0_DROME	Q4v6v0 drosophila	1231	58	11.6	296	2	Q2QJDO_9CYAN	Q2qjdo symploca at
1159	58.5	11.7	764	2	Q21580_GLOIN	Q21580 gliomus intr	1232	58	11.6	299	2	Q7XBT0_ORYSA	Q7xbt0 oryza sativ
1160	58.5	11.7	787	1	ADA32_HUMAN	Q8tc27 homo sapien	1233	58	11.6	299	2	Q9FRP5_ORYSA	Q9frp5 oryza sativ
1161	58.5	11.7	787	2	Q22QJ7_TETTH	Q22qj7 tetrahymena	1234	58	11.6	305	2	Q7Z7Y8_9AGAR	Q7z7y8 malloctybe s
1162	58.5	11.7	799	2	Q175Q9_AEDAE	Q175q9 aedes aegyp	1235	58	11.6	305	2	Q6D150_BRARE	Q6d150 brachydanio
1163	58.5	11.7	813	2	Q9ULN3_HUMAN	Q9uln3 homo sapien	1236	58	11.6	310	2	Q207G0_9HOMO	Q207g0 hericium am
1164	58.5	11.7	841	2	Q3KQJ3_HUMAN	Q3kqj3 homo sapien	1237	58	11.6	318	2	Q90Z81_BRARE	Q90z81 brachydanio
1165	58.5	11.7	847	2	Q6R6C8_LISIV	Q6r6c8 listeria iv	1238	58	11.6	320	2	Q199T1_9AGAR	Q199t1 naucoria vi
1166	58.5	11.7	882	2	Q5EW24_TRITU	Q5ew24 triticum tu	1239	58	11.6	331	2	Q6R7N8_9AGAR	Q6r7n8 phaecocollyb
1167	58.5	11.7	894	2	Q17429_CABEL	Q17429 caenorhabdi	1240	58	11.6	331	2	Q207F1_9APHY	Q207f1 trechispora
1168	58.5	11.7	895	2	Q9LX29_ARATH	Q9lx29 arabidopsis	1241	58	11.6	332	2	Q7Z816_INOCYBE	Q7z816 inocybe gla
1169	58.5	11.7	898	2	Q8MQG2_CABEL	Q8mqg2 caenorhabdi	1242	58	11.6	334	2	Q7Z7Z7_9AGAR	Q7z7z7 inocybe que
1170	58.5	11.7	901	2	Q6AV10_ORYSA	Q6av10 oryza sativ	1243	58	11.6	334	2	Q7Z818_9AGAR	Q7z818 inocybe flo
1171	58.5	11.7	907	2	Q5EW20_WHEAT	Q5ew20 triticum ae	1244	58	11.6	334	2	Q7Z8E6_9AGAR	Q7z8e6 inocybe cal
1172	58.5	11.7	907	2	Q347C9_TRIMO	Q347c9 triticum mo	1245	58	11.6	334	2	Q1KLK3_9AGAR	Q1klk3 lacrymaria
1173	58.5	11.7	925	2	Q9U4E4_CABEL	Q9u4e4 caenorhabdi	1246	58	11.6	335	2	Q7Z826_9AGAR	Q7z826 inocybe cer
1174	58.5	11.7	925	2	Q44191_CABEL	Q44191 caenorhabdi	1247	58	11.6	336	2	Q207H4_9AGAR	Q207h4 tubaria con
1175	58.5	11.7	960	2	Q8MM07_CABEL	Q8mm07 caenorhabdi	1248	58	11.6	337	2	Q207H3_9HOMO	Q207h3 phallus had
1176	58.5	11.7	962	1	KR73_ICHV1	Q00094 ictalurid h	1249	58	11.6	339	2	Q2ERZ1_9HOMO	Q2erz1 boletellus
1177	58.5	11.7	974	2	Q6DI14_XENTR	Q6di14 xenopus tro	1250	58	11.6	342	2	Q68FN3_MOUSE	Q68fn3 mus musculus
1178	58.5	11.7	994	2	Q22QJ5_TETTH	Q22qj5 tetrahymena	1251	58	11.6	346	2	Q27S85_9AGAR	Q27s85 agrocyste pr
1179	58.5	11.7	1033	2	Q7QK34_ANOGA	Q7qk34 anopheles g	1252	58	11.6	347	2	Q1KM11_9AGAR	Q1km11 catathelasm
1180	58.5	11.7	1061	2	Q4T8L6_TETNG	Q4t8l6 tetraodon n	1253	58	11.6	347	2	Q1KM12_9AGAR	Q1km12 camarophyll
1181	58.5	11.7	1238	1	JAG2_HUMAN	Q9y219 homo sapien	1254	58	11.6	347	2	Q27S73_9AGAR	Q27s73 mycena gale
1182	58.5	11.7	1276	1	Q28XG9_DROPS	Q28xg9 drosophila	1255	58	11.6	347	2	Q207H7_9AGAR	Q207h7 myctomyce
1183	58.5	11.7	1592	1	SORL_CHICK	Q98930 g sortilin-	1256	58	11.6	347	2	Q1KLA3_9AGAR	Q1kla3 plicaturops
1184	58.5	11.7	1712	1	LTBP1_RAT	Q00918 rattus norv	1257	58	11.6	348	2	Q1KM13_9AGAR	Q1km13 camarophyll
1185	58.5	11.7	2019	2	Q68FEO_MOUSE	Q68feo mus musculus	1258	58	11.6	348	2	Q1KM06_9AGAR	Q1km06 cortinarius
1186	58.5	11.7	2146	1	CRB_DROME	P10040 drosophila	1259	58	11.6	348	2	Q1KLL9_9AGAR	Q1kl19 gymnopus dr
1187	58.5	11.7	2146	1	Q4T7A2_TETNG	Q4t7a2 tetraodon n	1260	58	11.6	348	2	Q1KLL8_9AGAR	Q1kl18 hebeloma ve
1188	58.5	11.7	2189	2	Q9BI05_EIMTE	Q9bi05 elmeria ten	1261	58	11.6	348	2	Q27S76_9AGAR	Q27s76 lepieta iri
1189	58.5	11.7	2414	2	Q6DFL6_XENLA	Q6dfl6 xenopus lae	1262	58	11.6	348	2	Q19LA5_9HOMO	Q19la5 tulasnella
1190	58.5	11.7	2427	2	Q8MQ36_CABEL	Q8mq36 caenorhabdi	1263	58	11.6	349	2	Q1KLA1_9AGAR	Q1kla1 pseudoarml
1191	58.5	11.7	2764	2	Q9WTB5_MOUSE	Q9wtb5 mus musculus	1264	58	11.6	349	2	Q1KIK9_9AGAR	Q1kik9 infundibuli
1192	58.5	11.7	2764	2	Q5NBW8_MOUSE	Q5nbw8 mus musculus	1265	58	11.6	349	2	Q1KLM2_9AGAR	Q1klm2 flammula al
1193	58.5	11.7	2774	2	Q4Z799_PLABE	Q4z799 plasmodium	1266	58	11.6	349	2	Q1HHT9_9AGAR	Q1hht9 simocybe se
1194	58.5	11.7	3004	2	Q24550_DROME	Q24550 drosophila	1267	58	11.6	349	2	Q1KLA2_9AGAR	Q1kla2 plicaturops
1195	58.5	11.7	3004	2	Q3VYN8_DROME	Q3vyn8 drosophila	1268	58	11.6	350	2	Q1KM09_9AGAR	Q1km09 chrysomphal
1196	58.5	11.7	3019	2	Q4RU98_TETNG	Q4ru98 tetraodon n	1269	58	11.6	350	2	Q1KLL4_9AGAR	Q1kl14 hydrotus ma
1197	58.5	11.7	3087	2	Q8WRD2_PLABE	Q8wrd2 plasmodium	1270	58	11.6	350	2	Q1KM08_CLINE	Q1km08 cliticocye n
1198	58.5	11.7	3138	2	Q17L45_AEDAE	Q17l45 aedes aegyp	1271	58	11.6	350	2	Q1KLB0_9AGAR	Q1klb0 marasmus r
1199	58.5	11.7	3222	2	Q6V0I7_HUMAN	Q6v0i7 homo sapien	1272	58	11.6	351	2	Q1KLA8_9AGAR	Q1kla8 mycena aff.

1273	58	11.6	351	2	Q1KLA4_9AGAR	Q1kla4 pleuroflamm	1346	58	11.6	694	2	Q5TWT0_ANOGA	Q5twt0 anopheles g
1274	58	11.6	352	2	Q1HHT8_9AGAR	Q1hht8 stropharia	1347	58	11.6	696	2	Q1KLL0_9AGAR	Q1kll0 camarophyll
1275	58	11.6	352	2	Q27T06_9HOMO	Q27t06 utrobasisid	1348	58	11.6	698	2	Q5US90_9APHY	Q5us90 athelia bom
1276	58	11.6	353	2	Q1KLA9_9AGAR	Q1kla9 melanoleuca	1349	58	11.6	699	2	Q5U7W9_COPCM	Q5u7w9 coprinus co
1277	58	11.6	353	2	Q207H5_9AGAR	Q207h5 tricholomop	1350	58	11.6	700	2	Q5S2C1_9AGAR	Q5s2c1 collybia tu
1278	58	11.6	354	2	Q1KLA6_9AGAR	Q1kla6 mycena aura	1351	58	11.6	701	2	Q1KLL6_9AGAR	Q1kll6 hygrophorus
1279	58	11.6	354	2	Q1KLM5_9HOMO	Q1klm5 cyathus str	1352	58	11.6	705	2	Q5S3M3_9AGAR	Q5s3m3 marasmius a
1280	58	11.6	357	2	Q2HMX2_9AGAR	Q2hmx2 asterophora	1353	58	11.6	711	2	Q2ERY9_9HOMO	Q2ery9 conioophora
1281	58	11.6	357	2	Q2HXY7_9AGAR	Q2hxy7 tricholoma	1354	58	11.6	716	2	Q207F5_9HETE	Q207f5 tremelloiden
1282	58	11.6	358	2	Q2HXY9_9AGAR	Q2hxy9 lyophyllum	1355	58	11.6	721	2	Q5S2C0_9AGAR	Q5s2c0 rhodocollyb
1283	58	11.6	358	2	Q2HXZ0_9AGAR	Q2hxz0 lyophyllum	1356	58	11.6	728	1	Q5S2C0_9AGAR	Q5s2c0 rhodocollyb
1284	58	11.6	358	2	Q2HXZ1_9AGAR	Q2hxz1 calocybe ca	1357	58	11.6	728	1	Q5S2C0_9AGAR	Q5s2c0 rhodocollyb
1285	58	11.6	361	2	Q207F2_9APHY	Q207f2 trechispora	1358	58	11.6	741	2	Q2FNS9_METHU	Q2fns9 methanospir
1286	58	11.6	367	2	Q4RUJ5_TETNG	Q4ruj5 tetraodon n	1359	58	11.6	744	2	Q4DJ56_TRYCR	Q4dj56 trypanosoma
1287	58	11.6	370	2	Q207F9_9AGAR	Q207f9 lactarius l	1360	58	11.6	750	2	Q4RTV7_TETNG	Q4rtv7 tetraodon n
1288	58	11.6	373	2	Q1L686_BRARE	Q1l686 brachydania	1361	58	11.6	754	2	Q5TNY8_ANOGA	Q5tny8 anopheles g
1289	58	11.6	398	2	Q2C1Q0_9GAMM	Q2c1q0 photobacter	1362	58	11.6	755	1	COMP_RAT	P35444 rattus norv
1290	58	11.6	413	2	Q2SX94_MYCVN	Q2sx94 mycobacteri	1363	58	11.6	770	2	Q873V7_9AGAR	Q873v7 chondroster
1291	58	11.6	413	2	Q90ZE3_BRARE	Q90ze3 brachydania	1364	58	11.6	801	2	Q4D260_TRYCR	Q4d260 trypanosoma
1292	58	11.6	415	2	Q6NP02_DROME	Q6np02 brachydania	1365	58	11.6	820	2	Q9FFX8_ARATH	Q9ffx8 arabidopsis
1293	58	11.6	418	2	Q39ZC0_GEOMG	Q39zc0 geobacter m	1366	58	11.6	848	2	Q873T2_9AGAR	Q873t2 henningsomy
1294	58	11.6	422	2	Q1KLA0_9AGAR	Q1kla0 rhodocycbe m	1367	58	11.6	849	2	Q873U3_9HOMO	Q873u3 lycoperdon
1295	58	11.6	432	2	Q9NPM2_HUMAN	Q9npm2 homo sapien	1368	58	11.6	863	2	Q5S3M4_9HOMO	Q5s3m4 hygrophorop
1296	58	11.6	448	2	Q8PJ71_XANAC	Q8pj71 xanthomonas	1369	58	11.6	869	2	Q6NS01_XENLA	Q6ns01 xenopus lae
1297	58	11.6	461	2	Q3BRR0_XANCS	Q3br00 xanthomonas	1370	58	11.6	878	2	Q42126_XENLA	Q42126 xenopus lae
1298	58	11.6	465	2	Q2KGU4_MAGGR	Q2kgu4 magnaporthe	1371	58	11.6	880	2	Q6QJD4_9APHY	Q6qjd4 cortinariu
1299	58	11.6	479	2	Q6MGL5_BDEBA	Q6mgl5 bdellovibri	1372	58	11.6	882	2	Q27T04_9APHY	Q27t04 vullennia
1300	58	11.6	491	2	Q2K017_RHIEC	Q2k017 rhizobium e	1373	58	11.6	884	2	Q27S75_9AGAR	Q27s75 macrolepiot
1301	58	11.6	504	2	Q7QJ41_ANOGA	Q7qj41 anopheles g	1374	58	11.6	884	2	Q5U7W5_ARMME	Q5u7w5 armillaria
1302	58	11.6	515	2	Q6QF59_HETAN	Q6qf59 heterobasid	1375	58	11.6	889	2	Q5S3M2_9APHY	Q5s3m2 phyllocoopi
1303	58	11.6	525	2	Q24433_ARATH	Q24433 arabidopsis	1376	58	11.6	891	2	Q9SHG9_ARATH	Q9shg9 arabidopsis
1304	58	11.6	551	2	Q09967_CABEL	Q09967 caenorhabdi	1377	58	11.6	892	2	Q5EGJ2_9HOMO	Q5egj2 cotyldia s
1305	58	11.6	569	2	Q7PMP9_ANOGA	Q7pmp9 anopheles g	1378	58	11.6	898	2	Q5RM00_9HOMO	Q5rm00 fomitiporia
1306	58	11.6	576	2	Q9Y3V7_HUMAN	Q9y3v7 homo sapien	1379	58	11.6	898	2	Q5UPZ4_HUMAN	Q5upz4 macaca fusc
1307	58	11.6	578	2	Q8PLD7_XANAC	Q8pld7 xanthomonas	1380	58	11.6	899	2	Q5S2C2_9HOMO	Q5s2c2 boletellus
1308	58	11.6	600	2	Q207F4_9HOMO	Q207f4 hydrellum g	1381	58	11.6	908	2	Q5S3L8_9HOMO	Q5s3l8 strobilomyc
1309	58	11.6	608	2	Q4P9C1_USTWA	Q4p9c1 ustilago ma	1382	58	11.6	913	2	Q8AY18_RANES	Q8ay18 rana escul
1310	58	11.6	608	2	Q627A0_CAEBR	Q627a0 caenorhabdi	1383	58	11.6	917	2	Q9UVA3_AGABI	Q9uva3 agaricus bi
1311	58	11.6	628	2	Q9VER6_DROME	Q9ver6 drosophila	1384	58	11.6	917	2	Q6RY19_AMPAP	Q6ry19 amanita pha
1312	58	11.6	629	2	Q1KM07_9AGAR	Q1km07 conocybe la	1385	58	11.6	949	2	Q3V7A7_9PRIM	Q3v7a7 macaca fusc
1313	58	11.6	639	2	Q5RLZ7_9AGAR	Q5rlz7 malloccybe d	1386	58	11.6	980	1	TSP4_RAT	P49744 rattus norv
1314	58	11.6	640	2	Q1N0R4_9GAMM	Q1n0r4 oceanobacte	1387	58	11.6	1015	2	Q3UGT7_MOUSE	Q3ugt7 mus musculu
1315	58	11.6	641	2	Q1KLM4_9AGAR	Q1klm4 agrocycbe er	1388	58	11.6	1026	2	Q8SWY0_DROME	Q8swy0 drosophila
1316	58	11.6	645	2	Q5S3M1_FLEOS	Q5s3m1 pleurotus o	1389	58	11.6	1121	2	Q966P9_CAEL	Q966p9 caenorhabdi
1317	58	11.6	646	2	Q5S3M0_9AGAR	Q5s3m0 pleuteus rom	1390	58	11.6	1123	2	Q6V7X2_OROMI	Q6v7x2 orobanche m
1318	58	11.6	654	2	Q5U7W6_9AGAR	Q5u7w6 ampollocit	1391	58	11.6	1123	2	Q966Q0_CABEL	Q966q0 caenorhabdi
1319	58	11.6	655	2	Q1KLL3_9AGAR	Q1kll3 hygrocycbe c	1392	58	11.6	1148	1	Q5S2C2_HUMAN	Q5s2c2 caenorhabdi
1320	58	11.6	656	2	Q27T09_9HOMO	Q27t09 tulaanella	1393	58	11.6	1184	2	Q86V58_HUMAN	Q86v58 homo sapien
1321	58	11.6	657	2	Q207H2_9AGAR	Q207h2 rickenella	1394	58	11.6	1200	2	Q8VD07_MOUSE	Q8vd07 mus musculu
1322	58	11.6	667	2	Q27S81_9AGAR	Q27s81 clavulinops	1395	58	11.6	1217	1	EGF_MOUSE	P01132 mus musculu
1323	58	11.6	669	2	Q1KLK6_9AGAR	Q1klk6 kuehneromyc	1396	58	11.6	1217	2	Q569W5_MOUSE	Q569w5 mus musculu
1324	58	11.6	669	2	Q5S3L6_9AGAR	Q5s3l6 oudemansiel	1397	58	11.6	1231	2	Q8UIU0_HUMAN	Q8uiu0 homo sapien
1325	58	11.6	670	2	Q1KLL2_9AGAR	Q1kll2 hygrocycbe m	1398	58	11.6	1231	2	Q8UIU1_HUMAN	Q8uiu1 homo sapien
1326	58	11.6	670	2	Q27T08_9HOMO	Q27t08 tulaanella	1399	58	11.6	1241	2	Q1WMR3_9AGAR	Q1wmr3 coprinellus
1327	58	11.6	671	2	Q5S2B9_9APHY	Q5s2b9 hyphoderma	1400	58	11.6	1249	1	APAF_RAT	Q9epv5 rattus norv
1328	58	11.6	675	2	Q27S82_9AGAR	Q27s82 cantharocycb	1401	58	11.6	1275	2	Q61PE4_CAEBR	Q61pe4 caenorhabdi
1329	58	11.6	676	2	Q27T07_9HOMO	Q27t07 tulaanella	1402	58	11.6	1296	2	Q6AWM6_DROME	Q6awm6 drosophila
1330	58	11.6	677	2	Q5S3L9_9APHY	Q5s3l9 ramaria rub	1403	58	11.6	1311	2	Q4RUS3_TETNG	Q4rus3 tetraodon n
1331	58	11.6	685	2	Q1KLM1_9AGAR	Q1klm1 gloiocephal	1404	58	11.6	1420	2	Q4SYJ8_SCHMD	Q4syj8 schmidtea m
1332	58	11.6	686	2	Q5RM01_9AGAR	Q5rm01 hygrocycbe c	1405	58	11.6	1428	2	Q44341_HALRU	Q44341 haliotis ru
1333	58	11.6	687	2	Q1PB62_9AGAR	Q1pb62 hydropus cf	1406	58	11.6	1440	2	Q2HAU6_CHAGB	Q2haue chaetomium
1334	58	11.6	687	2	Q7Z8B0_9AGAR	Q7z8b0 phaeomarasam	1407	58	11.6	1469	2	Q6PD04_MOUSE	Q6pd04 mus musculu
1335	58	11.6	688	2	Q27S77_9AGAR	Q27s77 incocybe coo	1408	58	11.6	1477	2	Q4H3A4_CLOIN	Q4h3a4 ciona intes
1336	58	11.6	688	2	Q1KLL5_9APHY	Q1kll5 hydnoopolyc	1409	58	11.6	1483	2	Q4CNR3_TRYCR	Q4cnr3 trypanosoma
1337	58	11.6	689	2	Q1KML7_9AGAR	Q1klm7 hemimycena	1410	58	11.6	1517	2	Q6KAS1_MOUSE	Q6kas1 mus musculu
1338	58	11.6	690	2	Q1KML4_9AGAR	Q1klm4 basoipora m	1411	58	11.6	1517	2	Q3UPH7_MOUSE	Q3uph7 mus musculu
1339	58	11.6	690	2	Q1KML0_9AGAR	Q1klm0 cheimomophy	1412	58	11.6	1673	2	Q4RSP7_TETNG	Q4rsp7 tetraodon n
1340	58	11.6	691	2	Q1KLL1_9AGAR	Q1kll1 hygrophorus	1413	58	11.6	1686	2	Q6P7J9_HUMAN	Q6p7j9 homo sapien
1341	58	11.6	691	2	Q5S3M8_FLAVE	Q5s3m8 flammulina	1414	58	11.6	1790	1	LAMB1_DROME	P11046 drosophila
1342	58	11.6	693	2	Q1KLM0_9AGAR	Q1klm0 gymnocypus co	1415	58	11.6	1805	2	Q7QVW0_GIALA	Q7qvwo platydia lam
1343	58	11.6	693	2	Q5U7W1_9AGAR	Q5u7w1 clitocybe s	1416	58	11.6	2030	2	Q2WBY6_PLADU	Q2wby6 platynoreis
1344	58	11.6	694	2	Q5U7W7_9AGAR	Q5u7w7 amanita bru	1417	58	11.6	2061	2	Q4SRM9_TETNG	Q4srm9 tetraodon n
1345	58	11.6	694	2	Q5U7W3_9AGAR	Q5u7w3 clavaria zo	1418	58	11.6	2183	2	Q2GN01_CHAGB	Q2gn01 chaetomium

1419	58	11.6	2192	2	Q804R1_BRARE	Q804r1 brachydanio	1492	57.5	11.5	594	1	CHDH_HUMAN	Q8ne62 homo sapien
1420	58	11.6	2225	2	Q571J3_MOUSE	Q571j3 mus musculus	1493	57.5	11.5	601	2	Q656X3_ORISA	Q656x3 oryza sativ
1421	58	11.6	2277	2	Q4CRM2_TRYCR	Q4crm2 trypanosoma	1494	57.5	11.5	604	1	ENR1_HUMAN	Q14264 h herv-r-7q
1422	58	11.6	2506	2	Q9WJD2_VIRU	Q9wj22 venezuelan	1495	57.5	11.5	604	2	Q4W2L3_PANTR	Q4w2l3 pan troglod
1423	58	11.6	2516	2	Q7TQ52_MOUSE	Q7tq52 mus musculus	1496	57.5	11.5	625	2	Q2QS63_ORISA	Q2qs63 oryza sativ
1424	58	11.6	2526	2	Q7TQ51_MOUSE	Q7tq51 mus musculus	1497	57.5	11.5	625	2	Q8MPM6_GIALA	Q8mpm6 giardia lam
1425	58	11.6	2531	1	NOTC1_MOUSE	Q1705 mus musculus	1498	57.5	11.5	644	2	Q5NKM3_CRYNV	Q5nkm3 cryptococcu
1426	58	11.6	2531	2	Q8K428_MOUSE	Q8k428 mus musculus	1499	57.5	11.5	667	2	Q7RVRO_NEUCR	Q7rvro neurospora
1427	58	11.6	2531	2	Q7TQ50_MOUSE	Q7tq50 mus musculus	1500	57.5	11.5	680	2	Q9QW15_9MURI	Q9qw15 mus sp. bet
1428	58	11.6	2660	2	Q7QL19_ANOGA	Q7ql19 anopheles g							
1429	58	11.6	2812	1	ZAN_HUMAN	Q9v493 homo sapien							
1430	58	11.6	2824	2	Q9W7R3_BRARE	Q9w7r3 brachydanio							
1431	58	11.6	2906	2	Q9WUH9_RAT	Q9wuh9 rattus norv							
1432	58	11.6	2907	1	FEN2_MOUSE	Q61555 mus musculus							
1433	58	11.6	3301	1	CELK3_MOUSE	Q91z10 mus musculus							
1434	58	11.6	3452	2	Q4D8D4_TRYCR	Q4d8d4 trypanosoma							
1435	58	11.6	4056	2	Q2PDM3_DROME	Q2pdm3 drosophila							
1436	58	11.6	4542	2	Q23UF9_TETTH	Q23uf9 tetrahymena							
1437	58	11.6	4573	2	Q5TWP0_ANOGA	Q5tmp0 anopheles g							
1438	58	11.6	4856	2	Q7P2B3_ANOGA	Q7p2b3 anopheles g							
1439	58	11.6	4856	2	Q61EU2_CAEBR	Q61ej2 caenorhabdi							
1440	57.5	11.5	68	1	TF17_HADVE	P81803 hadronyche							
1441	57.5	11.5	98	1	KRA32_HUMAN	Q9byr7 homo sapien							
1442	57.5	11.5	98	2	Q24JK5_BOVIN	Q24jx9 bos taurus							
1443	57.5	11.5	101	2	Q9XG33_GERHY	Q9xgj3 gerbera hyb							
1444	57.5	11.5	110	1	ICE2B_HUMAN	Q14633 homo sapien							
1445	57.5	11.5	110	2	Q5TA80_HUMAN	Q5ta80 homo sapien							
1446	57.5	11.5	114	2	Q4XQB6_PLACH	Q4xqb6 plasmodium							
1447	57.5	11.5	116	2	Q1JSV3_TOXGO	Q1jsv3 toxoplasma							
1448	57.5	11.5	123	2	Q83078_9VIRU	Q83078 lychnis rin							
1449	57.5	11.5	132	2	Q4RD47_TETNG	Q4rd47 tetraodon n							
1450	57.5	11.5	139	2	Q61101_DROME	Q61101 drosophila							
1451	57.5	11.5	157	2	Q5ISQ5_MACFA	Q5isq5 macaca fasc							
1452	57.5	11.5	170	2	Q52VK0_CIOIN	Q52vk0 ciona intes							
1453	57.5	11.5	176	2	Q59K89_CANAL	Q59k89 candida alb							
1454	57.5	11.5	176	2	Q4ZNP7_PSEU2	Q4znf7 pseudomonas							
1455	57.5	11.5	205	2	Q96LP4_HUMAN	Q96lp4 homo sapien							
1456	57.5	11.5	217	2	Q8NEE7_HUMAN	Q8nee7 homo sapien							
1457	57.5	11.5	222	2	Q7X247_GRIJA	Q7x247 griffithia							
1458	57.5	11.5	226	2	Q8BYT9_MOUSE	Q8byt9 mus musculus							
1459	57.5	11.5	237	1	ULT1_ARATH	Q8gza8 arabidopsis							
1460	57.5	11.5	257	2	Q6NW92_BRARE	Q6nw92 brachydanio							
1461	57.5	11.5	269	2	Q6ALJ36_DESPS	Q6al36 desulfotale							
1462	57.5	11.5	275	2	Q7M9D7_WOLSU	Q7m9d7 wolinnella s							
1463	57.5	11.5	292	2	Q29S19_BOVIN	Q29s19 bos taurus							
1464	57.5	11.5	298	2	Q4CR12_TRYCN	Q4cr12 trypanosoma							
1465	57.5	11.5	298	2	Q5P1X1_AZOSE	Q5plx1 azoarcus sp							
1466	57.5	11.5	300	2	Q4RKB9_TETNG	Q4rkb9 tetraodon n							
1467	57.5	11.5	308	2	Q5YUP0_NOCFA	Q5yup0 nocardia fa							
1468	57.5	11.5	319	2	Q9V6U6_DROME	Q9v6u6 drosophila							
1469	57.5	11.5	322	2	Q72761_COWPX	Q72761 cowpox viru							
1470	57.5	11.5	367	2	Q9ZVY4_ARATH	Q9zv4 arabidopsis							
1471	57.5	11.5	368	2	Q3NBU8_9PROT	Q3nb8 nitrosomona							
1472	57.5	11.5	368	2	Q1LDY0_RALME	Q1ldy0 ralstonia m							
1473	57.5	11.5	368	2	Q46U28_RALEJ	Q46u28 ralstonia e							
1474	57.5	11.5	371	2	Q5Z0J9_NOCFA	Q5z0j9 nocardia fa							
1475	57.5	11.5	373	2	Q4UEJ5_THEAN	Q4uej5 theileria a							
1476	57.5	11.5	383	2	Q6XYN4_CRYNV	Q6xyn4 cryptococcu							
1477	57.5	11.5	434	2	Q5HRJ3_STAEO	Q5hrj3 staphylococ							
1478	57.5	11.5	434	2	Q8CTS4_STAES	Q8cts4 staphylococ							
1479	57.5	11.5	450	2	Q869J7_9MYRI	Q869j7 glomeris ma							
1480	57.5	11.5	458	2	Q8ZVP8_SALTI	Q8zvp8 salmonella							
1481	57.5	11.5	472	2	Q68ST7_9AGAR	Q68st7 pleurotus d							
1482	57.5	11.5	492	1	FSCN2_HUMAN	Q14926 homo sapien							
1483	57.5	11.5	499	2	Q3H189_9ACTO	Q3h189 nocardioid							
1484	57.5	11.5	507	2	Q56BV3_9CAUD	Q56bv3 enterobacte							
1485	57.5	11.5	508	2	Q6DHG1_BRARE	Q6dhl1 brachydanio							
1486	57.5	11.5	527	2	Q4SRF3_TETNG	Q4srf3 tetraodon n							
1487	57.5	11.5	542	2	Q80T13_MOUSE	Q80t13 mus musculus							
1488	57.5	11.5	544	2	Q8VCG2_MOUSE	Q8vcg2 mus musculus							
1489	57.5	11.5	581	2	Q8NAV8_HUMAN	Q8nav8 homo sapien							
1490	57.5	11.5	586	2	Q4RJE7_TETNG	Q4rje7 tetraodon n							
1491	57.5	11.5	591	2	Q6LBN5_HUMAN	Q6lbn5 homo sapien							

ALIGNMENTS

RESULT 1

ID	PROK1_HUMAN	STANDARD;	PRT;	105 AA.
AC	P58294;			
DT	26-SEP-2001,	integrated into UniProtKB/Swiss-Prot.		
DT	26-SEP-2001,	sequence version 1.		
DT	13-JUN-2006,	entry version 37.		
DE	Prokineticin-1 precursor [Endocrine-gland-derived vascular endothelial growth factor] (EG-VEGF) (Mambakine).			
DE	Name=PROK1; ORFNames=UNQ600/PRO1186;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;			
OC	Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE [MRNA].			
RX	MEDLINE=21419730; PubMed=11259612;			
RA	Li M., Bullock C.M., Knauer D.J., Ehler F.J., Zhou Q.-Y.;			
RT	"Identification of two prokineticin cDNAs: recombinant proteins			
RT	potentially contract gastrointestinal smooth muscle.";			
RL	Mol. Pharmacol. 59:692-698 (2001).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE [MRNA].			
RX	MEDLINE=21419730; PubMed=11259612; DOI=10.1038/35091000;			
RA	LeCouter J., Kowalski J., Foster J., Haas P., Zhang Z.,			
RA	Dillard-Teim L., Frantz G., Rangel L., DeGuzman L., Keller G.-A.,			
RA	Peale F., Gurney A., Hillan K.J., Ferrara N.;			
RT	"Identification of an angiogenic mitogen selective for endocrine gland			
RT	endothelium.";			
RL	Nature 412:877-884 (2001).			
RN	[3]			
RP	NUCLEOTIDE SEQUENCE [MRNA].			
RA	Fraser C.;			
RT	"Mambakine, a snake venom related endocrine hormone that controls			
RT	macrophages.";			
RL	Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].			
RX	MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;			
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,			
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,			
RA	Eaton D., Foster J.S., Grimaldi C., Gu Q., Haas P.E., Heldens S.,			
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,			
RA	Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,			
RA	Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,			
RA	Randlen R.L., Watanabe C., Wiedand D., Woods K., Xie M.-H.,			
RA	Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,			
RA	Wood W.I., Godowski P.J., Gray A.M.;			
RT	"The secreted protein discovery initiative (SPDI), a large-scale			
RT	effort to identify novel human secreted and transmembrane proteins: a			
RT	bioinformatics assessment.";			
RL	Genome Res. 13:2265-2270 (2003).			
RN	[5]			
RP	PROTEIN SEQUENCE OF 20-34.			
RX	PubMed=15340161; DOI=10.1110/ps.04682504;			
RA	Zhang Z., Henzel W.J.;			
RT	"Signal peptide prediction based on analysis of experimentally			
RT	verified cleavage sites.";			

RN NUCLEOTIDE SEQUENCE.
 RP TISSUE=Testis;
 RG NIH MGC Project;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
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 CC -----
 DR EMBL; BC025399; AAH25399.1; -; mRNA.
 DR HSSP; P25687; LIMT.
 DR Ensembl; ENSG00000143125; Homo sapiens.
 DR RZPD-ProtExp; IOH11285; -;
 DR RZPD-ProtExp; RZPD0839A10127; -;
 DR RZPD-ProtExp; RZPD0839A10128; -;
 DR RZPD-ProtExp; W1161; -;
 DR RZPD-ProtExp; IPR009523; Prokineticin.
 DR PANTHER; PTHR18821; Prokineticin; 1.
 DR Pfam; PF06607; Prokineticin; 1.
 SQ SEQUENCE 105 AA; 11729 MW; E570FDE30EFB52D2 CRC64;

 Query Match 99.8%; Score 497; DB 2; Length 105;
 Best Local Similarity 98.8%; Pred. No. 3.6e-47;
 Matches 85; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 QY 1 AVITGACERDVOCAGTCCCAISLWLRLGRLMCTPLGREGECHPGSHKVPFRKRKHHTCP 60
 DB 20 AVITGACERDVOCAGTCCCAISLWLRLGRLMCTPLGREGECHPGSHKVPFRKRKHHTCP 79

 QY 61 CLPNLLCSRFPDGRYRCSDLNKINF 86
 DB 80 CLPNLLCSRFPDGRYRCSDLNKINF 105

 RESULT 4
 PROK1_RAT STANDARD; PRT; 105 AA.
 ID Q8K414;
 AC Q8K414;
 DT 19-JUL-2003, integrated into UniProtKB/Swiss-Prot.
 DT 01-JUN-2002, sequence version 1.
 DT 18-APR-2006, entry version 25.
 DE Prokineticin-1 precursor (Endocrine-gland-derived vascular endothelial growth factor) (EG-VEGF).
 GN Name=Proki;
 OS Rattus norvegicus [Rat].
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=22050031; PubMed=12054613; DOI=10.1016/S0006-291X(02)00239-5;
 RA Masuda Y., Takatsu Y., Terao Y., Kumano S., Ishibashi Y., Suenaga M., Abe M., Fukusumi S., Watanabe T., Shintani Y., Yamada T., Hinuma S., Inatomi N., Ohtaki T., Onda H., Fujino M.;
 RT "Isolation and identification of EG-VEGF/prokineticins as cognate ligands for two orphan G-protein-coupled receptors.";
 RL Biochem. Biophys. Res. Commun. 293:396-402(2002).
 CC -1- FUNCTION: Potently contract gastrointestinal (GI) smooth muscle. Induces proliferation, migration and fenestration (the formation of membrane discontinuities) in capillary endothelial cells derived from endocrine glands. Has little or no effect on a variety of other endothelial and non-endothelial cell types (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted protein (By similarity).
 CC -1- SIMILARITY: Belongs to the prokinectin family.
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 CC -----
 DR EMBL; AY089983; AA09104.1; -; mRNA.
 DR UniGene; Rn.82757; -.

DR HSSP; P25687; LIMT.
 DR Ensembl; ENSRNOG0000018201; Rattus norvegicus.
 DR RGD; 620898; Proki.
 DR GO; GO:0008283; P:cell proliferation; TAS.
 DR GO; GO:0045765; P:regulation of angiogenesis; NAS.
 DR InterPro; IPR009523; Prokineticin.
 DR PANTHER; PTHR18821; Prokineticin; 1.
 DR Pfam; PF06607; Prokineticin; 1.
 DR Growth factor; Mitogen; Signal.
 FT SIGNAL 1 19 Potential.
 FT CHAIN 20 105 Prokineticin-1.
 FT /FTID=PRO_0000025808.
 FT DISULFID 26 38 By similarity.
 FT DISULFID 32 50 By similarity.
 FT DISULFID 37 78 By similarity.
 FT DISULFID 60 86 By similarity.
 FT DISULFID 80 96 By similarity.
 SQ SEQUENCE 105 AA; 11643 MW; 8DF0C42122B1C5B6 CRC64;

 Query Match 95.0%; Score 473; DB 1; Length 105;
 Best Local Similarity 91.9%; Pred. No. 1.7e-44;
 Matches 79; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

 QY 1 AVITGACERDVOCAGTCCCAISLWLRLGRLMCTPLGREGECHPGSHKVPFRKRKHHTCP 60
 DB 20 AVITGACERDVOCAGTCCCAISLWLRLGRLMCTPLGREGECHPGSHKVPFRKRKHHTCP 79

 QY 61 CLPNLLCSRFPDGRYRCSDLNKINF 86
 DB 80 CSPSLLCSRFPDGRYRCSDLNKINF 105

 RESULT 5
 Q8K457_MOUSE PRELIMINARY; PRT; 81 AA.
 ID Q8K457_MOUSE
 AC Q8K457_MOUSE
 DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
 DT 01-OCT-2002, sequence version 1.
 DT 07-FEB-2006, entry version 12.
 DE Prokineticin 1 (Fragment).
 GN Name=Proki; Synonym=PK1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6;
 RX MEDLINE=22022134; PubMed=12024206; DOI=10.1038/417405a;
 RA Cheng M.Y., Bullock C.M., Li C., Lee A.G., Bermak J.C., Belluzzi J., Weaver D.R., Leslie F.M., Zhou Q.-Y.;
 RA "Prokineticin 2 transmits the behavioural circadian rhythm of the suprachiasmatic nucleus.";
 RL Nature 417:405-410(2002).
 CC -----
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 CC -----
 DR EMBL; AF487281; AA049573.1; -; mRNA.
 DR HSSP; P25687; LIMT.
 DR Ensembl; ENSMUSG00000046213; Mus musculus.
 DR MGI; MGI:2180370; Proki.
 DR GO; GO:0005576; C:extracellular region; IDA.
 DR GO; GO:0000187; P:activation of MAPK activity; IDA.
 DR GO; GO:0007623; P:circadian rhythm; TAS.
 DR GO; GO:0008284; P:positive regulation of cell proliferation; IDA.
 DR GO; GO:0045765; P:regulation of angiogenesis; IDA.
 DR InterPro; IPR009523; Prokineticin.
 DR PANTHER; PTHR18821; Prokineticin; 1.
 DR Pfam; PF06607; Prokineticin; 1.
 FT NON TER 1 1
 SQ SEQUENCE 81 AA; 9192 MW; 7BBE3EC6B16A8011 CRC64;

Query Match 86.7%; Score 432; DB 2; Length 81;
 Best Local Similarity 87.7%; Pred. No. 4.5e-40;
 Matches 71; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 6 ACERDVQCGAGTCCALSLWRLGLRMCTPLGREGECHPGSHKVPFFFRKRKHTTCCPLPNL 65
 DB 1 ACERDVQCGAGTCCALSLWRLGLRMCTPLGREGECHPGSHKVPFFFRKRKHTTCCPLPNL 60

QY 66 LCSPFPDGRYRCSDMLKNINF 86
 DB 61 LCSPFPDGRYRCSDMLKNINF 81

RESULT 6
 Q32FI2_BOVIN
 ID Q32FI2_BOVIN PRELIMINARY; PRT; 81 AA.
 AC Q32FI2_BOVIN PRELIMINARY; PRT; 81 AA.
 DT 27-SEP-2005, integrated into UniProtKB/TrEMBL.
 DT 27-SEP-2005, sequence version 1.
 DT 18-APR-2006, entry version 4.
 DE Prokineticin-1 (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=15932929; DOI=10.1210/en.2005-0297;
 RA Kisliouk T., Podlovni H., Spanel-Borowski K., Ovadia O., Zhou Q.Y.,
 RA Meidan R.;
 RT "Prokineticins (endocrine gland-derived vascular endothelial growth
 factor and bFGF) in the bovine ovary: expression and role as mitogens
 and survival factors for corpus luteum-derived endothelial cells.";
 RT Endocrinology 146:3950-3958(2005).
 RL [1]
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EMBL: AY877432; AAX81517.1; -; mRNA.
 InterPro: IPR009523; Prokineticin.
 PANTHER: PTHR18821; Prokineticin; 1.
 Pfam: PF06607; Prokineticin; 1.
 NON TER 1
 SQ SEQUENCE 81 AA; 9086 MW; 228834A7B83BA536 CRC64;

Query Match 83.7%; Score 417; DB 2; Length 81;
 Best Local Similarity 87.7%; Pred. No. 2.1e-38;
 Matches 71; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 6 ACERDVQCGAGTCCALSLWRLGLRMCTPLGREGECHPGSHKVPFFFRKRKHTTCCPLPNL 65
 DB 1 ACERDVQCGAGTCCALSLWRLGLRMCTPLGREGECHPGSHKVPFFFRKRKHTTCCPLPNL 60

QY 66 LCSPFPDGRYRCSDMLKNINF 86
 DB 61 LCSPFPDGRYRCSDMLKNINF 81

RESULT 7
 Q2XXR8_VARVA
 ID Q2XXR8_VARVA PRELIMINARY; PRT; 104 AA.
 AC Q2XXR8_VARVA PRELIMINARY; PRT; 104 AA.
 DT 20-DEC-2005, integrated into UniProtKB/TrEMBL.
 DT 20-DEC-2005, sequence version 1.
 DT 18-APR-2006, entry version 5.
 DE AVIToxin-VAR1 precursor.
 OS Varanus varius (Lace monitor).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
 OC NCBI_TaxID=8559;
 RN [1]

RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Compound mandibular venom gland;
 RX PubMed=16292255; DOI=10.1038/nature04328;
 RA Fry B.G., Vidal N., Norman J.A., Vonk F.J., Scheib H., Ramjan S.F.,
 RA Kuruppu S., Fung K., Blair Hedges S., Richardson M.K., Hodgson W.C.,
 RA Ignjatovic V., Summerhayes R., Kochva E.;
 RT "Early evolution of the venom system in lizards and snakes.";
 RL Nature 439:584-588(2006).
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EMBL: DQ139877; AAZ75583.1; -; mRNA.
 SMR: Q2XXR8; 20-97.
 InterPro: IPR009523; Prokineticin.
 PANTHER: PTHR18821; Prokineticin; 1.
 Pfam: PF06607; Prokineticin; 1.
 Signal.
 FT SIGNAL 1 19 Potential.
 FT CHAIN 20 104 AVIToxin-VAR1.
 SQ SEQUENCE 104 AA; 11217 MW; C25A96B3B59D3AA3 CRC64;

Query Match 69.3%; Score 345; DB 2; Length 104;
 Best Local Similarity 64.3%; Pred. No. 2.6e-30;
 Matches 54; Conservative 15; Mismatches 15; Indels 0; Gaps 0;

QY 1 AVITGACERDVQCGAGTCCALSLWRLGLRMCTPLGREGECHPGSHKVPFFFRKRKHTTCCP 60
 DB 20 AVITGACERDVQCGAGTCCALSLWRLGLRMCTPLGREGECHPGSHKVPFFFRKRKHTTCCP 79

QY 61 CLPNLLCSRFDPGRYRCSDMLKNI 84
 DB 80 CLPNLLCSRFDPGRYRCSDMLKNI 103

RESULT 8
 Q2XXR7_VARVA
 ID Q2XXR7_VARVA PRELIMINARY; PRT; 104 AA.
 AC Q2XXR7_VARVA PRELIMINARY; PRT; 104 AA.
 DT 20-DEC-2005, integrated into UniProtKB/TrEMBL.
 DT 20-DEC-2005, sequence version 1.
 DT 18-APR-2006, entry version 5.
 DE AVIToxin-VAR2 precursor.
 OS Varanus varius (Lace monitor).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
 OC NCBI_TaxID=8559;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Compound mandibular venom gland;
 RX PubMed=16292255; DOI=10.1038/nature04328;
 RA Fry B.G., Vidal N., Norman J.A., Vonk F.J., Scheib H., Ramjan S.F.,
 RA Kuruppu S., Fung K., Blair Hedges S., Richardson M.K., Hodgson W.C.,
 RA Ignjatovic V., Summerhayes R., Kochva E.;
 RT "Early evolution of the venom system in lizards and snakes.";
 RL Nature 439:584-588(2006).
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EMBL: DQ139878; AAZ75584.1; -; mRNA.
 SMR: Q2XXR7; 20-97.
 InterPro: IPR009523; Prokineticin.
 PANTHER: PTHR18821; Prokineticin; 1.
 Pfam: PF06607; Prokineticin; 1.
 Signal.
 FT SIGNAL 1 19 Potential.
 FT CHAIN 20 104 AVIToxin-VAR2.
 SQ SEQUENCE 104 AA; 11191 MW; C25A83A6B59D3AA3 CRC64;

Query Match 68.3%; Score 340; DB 2; Length 104;
 Best Local Similarity 63.1%; Pred. No. 9.4e-30;
 Matches 53; Conservative 16; Mismatches 15; Indels 0; Gaps 0;

[illegible]

RESULT 9	
VPRA_DENPO	
ID	VPRA_DENPO
AC	STANDARD; PRT; 81 AA.
P25687;	
DT	01-MAY-1992, integrated into UniProtKB/Swiss-Prot.
DT	19-JUL-2005, sequence version 3.
DT	30-MAY-2006, entry version 38.
DE	Intestinal toxin 1 (Mamba intestinal toxin 1) (MIT 1) (MIT)
DE	(protein A).
OS	Dendroaspis polylepsis polylepsis (Black mamba).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC	Elapidae; Elapinae; Dendroaspis.
OX	NCBI_Taxid=8620;

[1]
RP PROTEIN SEQUENCE OF 1-80.
RC
RC TISSUE=Venom;
RX MEDLINE=81115818; PubMed=7461607;
RA Joubert F.J., Strydom D.J.;
RT "Snake venom. The amino acid sequence of protein A from Dendroaspis
RT polylepsis polylepsis (black mamba) venom.";
RL Hoppe-Seyler's Z. Physiol. Chem. 361:1787-1794(1980).
[2]
RP PROTEIN SEQUENCE, AND CHARACTERIZATION.
RC
RC TISSUE=Venom;
RX MEDLINE=20036442; PubMed=10567694; DOI=10.1016/S0014-5793(99)01459-3;
RA Schweitz H., Pascaud P., Diochot S., Moinier D., Lazdunski M.;
RT "MT1, a black mamba toxin with a new and highly potent activity on
RT intestinal contraction.";
RL FEBS Lett. 461:183-188(1998).

[3] STRUCTURE BY NMR OF 1-81, AND DISULFIDE BONDS.
 RC TISSUE=Venom;
 RX MEDLINE=98437381; PubMed=9761684; DOI=10.1006/jmbi.1998.2057;
 RA Boislavouyer J., Albrand J.-P., Blackledge M., Jaquinod M.,
 RC Schweitz H., Lazdunski M., Marion D.;
 RT "A structural homologue of colipase in black mamba venom revealed by
 RT NMR floating disulphide bridge analysis.";
 RL J. Mol. Biol. 283:205-219(1998).
 CC -I- FUNCTION: Potently contracts gastrointestinal (GI) smooth muscle.
 CC May act on potassium channels, but not on Kv1.1, Kv1.2, Kv1.3,
 CC Kv1.4, Kv1.5, Kv2.1, Kv3.4, Kv4.2, TREK-1, HERG, KCNQ1, KCNQ2,
 CC KCNQ3, IRK1, IRK2, ROMK1, GIRK1,2 and GIRK4.
 CC -I- SUBCELLULAR LOCATION: Secreted protein.
 CC -I- SIMILARITY: Belongs to the prokinectin family.

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 PDB; 1IMT; NMR; @=1-80.
 InterPro: IPR009523; Prokineticin.
 Pfam: PF06607; Prokineticin; 1.
 3D-structure; Direct protein sequencing; Toxin.
 Intestinal toxin 1.
 CHAIN 1 81
 /FTID=PRO 0000165469.

	7	19	
PT	DISULFID		
PT	DISULFID	31	
PT	DISULFID	18	
PT	DISULFID	59	
PT	DISULFID	41	
PT	DISULFID	67	
PT	DISULFID	61	
PT	VARIANT	72	
PT	CONFLICT	18	
PT	CONFLICT	22	
PT	CONFLICT	22	

P - A Q (in protein A').
S - A C (in Ref. 1).
C - A C (in Ref. 1).

FT	CONFLICT	54	54	R -> RK (in Ref. 1).
FT	STRAND	5	6	
FT	STRAND	8	9	
FT	HELIX	10	12	
FT	TURN	13	13	
FT	TURN	15	16	
FT	TURN	17	21	
FT	STRAND	23	24	
FT	TURN	26	27	
FT	STRAND	29	33	
FT	TURN	35	35	
FT	TURN	37	38	
FT	STRAND	40	41	
FT	TURN	43	44	
FT	STRAND	48	49	
FT	STRAND	52	52	
FT	STRAND	57	58	
FT	STRAND	62	62	
FT	TURN	64	65	
FT	STRAND	67	72	
FT	TURN	73	74	
FT	STRAND	75	79	
SQ	SEQUENCE	81 AA; 8604 MW; 5F6B703434338B03 CRC64;		

Query Match	63.3%; Score 315; DB 1; Length 81;
Best Local Similarity	62.3%; Pred. No. 4.3e-17;
Matches	48; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

Qy	1	AVITGACERDVOCAGCTCCCAISLWTLGLRMCTPLGREGHECHPGSHKVPFPRKRKHHTCP	60
Db	1	AVITGACERDLQCGKGTCCAVSLWIKSVRCPTVGTSGEDCHPASHKIPFSGQRMHHTCP	60
Qy	61	CLPNLLCSRPFDGRYRC	77
Db	61	CAPNLACVQTSPPKFKC	77

RESULT 10		
QARVU3	TETNG	PRELIMINARY; PRT; 106 AA.
AC	QARVU3	TETNG
DT	19-JUL-2005,	integrated into UniProtKB/TrEMBL.
DT	19-JUL-2005,	sequence version 1.
DT	07-FEB-2006,	entry version 4.
DE	Chromosome 9	SCAF14991, whole genome shotgun sequence. (Fragment).
GN	ORFNames=GSTENG0028169001;	
OS	Tetraodon nigroviridis	(Green puffer).
OC	Eukaryota; Metazoa; Chordata; Craniata;	Vertebrata; Euteleostomi;
OC	Actinopterygii; Neopterygii; Teleostei;	Euteleostei; Neoteleostei;
OC	Acanthomorpha; Acanthopterygii; Percomorpha;	Tetraodontiformes;
OC	Tetraodontidae; Tetraodontidae;	Tetraodon.
OX	NCBI_TaxID=99883;	
RN	[1]	

NUCLEOTIDE SEQUENCE.		
RP	PubMed=15496914; DOI=10.1038/nature03025;	
RX	Jallion O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,	
RA	Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,	
RA	Nicaud S., Jaffe D., Fisher S., Lufalla G., Dossat C., Segures B.,	
RA	Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,	
RA	Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,	
RA	Biemont C., Skalli Z., Cattolico L., Poullain J., De Bernardis V.,	
RA	Cruaud C., Duprat S., Bröttier P., Coutanceau J.-P., Guzy J.,	
RA	Barra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,	
RA	Kellis M., Wolff J.-N., Guigo R., Zody M.C., Mesirov J.,	
RA	Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,	
RA	Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,	
RA	Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.,	
RT	"Genome duplication in the teleost fish Tetraodon nigroviridis reveals	
RL	the early vertebrate proto-karyotype."	
RL	Nature 431:946-957(2004).	
RN	[2]	

NUCLEOTIDE SEQUENCE.	
RP	Genoscope; Whitehead Institute Centre for Genome Research;
RG	

Search completed: November 29, 2007, 17:25:54
Job time : 192.445 secs

GenCore version 6.2.1
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 OM protein - protein search, using sw model
 Run on: November 29, 2007, 17:21:19 ; Search time 69 Seconds
 (without alignments)
 1014.355 Million cell updates/sec

Title: US-10-692-299-2_COPY_20_105
 Perfect score: 498
 Sequence: 1 AVITGACRDVQAGTCCA.....CSRFPDGRYRCMDLKNINF 86

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 352611 seqs, 817857308 residues

Total number of hits satisfying chosen parameters: 352611

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : Published Applications AA Main:

- 1: /EMC_Celerra_SIDS2/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /EMC_Celerra_SIDS2/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 3: /EMC_Celerra_SIDS2/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 4: /EMC_Celerra_SIDS2/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 5: /EMC_Celerra_SIDS2/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 6: /EMC_Celerra_SIDS2/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	498	100.0	86	4	US-10-016-481-3
2	498	100.0	86	4	US-10-323-157-3
3	498	100.0	86	4	US-10-417-426-9
4	498	100.0	86	4	US-10-333-192-21
5	498	100.0	86	5	US-10-680-554-5
6	498	100.0	86	5	US-10-713-567-3
7	498	100.0	86	5	US-10-811-328-3
8	498	100.0	86	5	US-10-912-907-3
9	498	100.0	86	5	US-10-415-724-3
10	498	100.0	86	5	US-10-871-152-22
11	498	100.0	86	5	US-10-503-554A-82
12	498	100.0	86	5	US-10-343-055A-117
13	498	100.0	86	5	US-10-415-724-3
14	498	100.0	86	5	US-10-542-664-1
15	498	100.0	86	5	US-10-576-066-2
16	498	100.0	86	6	US-11-073-420-11
17	498	100.0	86	6	US-11-304-129-21
18	498	100.0	86	6	US-11-048-649-9
19	498	100.0	86	6	US-11-384-222-7
20	498	100.0	86	6	US-11-529-695-3
21	498	100.0	87	4	US-10-016-481-18
22	498	100.0	87	4	US-10-323-157-18
23	498	100.0	87	5	US-10-713-567-18
24	498	100.0	87	5	US-10-811-328-18
25	498	100.0	87	5	US-10-912-907-18
26	498	100.0	87	5	US-10-415-724-18
27	498	100.0	87	5	US-10-415-724-18

28	498	100.0	87	6	US-11-529-695-18	Sequence 18, Appl
29	498	100.0	89	4	US-10-016-481-15	Sequence 15, Appl
30	498	100.0	89	4	US-10-323-157-15	Sequence 15, Appl
31	498	100.0	89	5	US-10-713-567-15	Sequence 15, Appl
32	498	100.0	89	5	US-10-811-328-15	Sequence 15, Appl
33	498	100.0	89	5	US-10-912-907-15	Sequence 15, Appl
34	498	100.0	89	5	US-10-415-724-15	Sequence 15, Appl
35	498	100.0	89	5	US-10-415-724-15	Sequence 15, Appl
36	498	100.0	89	6	US-11-529-695-15	Sequence 15, Appl
50	498	100.0	105	3	US-09-886-242A-2	Sequence 2, Appl
52	498	100.0	105	3	US-09-965-528-11	Sequence 11, Appl
65	498	100.0	105	3	US-09-997-428-371	Sequence 371, Appl
69	498	100.0	105	3	US-09-796-753-64	Sequence 64, Appl
111	498	100.0	105	3	US-09-969-984-11	Sequence 11, Appl
112	498	100.0	105	4	US-10-016-481-2	Sequence 2, Appl
113	498	100.0	105	4	US-10-027-603-2	Sequence 2, Appl
135	498	100.0	105	4	US-10-132-812-16	Sequence 16, Appl
294	498	100.0	105	4	US-10-223-085-172	Sequence 172, Appl
300	498	100.0	105	4	US-10-219-065-166	Sequence 166, Appl
328	498	100.0	105	4	US-10-223-084-172	Sequence 172, Appl
329	498	100.0	105	4	US-10-223-088-172	Sequence 172, Appl
330	498	100.0	105	4	US-10-223-090-172	Sequence 172, Appl
335	498	100.0	105	4	US-10-212-355-5	Sequence 5, Appl
336	498	100.0	105	4	US-10-223-087-172	Sequence 172, Appl
337	498	100.0	105	4	US-10-323-157-2	Sequence 2, Appl
339	498	100.0	105	4	US-10-223-083-172	Sequence 172, Appl
342	498	100.0	105	4	US-10-223-089-172	Sequence 172, Appl
391	498	100.0	105	4	US-10-212-201-5	Sequence 5, Appl
502	498	100.0	105	4	US-10-223-081-172	Sequence 172, Appl
536	498	100.0	105	4	US-10-223-082-172	Sequence 172, Appl
647	498	100.0	105	4	US-10-305-654-172	Sequence 172, Appl
658	498	100.0	105	4	US-10-081-056-172	Sequence 172, Appl
664	498	100.0	105	4	US-10-333-192-23	Sequence 23, Appl
667	498	100.0	105	4	US-10-680-755A-5	Sequence 5, Appl
668	498	100.0	105	4	US-10-680-800A-5	Sequence 5, Appl
676	498	100.0	105	5	US-10-713-567-2	Sequence 2, Appl
680	498	100.0	105	5	US-10-931-886-470	Sequence 470, Appl
681	498	100.0	105	5	US-10-811-328-2	Sequence 2, Appl
682	498	100.0	105	5	US-10-912-907-2	Sequence 2, Appl
683	498	100.0	105	5	US-10-692-299-2	Sequence 2, Appl
684	498	100.0	105	5	US-10-415-724-2	Sequence 2, Appl
686	498	100.0	105	5	US-10-977-113-31	Sequence 31, Appl
687	498	100.0	105	5	US-10-990-246-5	Sequence 5, Appl
688	498	100.0	105	5	US-10-955-952-470	Sequence 470, Appl
689	498	100.0	105	5	US-10-503-554A-84	Sequence 84, Appl
690	498	100.0	105	5	US-10-950-374-371	Sequence 371, Appl
691	498	100.0	105	5	US-10-982-168-5	Sequence 5, Appl
693	498	100.0	105	5	US-10-973-115B-470	Sequence 470, Appl
699	498	100.0	105	5	US-10-504-588-4	Sequence 4, Appl
702	498	100.0	105	5	US-10-415-724-2	Sequence 2, Appl
703	498	100.0	105	5	US-10-549-241-8	Sequence 8, Appl
705	498	100.0	105	5	US-10-964-241-470	Sequence 470, Appl
706	498	100.0	105	6	US-11-052-721-2	Sequence 2, Appl
707	498	100.0	105	6	US-11-290-153-470	Sequence 470, Appl
708	498	100.0	105	6	US-11-304-129-23	Sequence 23, Appl
709	498	100.0	105	6	US-11-265-762-64	Sequence 64, Appl
710	498	100.0	105	6	US-11-549-232-5	Sequence 5, Appl
711	498	100.0	105	6	US-11-549-227-5	Sequence 5, Appl
712	498	100.0	105	6	US-11-548-814-5	Sequence 5, Appl
713	498	100.0	105	6	US-11-550-982-5	Sequence 5, Appl
714	498	100.0	105	6	US-11-549-237-5	Sequence 5, Appl
715	498	100.0	105	6	US-11-548-805-5	Sequence 5, Appl
716	498	100.0	105	6	US-11-549-223-5	Sequence 5, Appl
717	498	100.0	105	6	US-11-550-993-5	Sequence 5, Appl
718	498	100.0	105	6	US-11-551-002-5	Sequence 5, Appl
719	498	100.0	105	6	US-11-548-810-5	Sequence 5, Appl
720	498	100.0	105	6	US-11-548-819-5	Sequence 5, Appl
721	498	100.0	105	6	US-11-548-824-5	Sequence 5, Appl
722	498	100.0	105	6	US-11-529-695-2	Sequence 2, Appl
723	498	100.0	105	6	US-11-548-830-5	Sequence 5, Appl
724	498	100.0	105	6	US-11-443-428A-862623	Sequence 862623, Appl
725	498	100.0	105	6	US-11-443-428A-862624	Sequence 862624, Appl
726	498	100.0	105	6	US-11-443-428A-862625	Sequence 862625, Appl

727	498	100.0	105	6	US-11-443-428A-862626	Sequence 862626,	800	455	91.4	86	5	US-10-871-152-23	Sequence 23, Appl
728	498	100.0	105	6	US-11-548-826-5	Sequence 5, Appli	801	455	91.4	86	5	US-10-503-554A-109	Sequence 109, App
729	498	100.0	105	6	US-11-551-008-5	Sequence 5, Appli	802	455	91.4	86	5	US-10-073-420-12	Sequence 12, Appl
730	498	100.0	105	6	US-11-537-382-2	Sequence 2, Appli	803	455	91.4	86	6	US-11-048-649-10	Sequence 10, Appl
731	498	100.0	105	6	US-11-549-241-5	Sequence 5, Appli	804	455	91.4	86	6	US-11-529-695-28	Sequence 28, Appl
732	497	99.8	86	4	US-10-333-192-20	Sequence 20, Appl	805	455	91.4	105	4	US-10-470-351-6	Sequence 6, Appli
733	497	99.8	86	5	US-10-503-554A-81	Sequence 81, Appl	806	455	91.4	105	5	US-10-549-241-10	Sequence 10, App
734	497	99.8	86	5	US-10-542-664-2	Sequence 2, Appli	807	455	91.4	105	5	US-10-503-554A-107	Sequence 107, App
735	497	99.8	86	5	US-10-576-066-3	Sequence 3, Appli	808	413	82.9	86	4	US-10-016-481-14	Sequence 14, Appl
736	497	99.8	86	6	US-11-304-129-20	Sequence 20, Appl	809	413	82.9	86	4	US-10-323-157-14	Sequence 14, Appl
737	497	99.8	105	4	US-10-132-812-18	Sequence 18, Appl	810	413	82.9	86	4	US-10-417-426-21	Sequence 21, Appl
738	497	99.8	105	4	US-10-333-192-22	Sequence 22, Appl	811	413	82.9	86	5	US-10-680-554-16	Sequence 16, Appl
739	497	99.8	105	5	US-10-467-554-3	Sequence 3, Appli	812	413	82.9	86	5	US-10-713-567-14	Sequence 14, Appl
740	497	99.8	105	5	US-10-503-554A-83	Sequence 83, Appl	813	413	82.9	86	5	US-10-811-328-14	Sequence 14, Appl
741	497	99.8	105	5	US-10-475-075-194	Sequence 194, App	814	413	82.9	86	5	US-10-912-907-14	Sequence 14, Appl
742	497	99.8	105	6	US-11-304-129-22	Sequence 22, Appl	815	413	82.9	86	5	US-10-415-724-14	Sequence 14, Appl
743	497	99.8	105	6	US-11-371-354-76695	Sequence 76695, A	816	413	82.9	86	5	US-10-977-113-17	Sequence 17, Appl
744	497	99.8	105	6	US-11-371-354-76648	Sequence 76648, A	817	413	82.9	86	5	US-10-871-152-28	Sequence 28, Appl
745	497	99.8	105	6	US-11-218-141-1728	Sequence 1728, Ap	818	413	82.9	86	5	US-10-415-724-14	Sequence 14, Appl
746	494	99.2	85	4	US-10-016-481-16	Sequence 16, Appl	819	413	82.9	86	6	US-11-073-420-17	Sequence 17, Appl
747	494	99.2	85	4	US-10-323-157-16	Sequence 16, Appl	820	413	82.9	86	6	US-11-048-649-21	Sequence 21, Appl
748	494	99.2	85	5	US-10-713-567-16	Sequence 16, Appl	821	413	82.9	86	6	US-11-529-695-14	Sequence 14, Appl
749	494	99.2	85	5	US-10-811-328-16	Sequence 16, Appl	822	376	75.5	81	4	US-10-016-481-13	Sequence 13, Appl
750	494	99.2	85	5	US-10-912-907-16	Sequence 16, Appl	823	376	75.5	81	4	US-10-323-157-13	Sequence 13, Appl
751	494	99.2	85	5	US-10-415-724-16	Sequence 16, Appl	824	376	75.5	81	4	US-10-417-426-20	Sequence 20, Appl
752	494	99.2	85	5	US-10-415-724-16	Sequence 16, Appl	825	376	75.5	81	5	US-10-680-554-15	Sequence 15, Appl
753	494	99.2	85	6	US-11-529-695-16	Sequence 16, Appl	826	376	75.5	81	5	US-10-713-567-13	Sequence 13, Appl
754	494	99.2	86	5	US-10-713-567-20	Sequence 20, Appl	827	376	75.5	81	5	US-10-811-328-13	Sequence 13, Appl
755	494	99.2	86	5	US-10-811-328-20	Sequence 20, Appl	828	376	75.5	81	5	US-10-912-907-13	Sequence 13, Appl
756	494	99.2	86	6	US-11-529-695-20	Sequence 20, Appl	829	376	75.5	81	5	US-10-415-724-13	Sequence 13, Appl
757	492	98.8	105	6	US-10-977-113-30	Sequence 30, Appl	830	376	75.5	81	5	US-10-977-113-16	Sequence 16, Appl
758	492	98.8	105	6	US-11-073-420-28	Sequence 28, Appl	831	376	75.5	81	5	US-10-871-152-27	Sequence 27, Appl
759	491	98.6	105	5	US-10-475-075-193	Sequence 193, App	832	376	75.5	81	6	US-10-415-724-13	Sequence 13, Appl
760	491	98.6	105	5	US-10-475-075-477	Sequence 477, App	833	376	75.5	81	6	US-11-048-649-20	Sequence 20, Appl
761	489	98.2	105	6	US-11-073-420-31	Sequence 31, Appl	834	376	75.5	81	6	US-11-529-695-13	Sequence 13, Appl
762	486	97.6	105	5	US-10-664-025-5350	Sequence 5350, Ap	835	376	75.5	81	6	US-10-631-441-2421	Sequence 2421, Ap
763	478	96.0	86	4	US-10-016-481-17	Sequence 17, Appl	836	361	72.5	80	4	US-10-417-426-13	Sequence 13, Appl
764	478	96.0	86	4	US-10-323-157-17	Sequence 17, Appl	837	315	63.3	80	4	US-10-467-019-21	Sequence 21, Appl
765	478	96.0	86	5	US-10-713-567-17	Sequence 17, Appl	838	315	63.3	80	4	US-10-470-951-64	Sequence 64, Appl
766	478	96.0	86	5	US-10-811-328-17	Sequence 17, Appl	839	315	63.3	80	4	US-10-333-192-34	Sequence 34, Appl
767	478	96.0	86	5	US-10-912-907-17	Sequence 17, Appl	840	315	63.3	80	5	US-10-977-113-15	Sequence 15, Appl
768	478	96.0	86	5	US-10-415-724-17	Sequence 17, Appl	841	315	63.3	80	5	US-10-977-113-15	Sequence 15, Appl
769	478	96.0	86	6	US-10-415-724-17	Sequence 17, Appl	842	315	63.3	80	5	US-10-871-152-26	Sequence 26, Appl
770	478	96.0	86	6	US-11-529-695-17	Sequence 17, Appl	843	315	63.3	80	5	US-10-503-554A-21	Sequence 21, Appl
771	476	95.6	82	5	US-10-977-113-11	Sequence 11, Appl	844	315	63.3	80	6	US-11-073-420-15	Sequence 15, Appl
772	473	95.0	86	4	US-10-470-951-37	Sequence 37, Appl	845	315	63.3	80	6	US-11-048-649-13	Sequence 13, Appl
773	473	95.0	86	4	US-10-362-504-49	Sequence 49, Appl	846	315	63.3	80	6	US-11-048-649-13	Sequence 13, Appl
774	473	95.0	86	5	US-10-680-554-10	Sequence 10, Appl	847	311.5	62.6	79	3	US-09-886-242A-5	Sequence 5, Appli
775	473	95.0	86	5	US-10-713-567-30	Sequence 30, Appl	848	311.5	62.6	79	4	US-10-027-603-5	Sequence 5, Appli
776	473	95.0	86	5	US-10-811-328-30	Sequence 30, Appl	849	311.5	62.6	79	5	US-10-692-399-5	Sequence 5, Appli
777	473	95.0	86	5	US-10-503-554A-138	Sequence 138, App	850	311.5	62.6	79	5	US-11-537-382-5	Sequence 5, Appli
778	473	95.0	86	6	US-11-529-695-30	Sequence 30, Appl	851	310.5	62.3	81	4	US-10-016-481-12	Sequence 12, Appl
779	473	95.0	105	4	US-10-470-951-31	Sequence 31, Appl	852	310.5	62.3	81	4	US-10-132-812-19	Sequence 19, Appl
780	473	95.0	105	4	US-10-362-504-43	Sequence 43, Appl	853	310.5	62.3	81	4	US-10-323-157-12	Sequence 12, Appl
781	473	95.0	105	5	US-10-503-554A-132	Sequence 132, App	854	310.5	62.3	81	5	US-10-680-554-12	Sequence 12, Appl
782	469	94.2	86	4	US-10-470-951-41	Sequence 41, Appl	855	310.5	62.3	81	5	US-10-713-567-12	Sequence 12, Appl
783	469	94.2	86	4	US-10-362-504-53	Sequence 53, Appl	856	310.5	62.3	81	5	US-10-811-328-12	Sequence 12, Appl
784	469	94.2	86	5	US-10-503-554A-142	Sequence 142, App	857	310.5	62.3	81	5	US-10-912-907-12	Sequence 12, Appl
785	469	94.2	105	4	US-10-470-951-35	Sequence 35, Appl	858	310.5	62.3	81	5	US-10-415-724-12	Sequence 12, Appl
786	469	94.2	105	4	US-10-362-504-47	Sequence 47, Appl	859	310.5	62.3	81	5	US-10-415-724-12	Sequence 12, Appl
787	469	94.2	105	5	US-10-503-554A-136	Sequence 136, App	860	310.5	62.3	81	6	US-11-529-695-12	Sequence 12, Appl
788	467	93.8	86	4	US-10-470-951-39	Sequence 39, Appl	861	291	58.4	80	4	US-10-467-019-22	Sequence 22, Appl
789	467	93.8	86	4	US-10-362-504-51	Sequence 51, Appl	862	291	58.4	80	5	US-10-503-554A-22	Sequence 22, Appl
790	467	93.8	86	5	US-10-503-554A-140	Sequence 140, App	863	291	58.4	81	4	US-10-016-481-6	Sequence 6, Appli
791	467	93.8	105	4	US-10-470-951-33	Sequence 33, Appl	864	291	58.4	81	4	US-10-323-157-6	Sequence 6, Appli
792	467	93.8	105	5	US-10-362-504-45	Sequence 45, Appl	865	291	58.4	81	4	US-10-417-426-5	Sequence 5, Appli
793	467	93.8	105	5	US-10-503-554A-134	Sequence 134, App	866	291	58.4	81	4	US-10-680-554-7	Sequence 7, Appli
794	455	91.4	86	4	US-10-417-426-10	Sequence 10, Appl	867	291	58.4	81	5	US-10-713-567-6	Sequence 6, Appli
795	455	91.4	86	4	US-10-470-951-8	Sequence 8, Appli	868	291	58.4	81	5	US-10-811-328-6	Sequence 6, Appli
796	455	91.4	86	5	US-10-680-554-8	Sequence 8, Appli	869	291	58.4	81	5	US-10-912-907-6	Sequence 6, Appli
797	455	91.4	86	5	US-10-713-567-28	Sequence 28, Appl	870	291	58.4	81	5	US-10-811-328-6	Sequence 6, Appli
798	455	91.4	86	5	US-10-811-328-28	Sequence 28, Appl	871	291	58.4	81	5	US-10-415-724-6	Sequence 6, Appli
799	455	91.4	86	5	US-10-977-113-12	Sequence 12, Appl	872	291	58.4	81	5	US-10-977-113-9	Sequence 9, Appli

873	291	58.4	81	5	US-10-871-152-18	Sequence 18, Appl	946	286	57.4	81	5	US-10-871-152-20	Sequence 20, Appl
874	291	58.4	81	5	US-10-503-554A-19	Sequence 19, Appl	947	286	57.4	81	5	US-10-503-554A-39	Sequence 39, Appl
875	291	58.4	81	5	US-10-415-724-6	Sequence 6, Appl	948	286	57.4	81	5	US-11-048-649-7	Sequence 7, Appl
876	291	58.4	81	5	US-10-542-664-3	Sequence 3, Appl	949	286	57.4	81	6	US-11-529-695-29	Sequence 29, Appl
877	291	58.4	81	5	US-10-576-066-1	Sequence 1, Appl	950	286	57.4	81	6	US-11-529-695-31	Sequence 31, Appl
878	291	58.4	81	6	US-11-073-420-9	Sequence 9, Appl	951	286	57.4	107	4	US-10-132-812-10	Sequence 10, Appl
879	291	58.4	81	6	US-11-048-649-5	Sequence 5, Appl	952	286	57.4	107	4	US-10-231-411-6	Sequence 6, Appl
880	291	58.4	81	6	US-11-529-695-6	Sequence 6, Appl	953	286	57.4	107	4	US-10-467-019-37	Sequence 37, Appl
881	291	58.4	100	3	US-09-886-242A-4	Sequence 4, Appl	954	286	57.4	107	4	US-10-467-019-55	Sequence 55, Appl
882	291	58.4	100	4	US-10-027-603-4	Sequence 4, Appl	955	286	57.4	107	4	US-10-362-504-69	Sequence 69, Appl
883	291	58.4	100	5	US-10-692-299-4	Sequence 4, Appl	956	286	57.4	107	5	US-10-503-554A-37	Sequence 37, Appl
884	291	58.4	100	6	US-11-537-382-4	Sequence 4, Appl	957	286	57.4	107	5	US-10-503-554A-55	Sequence 55, Appl
885	291	58.4	108	4	US-10-016-481-5	Sequence 5, Appl	958	286	57.4	107	5	US-10-549-241-6	Sequence 6, Appl
886	291	58.4	108	4	US-10-212-411-4	Sequence 4, Appl	959	286	57.4	107	6	US-11-384-222-6	Sequence 6, Appl
887	291	58.4	108	4	US-10-212-355-2	Sequence 2, Appl	960	284	57.0	81	6	US-11-073-420-37	Sequence 37, Appl
888	291	58.4	108	4	US-10-323-157-5	Sequence 5, Appl	961	284	57.0	108	5	US-10-713-567-34	Sequence 34, Appl
889	291	58.4	108	4	US-10-212-201-2	Sequence 2, Appl	962	284	57.0	108	5	US-10-977-113-6	Sequence 6, Appl
890	291	58.4	108	4	US-10-467-019-17	Sequence 17, Appl	963	284	57.0	108	6	US-11-073-420-6	Sequence 6, Appl
891	291	58.4	108	4	US-10-680-755A-2	Sequence 2, Appl	964	278.5	55.9	77	5	US-10-680-554-14	Sequence 14, Appl
892	291	58.4	108	4	US-10-680-800A-2	Sequence 2, Appl	965	278.5	55.9	77	5	US-10-713-567-32	Sequence 32, Appl
893	291	58.4	108	5	US-10-713-567-5	Sequence 5, Appl	966	278.5	55.9	77	5	US-10-811-328-32	Sequence 32, Appl
894	291	58.4	108	5	US-10-811-328-5	Sequence 5, Appl	967	278.5	55.9	77	5	US-11-529-695-32	Sequence 32, Appl
895	291	58.4	108	5	US-10-912-907-5	Sequence 5, Appl	968	270.5	54.3	102	5	US-10-680-554-6	Sequence 6, Appl
896	291	58.4	108	5	US-10-415-724-5	Sequence 5, Appl	969	270.5	54.3	129	4	US-10-132-812-14	Sequence 14, Appl
897	291	58.4	108	5	US-10-990-246-2	Sequence 2, Appl	970	270.5	54.3	129	4	US-10-231-411-2	Sequence 2, Appl
898	291	58.4	108	5	US-10-503-554A-17	Sequence 17, Appl	971	270.5	54.3	129	4	US-10-680-755A-29	Sequence 29, Appl
899	291	58.4	108	5	US-10-982-168-2	Sequence 2, Appl	972	270.5	54.3	129	4	US-10-680-800A-29	Sequence 29, Appl
900	291	58.4	108	5	US-10-504-588-6	Sequence 6, Appl	973	270.5	54.3	129	5	US-10-549-241-2	Sequence 2, Appl
901	291	58.4	108	5	US-10-415-724-5	Sequence 5, Appl	974	270.5	54.3	129	5	US-11-384-222-2	Sequence 2, Appl
902	291	58.4	108	5	US-10-549-241-4	Sequence 4, Appl	975	270.5	54.3	129	6	US-11-548-814-29	Sequence 29, Appl
903	291	58.4	108	6	US-11-384-222-4	Sequence 4, Appl	976	270.5	54.3	129	6	US-11-550-982-29	Sequence 29, Appl
904	291	58.4	108	6	US-11-549-232-2	Sequence 2, Appl	977	270.5	54.3	129	6	US-11-548-805-29	Sequence 29, Appl
905	291	58.4	108	6	US-11-549-227-2	Sequence 2, Appl	978	270.5	54.3	129	6	US-11-550-993-29	Sequence 29, Appl
906	291	58.4	108	6	US-11-548-814-2	Sequence 2, Appl	979	270.5	54.3	129	6	US-11-551-002-29	Sequence 29, Appl
907	291	58.4	108	6	US-11-550-982-2	Sequence 2, Appl	980	270.5	54.3	129	6	US-11-548-810-29	Sequence 29, Appl
908	291	58.4	108	6	US-11-549-237-2	Sequence 2, Appl	981	270.5	54.3	129	6	US-11-548-819-29	Sequence 29, Appl
909	291	58.4	108	6	US-11-549-222-2	Sequence 2, Appl	982	270.5	54.3	129	6	US-11-548-824-29	Sequence 29, Appl
910	291	58.4	108	6	US-11-548-805-2	Sequence 2, Appl	983	270.5	54.3	129	6	US-11-548-830-29	Sequence 29, Appl
911	291	58.4	108	6	US-11-550-993-2	Sequence 2, Appl	984	270.5	54.3	129	6	US-11-443-428A-790497	Sequence 790497
912	291	58.4	108	6	US-11-551-002-2	Sequence 2, Appl	985	270.5	54.3	129	6	US-11-548-826-29	Sequence 29, Appl
913	291	58.4	108	6	US-11-548-810-2	Sequence 2, Appl	986	270.5	54.3	129	6	US-11-551-008-29	Sequence 29, Appl
914	291	58.4	108	6	US-11-548-819-2	Sequence 2, Appl	987	267.5	53.7	77	4	US-10-417-426-11	Sequence 11, Appl
915	291	58.4	108	6	US-11-548-824-2	Sequence 2, Appl	988	267.5	53.7	77	5	US-10-680-554-13	Sequence 13, Appl
916	291	58.4	108	6	US-11-529-695-5	Sequence 5, Appl	989	267.5	53.7	77	5	US-10-977-113-14	Sequence 14, Appl
917	291	58.4	108	6	US-11-548-830-2	Sequence 2, Appl	990	267.5	53.7	77	5	US-10-871-152-24	Sequence 24, Appl
918	291	58.4	108	6	US-11-443-428A-790496	Sequence 790496	991	267.5	53.7	77	6	US-11-073-420-14	Sequence 14, Appl
919	291	58.4	108	6	US-11-548-826-2	Sequence 2, Appl	992	267.5	53.7	77	6	US-11-048-649-11	Sequence 11, Appl
920	291	58.4	108	6	US-11-551-008-2	Sequence 2, Appl	993	267.5	53.7	96	4	US-10-016-481-11	Sequence 11, Appl
921	291	58.4	108	6	US-11-549-241-2	Sequence 2, Appl	994	267.5	53.7	96	4	US-10-132-812-12	Sequence 12, Appl
922	291	58.4	116	4	US-10-680-755A-26	Sequence 26, Appl	995	267.5	53.7	96	4	US-10-323-157-11	Sequence 11, Appl
923	291	58.4	116	4	US-10-680-800A-26	Sequence 26, Appl	996	267.5	53.7	96	5	US-10-713-567-11	Sequence 11, Appl
924	291	58.4	116	6	US-11-548-814-26	Sequence 26, Appl	997	267.5	53.7	96	5	US-10-811-328-11	Sequence 11, Appl
925	291	58.4	116	6	US-11-550-982-26	Sequence 26, Appl	998	267.5	53.7	96	5	US-10-912-907-11	Sequence 11, Appl
926	291	58.4	116	6	US-11-548-805-26	Sequence 26, Appl	999	267.5	53.7	96	5	US-10-415-724-11	Sequence 11, Appl
927	291	58.4	116	6	US-11-550-993-26	Sequence 26, Appl	1000	267.5	53.7	96	5	US-10-415-724-11	Sequence 11, Appl
928	291	58.4	116	6	US-11-551-002-26	Sequence 26, Appl	1001	267.5	53.7	96	5	US-11-529-695-11	Sequence 11, Appl
929	291	58.4	116	6	US-11-548-810-26	Sequence 26, Appl	1002	265.5	53.3	102	4	US-10-417-426-8	Sequence 8, Appl
930	291	58.4	116	6	US-11-548-819-26	Sequence 26, Appl	1003	265.5	53.3	102	4	US-10-871-152-21	Sequence 21, Appl
931	291	58.4	116	6	US-11-548-824-26	Sequence 26, Appl	1004	265.5	53.3	102	6	US-11-048-649-8	Sequence 8, Appl
932	291	58.4	116	6	US-11-548-830-26	Sequence 26, Appl	1005	251.5	50.5	100	4	US-10-417-426-6	Sequence 6, Appl
933	291	58.4	116	6	US-11-548-826-26	Sequence 26, Appl	1006	251.5	50.5	100	5	US-10-871-152-19	Sequence 19, Appl
934	291	58.4	116	6	US-11-551-008-26	Sequence 26, Appl	1007	251.5	50.5	100	6	US-11-048-649-6	Sequence 6, Appl
935	286	57.4	80	6	US-10-977-113-10	Sequence 10, Appl	1008	250.5	50.3	75	4	US-10-417-426-12	Sequence 12, Appl
936	286	57.4	80	6	US-11-073-420-10	Sequence 10, Appl	1009	250.5	50.3	75	5	US-10-977-113-13	Sequence 13, Appl
937	286	57.4	81	4	US-10-467-019-39	Sequence 39, Appl	1010	250.5	50.3	75	5	US-10-871-152-25	Sequence 25, Appl
938	286	57.4	81	4	US-10-467-019-39	Sequence 39, Appl	1011	250.5	50.3	75	6	US-11-073-420-13	Sequence 13, Appl
939	286	57.4	81	5	US-10-362-504-71	Sequence 71, Appl	1012	250.5	50.3	75	6	US-11-048-649-12	Sequence 12, Appl
940	286	57.4	81	5	US-10-680-554-9	Sequence 9, Appl	1013	201.5	40.5	118	4	US-10-132-812-8	Sequence 8, Appl
941	286	57.4	81	5	US-10-680-554-11	Sequence 11, Appl	1014	109	21.9	23	4	US-10-680-755A-9	Sequence 9, Appl
942	286	57.4	81	5	US-10-713-567-29	Sequence 29, Appl	1015	109	21.9	23	4	US-10-680-800A-9	Sequence 9, Appl
943	286	57.4	81	5	US-10-713-567-31	Sequence 31, Appl	1016	109	21.9	23	6	US-11-548-814-9	Sequence 9, Appl
944	286	57.4	81	5	US-10-811-328-29	Sequence 29, Appl	1017	109	21.9	23	6	US-11-550-982-9	Sequence 9, Appl
945	286	57.4	81	5	US-10-811-328-31	Sequence 31, Appl	1018	109	21.9	23	6	US-11-548-805-9	Sequence 9, Appl

1019	109	21.9	23	6	US-11-550-993-9	Sequence 9, Appli
1020	109	21.9	23	6	US-11-551-002-9	Sequence 9, Appli
1021	109	21.9	23	6	US-11-548-810-9	Sequence 9, Appli
1022	109	21.9	23	6	US-11-548-819-9	Sequence 9, Appli
1023	109	21.9	23	6	US-11-548-824-9	Sequence 9, Appli
1024	109	21.9	23	6	US-11-548-830-9	Sequence 9, Appli
1025	109	21.9	23	6	US-11-548-826-9	Sequence 9, Appli
1026	109	21.9	23	6	US-11-551-008-9	Sequence 9, Appli
1027	108.5	21.8	221	5	US-10-579-596-5	Sequence 5, Appli
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1038	107.5	21.6	224	5	US-10-998-271-14	Sequence 14, Appl
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1040	107.5	21.6	224	5	US-10-579-596-4	Sequence 4, Appli
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	311.5	62.6	79	7	US-11-537-472-5
8	291	58.4	100	7	US-11-537-472-4
9	291	58.4	108	7	US-11-536-880-4
10	286	57.4	107	7	US-11-536-880-6
11	270.5	54.3	129	7	US-11-536-880-2
13	100.5	20.2	83	7	US-11-537-472-6
14	100.5	20.2	350	6	US-10-594-211-251
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16	97	19.5	266	7	US-11-537-235-428
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55	67.5	13.6	1641	7	US-11-649-663A-760
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92	63.5	12.8	197	6	US-10-767-701-51471
93	63.5	12.8	1353	7	US-11-649-663A-66
94	63.5	12.8	1509	7	US-11-649-663A-1838
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96	63.5	12.8	1801	7	US-11-649-663A-2660
97	63.5	12.8	3707	7	US-11-625-272-139
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154	61	12.2	1736	7	US-11-649-663A-664	Sequence 664, App	227	59	11.8	1303	7	US-11-649-663A-430	Sequence 430, App
155	61	12.2	1865	7	US-11-649-663A-2174	Sequence 2174, Ap	228	59	11.8	1553	7	US-11-649-663A-380	Sequence 380, App
156	61	12.2	1870	7	US-11-649-663A-4998	Sequence 4998, Ap	229	59	11.8	1703	7	US-11-649-663A-558	Sequence 558, App
157	61	12.2	1914	7	US-11-649-663A-20	Sequence 20, Appl	230	59	11.8	1733	7	US-11-649-663A-814	Sequence 814, App
158	61	12.2	1962	7	US-11-649-663A-1748	Sequence 1748, Ap	231	59	11.8	1814	7	US-11-649-663A-2750	Sequence 2750, Ap
159	61	12.2	2162	7	US-11-649-663A-2158	Sequence 2158, Ap	232	59	11.8	1847	7	US-11-649-663A-1182	Sequence 1182, Ap
160	61	12.2	2194	7	US-11-649-663A-2768	Sequence 2768, Ap	233	59	11.8	1948	7	US-11-649-663A-2702	Sequence 2702, Ap
161	61	12.2	2198	7	US-11-649-663A-1384	Sequence 1384, Ap	234	59	11.8	2047	7	US-11-649-663A-680	Sequence 680, App
162	61	12.2	255	6	US-10-767-701-42785	Sequence 42785, A	235	59	11.8	222	6	US-10-767-701-56855	Sequence 56855, A
163	61	12.2	183	7	US-11-689-173-6573	Sequence 6573, Ap	236	58.5	11.7	258	7	US-11-257-477-28	Sequence 28, Appl
164	61	12.2	183	7	US-11-689-173-9632	Sequence 9632, Ap	237	58.5	11.7	258	7	US-11-257-477-28	Sequence 28, Appl
165	61	12.2	183	7	US-11-689-173-9632	Sequence 9632, Ap	238	58.5	11.7	305	6	US-10-438-246-33140	Sequence 33140, A
166	61	12.2	183	7	US-11-689-173-9632	Sequence 9632, Ap	239	58.5	11.7	486	7	US-11-649-663A-82	Sequence 82, Appl
167	60.5	12.1	183	7	US-11-689-173-9632	Sequence 9632, Ap	240	58.5	11.7	584	7	US-11-403-116-468	Sequence 468, App
168	60.5	12.1	183	7	US-11-689-173-9632	Sequence 9632, Ap	241	58.5	11.7	584	7	US-11-403-116-470	Sequence 470, App
169	60.5	12.1	183	7	US-11-689-173-9632	Sequence 9632, Ap	242	58.5	11.7	584	7	US-11-403-116-470	Sequence 470, App
170	60.5	12.1	183	7	US-11-689-173-9632	Sequence 9632, Ap	243	58.5	11.7	584	7	US-11-403-116-470	Sequence 470, App
171	60.5	12.1	183	7	US-11-689-173-9632	Sequence 9632, Ap	244	58.5	11.7	584	7	US-11-403-116-470	Sequence 470, App
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175	60.5	12.1	183	7	US-11-689-173-9632	Sequence 9632, Ap	248	58.5	11.7	584	7	US-11-403-116-470	Sequence 470, App
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177	60.5	12.1	183	7	US-11-689-173-9632	Sequence 9632, Ap	250	58.5	11.7	584	7	US-11-403-116-470	Sequence 470, App
178	60.5	12.1	183	7	US-11-689-173-9632	Sequence 9632, Ap	251	58.5	11.7	584	7	US-11-403-116-470	Sequence 470, App
179	60.5	12.1	183	7	US-11-689-173-9632	Sequence 9632, Ap	252	58.5	11.7	584	7	US-11-403-116-470	Sequence 470, App
180	60.5	12.1	183	7	US-11-689-173-9632	Sequence 9632, Ap	253	58.5	11.7	584	7	US-11-403-116-470	Sequence 470, App
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249	58.5	11.7	1368	7	US-11-649-663A-4560	Sequence 4560, Ap	323	57.5	11.5	2052	7	US-11-649-663A-652	Sequence 652, App
250	58.5	11.7	1367	7	US-11-649-663A-2302	Sequence 2302, Ap	324	57.5	11.5	2119	7	US-11-649-663A-4798	Sequence 4798, Ap
251	58.5	11.7	1571	7	US-11-649-663A-2074	Sequence 2074, Ap	325	57.5	11.5	2137	7	US-11-649-663A-4852	Sequence 4852, Ap
252	58.5	11.7	1595	7	US-11-649-663A-4562	Sequence 4562, Ap	326	57.5	11.5	2574	7	US-11-649-663A-1990	Sequence 1990, Ap
253	58.5	11.7	1660	7	US-11-649-663A-2132	Sequence 2132, Ap	327	57.5	11.5	2871	6	US-10-529-351A-4185	Sequence 4185, Ap
254	58.5	11.7	1661	7	US-11-649-663A-1792	Sequence 1792, Ap	328	57.5	11.5	5109	7	US-11-649-663A-1520	Sequence 1520, Ap
255	58.5	11.7	1830	7	US-11-649-663A-1478	Sequence 1478, Ap	329	57	11.4	95	6	US-10-767-701-34249	Sequence 34249, A
256	58.5	11.7	1845	7	US-11-649-663A-1980	Sequence 1980, Ap	330	57	11.4	112	6	US-10-767-701-40551	Sequence 40551, A
257	58.5	11.7	1965	7	US-11-649-663A-1092	Sequence 1092, Ap	331	57	11.4	115	7	US-11-649-663A-5376	Sequence 5376, Ap
258	58.5	11.7	2012	7	US-11-649-663A-528	Sequence 528, App	332	57	11.4	141	7	US-11-360-355-138324	Sequence 138324,
259	58.5	11.7	2061	7	US-11-649-663A-1216	Sequence 1216, Ap	333	57	11.4	149	7	US-11-360-355-159798	Sequence 159798,
260	58	11.6	45	7	US-11-214-372B-120	Sequence 120, App	334	57	11.4	159	7	US-11-689-173-7143	Sequence 7143, Ap
261	58	11.6	83	6	US-10-767-701-40042	Sequence 40042, A	335	57	11.4	159	7	US-11-689-173-10034	Sequence 10034, A
262	58	11.6	115	7	US-11-689-173-8506	Sequence 8506, Ap	336	57	11.4	464	7	US-11-689-173-8731	Sequence 8731, Ap
263	58	11.6	127	6	US-10-767-701-45809	Sequence 45809, A	337	57	11.4	549	6	US-10-438-246-33486	Sequence 33486, A
264	58	11.6	299	6	US-10-438-246-18090	Sequence 18090, A	338	57	11.4	598	7	US-11-403-116-465	Sequence 465, App
265	58	11.6	299	6	US-10-438-246-25229	Sequence 25229, A	339	57	11.4	655	6	US-10-529-351A-1871	Sequence 1871, Ap
266	58	11.6	301	6	US-10-767-701-40000	Sequence 40000, A	342	57	11.4	850	7	US-11-649-663A-534	Sequence 534, App
267	58	11.6	525	7	US-11-713-768-76541	Sequence 76541, A	343	57	11.4	856	7	US-11-649-663A-1592	Sequence 1592, Ap
268	58	11.6	539	7	US-11-713-768-76540	Sequence 76540, A	344	57	11.4	984	7	US-11-649-663A-1592	Sequence 1592, Ap
269	58	11.6	710	7	US-11-649-663A-4112	Sequence 4112, Ap	345	57	11.4	1001	7	US-11-649-663A-1460	Sequence 1460, Ap
270	58	11.6	901	7	US-11-360-355-146763	Sequence 146763,	346	57	11.4	1027	7	US-11-649-663A-4296	Sequence 4296, Ap
271	58	11.6	1026	7	US-11-649-663A-1834	Sequence 1834, Ap	347	57	11.4	1131	7	US-11-649-663A-1604	Sequence 1604, Ap
272	58	11.6	1075	7	US-11-649-663A-3060	Sequence 3060, Ap	348	57	11.4	1215	7	US-11-649-663A-2800	Sequence 2800, Ap
273	58	11.6	1103	7	US-11-649-663A-2450	Sequence 2450, Ap	349	57	11.4	1242	7	US-11-649-663A-1678	Sequence 1678, Ap
274	58	11.6	1259	7	US-11-649-663A-5038	Sequence 5038, Ap	350	57	11.4	1274	7	US-11-649-663A-1848	Sequence 1848, Ap
275	58	11.6	1271	7	US-11-649-663A-2618	Sequence 2618, Ap	351	57	11.4	1310	7	US-11-649-663A-1186	Sequence 1186, Ap
276	58	11.6	1272	7	US-11-649-663A-422	Sequence 422, App	352	57	11.4	1365	7	US-11-649-663A-2290	Sequence 2290, Ap
277	58	11.6	1375	7	US-11-649-663A-622	Sequence 622, App	353	57	11.4	1396	7	US-11-649-663A-466	Sequence 466, App
278	58	11.6	1419	7	US-11-649-663A-132	Sequence 132, App	354	57	11.4	1418	7	US-11-649-663A-950	Sequence 950, App
279	58	11.6	1431	7	US-11-649-663A-2332	Sequence 2332, Ap	355	57	11.4	1432	7	US-11-649-663A-1100	Sequence 1100, Ap
280	58	11.6	1489	7	US-11-649-663A-2422	Sequence 2422, Ap	356	57	11.4	1444	7	US-11-649-663A-2626	Sequence 2626, Ap
281	58	11.6	1490	7	US-11-649-663A-2534	Sequence 2534, Ap	357	57	11.4	1445	7	US-11-649-663A-1452	Sequence 1452, Ap
282	58	11.6	1491	7	US-11-649-663A-382	Sequence 382, App	358	57	11.4	1485	7	US-11-649-663A-2522	Sequence 2522, Ap
283	58	11.6	1492	7	US-11-649-663A-2094	Sequence 2094, Ap	359	57	11.4	1533	7	US-11-649-663A-78	Sequence 78, Appl
284	58	11.6	1575	7	US-11-649-663A-2648	Sequence 2648, Ap	360	57	11.4	1555	7	US-11-649-663A-1366	Sequence 1366, Ap
285	58	11.6	1577	7	US-11-649-663A-396	Sequence 396, App	361	57	11.4	1596	7	US-11-649-663A-792	Sequence 792, App
286	58	11.6	1638	7	US-11-649-663A-660	Sequence 660, App	362	57	11.4	1709	7	US-11-649-663A-3210	Sequence 3210, Ap
287	58	11.6	1656	7	US-11-649-663A-3004	Sequence 3004, Ap	363	57	11.4	1737	7	US-11-649-663A-674	Sequence 674, App
288	58	11.6	1689	7	US-11-649-663A-1196	Sequence 1196, Ap	364	57	11.4	1750	7	US-11-649-663A-570	Sequence 570, App
289	58	11.6	1745	7	US-11-649-663A-960	Sequence 960, App	365	57	11.4	1751	7	US-11-649-663A-2426	Sequence 2426, Ap
290	58	11.6	1773	7	US-11-649-663A-1710	Sequence 1710, Ap	366	57	11.4	1764	7	US-11-649-663A-2034	Sequence 2034, Ap
291	58	11.6	2088	7	US-11-649-663A-4996	Sequence 4996, Ap	367	57	11.4	1867	7	US-11-649-663A-406	Sequence 406, App
292	58	11.6	2628	7	US-11-649-663A-2692	Sequence 2692, Ap	368	57	11.4	1868	7	US-11-649-663A-2604	Sequence 2604, Ap
293	57.5	11.5	280	7	US-11-656-491-5395	Sequence 5395, Ap	369	57	11.4	1872	7	US-11-649-663A-2266	Sequence 2266, Ap
294	57.5	11.5	328	7	US-11-713-768-9512	Sequence 9512, Ap	370	57	11.4	1872	7	US-11-649-663A-1664	Sequence 1664, Ap
295	57.5	11.5	369	6	US-10-767-701-47121	Sequence 47121, A	371	57	11.4	1945	7	US-11-649-663A-1972	Sequence 1972, Ap
296	57.5	11.5	420	7	US-11-713-768-9511	Sequence 9511, Ap	372	57	11.4	2017	7	US-11-649-663A-2682	Sequence 2682, Ap
297	57.5	11.5	442	7	US-11-689-173-3303	Sequence 9303, Ap	373	57	11.4	2045	7	US-11-649-663A-2726	Sequence 2726, Ap
298	57.5	11.5	493	7	US-11-713-768-9510	Sequence 9510, Ap	374	57	11.4	2072	7	US-11-649-663A-1184	Sequence 1184, Ap
299	57.5	11.5	493	7	US-11-713-768-9510	Sequence 9510, Ap	375	57	11.4	2079	7	US-11-649-663A-2126	Sequence 2126, Ap
300	57.5	11.5	678	7	US-11-649-663A-3924	Sequence 3924, Ap	376	57	11.4	2079	7	US-11-649-663A-2408	Sequence 2408, Ap
301	57.5	11.5	745	7	US-11-537-235-68	Sequence 68, Appl	377	57	11.4	2355	7	US-11-625-272-147	Sequence 147, App
302	57.5	11.5	745	7	US-11-553-810-68	Sequence 5, Appl	378	57	11.4	2386	7	US-11-707-223-32	Sequence 32, Appl
303	57.5	11.5	991	6	US-10-481-700-5	Sequence 5, Appl	379	57	11.4	2472	7	US-11-649-663A-1716	Sequence 1716, Ap
304	57.5	11.5	1070	7	US-11-649-663A-2300	Sequence 2300, Ap	380	57	11.4	2643	7	US-11-649-663A-1864	Sequence 1864, Ap
305	57.5	11.5	1092	7	US-11-649-663A-912	Sequence 912, App	381	57	11.4	2643	7	US-11-649-663A-1864	Sequence 1864, Ap
306	57.5	11.5	1223	7	US-11-649-663A-2472	Sequence 2472, Ap	382	57	11.4	3250	7	US-11-649-663A-2262	Sequence 2262, Ap
307	57.5	11.5	1232	7	US-11-649-663A-2840	Sequence 2840, Ap	383	57	11.4	3331	7	US-11-649-663A-1574	Sequence 1574, Ap
308	57.5	11.5	1356	7	US-11-716-794-17	Sequence 17, Appl	384	57	11.4	3682	7	US-11-649-663A-2486	Sequence 2486, Ap
309	57.5	11.5	1396	7	US-11-649-663A-1102	Sequence 1102, Ap	385	57	11.4	6498	7	US-11-726-028-8	Sequence 8, Appl
310	57.5	11.5	1504	7	US-11-649-663A-932	Sequence 932, App	386	57	11.4	62	7	US-11-518-590-508	Sequence 508, App
311	57.5	11.5	1506	7	US-11-649-663A-1992	Sequence 1992, Ap	387	56.5	11.3	143	6	US-10-438-246-33361	Sequence 33361, A
312	57.5	11.5	1530	7	US-11-649-663A-1862	Sequence 1862, Ap	388	56.5	11.3	231	7	US-11-360-355-151313	Sequence 151313,
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315	57.5	11.5	1709	7	US-11-649-663A-2970	Sequence 2970, Ap	391	56.5	11.3	439	7	US-11-713-768-6832	Sequence 6832, Ap
316	57.5	11.5	1754	7	US-11-649-663A-2600	Sequence 2600, Ap	392	56.5	11.3	462	7	US-11-713-768-6831	Sequence 6831, Ap
317	57.5	11.5	1758	7	US-11-649-663A-2310	Sequence 2310, Ap	393	56.5	11.3	463	7	US-11-649-663A-80	Sequence 80, Appl
318	57.5	11.5	1765	7	US-11-649-663A-2282	Sequence 2282, Ap	394	56.5	11.3	480	7	US-11-713-768-6830	Sequence 6830, Ap
319	57.5	11.5	1783	7	US-11-649-663A-902	Sequence 902, App	395	56.5	11.3	575	7	US-11-689-173-6159	Sequence 6159, Ap
320	57.5	11.5	1821	7	US-11-649-663A-2108	Sequence 2108, Ap	396	56.5	11.3	575	7	US-11-689-173-9411	Sequence 9411, Ap
321	57.5	11.5	1913	6	US-10-529-351A-5	Sequence 5, Appl		56.5	11.3	659	7	US-11-649-663A-614	Sequence 614, App

397	56.5	11.3	876	7	US-11-649-663A-144	Sequence 144, App	470	56	11.2	1572	7	US-11-649-663A-1326	Sequence 1326, Ap
398	56.5	11.3	909	7	US-11-649-663A-1506	Sequence 1506, Ap	471	56	11.2	1710	7	US-11-649-663A-1588	Sequence 1588, Ap
399	56.5	11.3	910	7	US-11-649-663A-2232	Sequence 2232, Ap	472	56	11.2	1721	7	US-11-649-663A-968	Sequence 968, App
400	56.5	11.3	914	6	US-10-438-246-20354	Sequence 20354, A	473	56	11.2	1761	7	US-11-649-663A-3708	Sequence 3708, Ap
401	56.5	11.3	923	7	US-11-649-663A-4314	Sequence 4314, Ap	474	56	11.2	1768	7	US-11-649-663A-1220	Sequence 1220, Ap
402	56.5	11.3	978	7	US-11-649-663A-1320	Sequence 120, App	475	56	11.2	1884	7	US-11-649-663A-2588	Sequence 2588, Ap
403	56.5	11.3	1042	7	US-11-649-663A-356	Sequence 356, App	476	56	11.2	1919	7	US-11-649-663A-978	Sequence 978, App
404	56.5	11.3	1042	7	US-11-649-663A-2500	Sequence 2500, Ap	477	56	11.2	1942	7	US-11-649-663A-1296	Sequence 1296, Ap
405	56.5	11.3	1052	7	US-11-649-663A-1750	Sequence 1750, Ap	478	56	11.2	1957	7	US-11-649-663A-2192	Sequence 2192, Ap
406	56.5	11.3	1136	7	US-11-649-663A-2400	Sequence 2400, Ap	479	56	11.2	1962	7	US-11-649-663A-1446	Sequence 1446, Ap
407	56.5	11.3	1150	7	US-11-713-768-86061	Sequence 86061, A	480	56	11.2	2052	7	US-11-649-663A-1454	Sequence 1454, Ap
408	56.5	11.3	1170	7	US-11-713-768-86060	Sequence 86060, A	481	56	11.2	2077	7	US-11-649-663A-778	Sequence 778, App
409	56.5	11.3	1190	6	US-10-438-246-19095	Sequence 19095, A	482	56	11.2	2101	7	US-11-649-663A-2010	Sequence 2010, Ap
410	56.5	11.3	1304	7	US-11-649-663A-2586	Sequence 2586, Ap	483	56	11.2	2110	7	US-11-649-663A-1564	Sequence 1564, Ap
411	56.5	11.3	1305	7	US-11-649-663A-2140	Sequence 2140, Ap	484	56	11.2	2415	7	US-11-649-663A-90	Sequence 90, Appl
412	56.5	11.3	1319	6	US-10-438-246-19056	Sequence 19056, A	485	56	11.2	2568	7	US-11-649-663A-722	Sequence 722, App
413	56.5	11.3	1319	6	US-10-438-246-25888	Sequence 25888, A	486	56	11.2	2782	7	US-11-625-272-151	Sequence 151, App
414	56.5	11.3	1337	7	US-11-649-663A-2460	Sequence 2460, Ap	487	56	11.2	5405	7	US-11-528-927-571	Sequence 571, App
415	56.5	11.3	1337	7	US-11-649-663A-518	Sequence 518, App	488	55.5	11.1	42	7	US-11-528-950-571	Sequence 571, App
416	56.5	11.3	1377	7	US-11-649-663A-2196	Sequence 2196, Ap	489	55.5	11.1	42	6	US-10-438-246-32293	Sequence 32293, A
417	56.5	11.3	1436	6	US-10-438-246-19057	Sequence 19057, A	490	55.5	11.1	97	6	US-10-767-701-32134	Sequence 32134, A
418	56.5	11.3	1478	7	US-11-649-663A-710	Sequence 710, App	491	55.5	11.1	183	6	US-10-767-701-45523	Sequence 45523, A
419	56.5	11.3	1610	7	US-11-649-663A-1688	Sequence 1688, Ap	492	55.5	11.1	184	6	US-10-767-701-45523	Sequence 45523, A
420	56.5	11.3	1617	7	US-11-649-663A-2448	Sequence 2448, Ap	493	55.5	11.1	264	7	US-11-713-768-89430	Sequence 89430, A
421	56.5	11.3	1655	6	US-10-438-246-25931	Sequence 25931, A	494	55.5	11.1	264	7	US-11-713-768-93186	Sequence 93186, A
422	56.5	11.3	1655	7	US-11-649-663A-2908	Sequence 2908, Ap	495	55.5	11.1	438	7	US-11-649-663A-1434	Sequence 1434, Ap
423	56.5	11.3	1680	7	US-11-649-663A-598	Sequence 598, App	496	55.5	11.1	439	7	US-11-713-768-6544	Sequence 6544, Ap
424	56.5	11.3	1695	7	US-11-649-663A-3178	Sequence 3178, App	497	55.5	11.1	470	7	US-11-713-768-6543	Sequence 6543, Ap
425	56.5	11.3	1779	7	US-11-649-663A-1438	Sequence 1438, Ap	498	55.5	11.1	505	7	US-11-713-768-6542	Sequence 6542, Ap
426	56.5	11.3	1782	7	US-11-649-663A-1652	Sequence 1652, Ap	499	55.5	11.1	839	7	US-11-649-663A-2580	Sequence 2580, Ap
427	56.5	11.3	1788	6	US-10-438-246-19513	Sequence 19513, A	500	55.5	11.1	843	6	US-10-438-246-10849	Sequence 10849, A
428	56.5	11.3	1796	7	US-11-649-663A-910	Sequence 910, App	501	55.5	11.1	1005	7	US-11-649-663A-1158	Sequence 1158, A
429	56.5	11.3	1814	7	US-11-649-663A-1302	Sequence 1302, App	502	55.5	11.1	1015	7	US-11-649-663A-330	Sequence 330, App
430	56.5	11.3	1865	7	US-11-649-663A-1078	Sequence 1078, App	503	55.5	11.1	1049	7	US-11-649-663A-624	Sequence 624, App
431	56.5	11.3	1865	7	US-11-649-663A-692	Sequence 692, App	504	55.5	11.1	1066	7	US-11-649-663A-1402	Sequence 1402, Ap
432	56.5	11.3	1933	7	US-11-649-663A-2226	Sequence 2226, Ap	505	55.5	11.1	1098	7	US-11-649-663A-400	Sequence 400, App
433	56.5	11.3	2250	7	US-11-649-663A-1394	Sequence 1394, Ap	506	55.5	11.1	1099	7	US-11-649-663A-1142	Sequence 1142, Ap
434	56.5	11.3	2440	7	US-11-649-663A-1294	Sequence 1294, Ap	507	55.5	11.1	1187	7	US-11-649-663A-1696	Sequence 1696, Ap
435	56.5	11.3	2773	7	US-11-649-663A-1466	Sequence 1466, Ap	508	55.5	11.1	1212	7	US-11-649-663A-1968	Sequence 1968, Ap
436	56.5	11.3	2791	7	US-11-649-663A-2826	Sequence 2826, Ap	509	55.5	11.1	1242	7	US-11-649-663A-4164	Sequence 4164, Ap
437	56.5	11.3	3409	7	US-11-257-477-165	Sequence 165, App	510	55.5	11.1	1307	7	US-11-649-663A-2318	Sequence 2318, Ap
438	56.5	11.3	4753	7	US-11-673-351-247	Sequence 247, App	511	55.5	11.1	1365	7	US-11-649-663A-662	Sequence 662, App
439	56	11.2	124	7	US-11-713-768-17338	Sequence 17338, A	512	55.5	11.1	1446	7	US-11-649-663A-1308	Sequence 1308, Ap
440	56	11.2	132	7	US-11-713-768-85497	Sequence 85497, A	513	55.5	11.1	1463	7	US-11-649-663A-1162	Sequence 1162, Ap
441	56	11.2	132	7	US-11-713-768-96353	Sequence 96353, A	514	55.5	11.1	1481	7	US-11-649-663A-2972	Sequence 2972, Ap
442	56	11.2	163	7	US-11-713-768-85496	Sequence 85496, A	515	55.5	11.1	1487	7	US-11-649-663A-2972	Sequence 2972, Ap
443	56	11.2	163	7	US-11-713-768-96352	Sequence 96352, A	516	55.5	11.1	1516	7	US-11-649-663A-718	Sequence 718, App
444	56	11.2	208	7	US-11-713-768-64492	Sequence 64492, A	517	55.5	11.1	1698	7	US-11-649-663A-3720	Sequence 3720, Ap
445	56	11.2	264	7	US-11-725-235-146	Sequence 146, App	518	55.5	11.1	1713	7	US-11-649-663A-726	Sequence 726, App
446	56	11.2	264	7	US-11-728-567-710	Sequence 710, App	519	55.5	11.1	1741	7	US-11-649-663A-526	Sequence 526, App
447	56	11.2	264	7	US-11-713-768-96351	Sequence 96351, A	520	55.5	11.1	1775	7	US-11-649-663A-2856	Sequence 2856, Ap
448	56	11.2	265	7	US-11-713-768-106290	Sequence 106290, A	521	55.5	11.1	1784	7	US-11-649-663A-2054	Sequence 2054, Ap
449	56	11.2	270	7	US-11-713-768-106289	Sequence 106289, A	522	55.5	11.1	1809	7	US-11-649-663A-2350	Sequence 2350, Ap
450	56	11.2	515	7	US-11-360-355-132122	Sequence 132122, A	523	55.5	11.1	1832	7	US-11-649-663A-1242	Sequence 1242, Ap
451	56	11.2	657	7	US-11-649-663A-512	Sequence 512, App	524	55.5	11.1	1847	7	US-11-649-663A-3118	Sequence 3118, Ap
452	56	11.2	754	7	US-11-713-768-81272	Sequence 81272, A	525	55.5	11.1	1951	7	US-11-649-663A-998	Sequence 998, App
453	56	11.2	826	7	US-11-713-768-81271	Sequence 81271, A	526	55.5	11.1	1962	7	US-11-649-663A-1378	Sequence 1378, Ap
454	56	11.2	849	7	US-11-713-768-81270	Sequence 81270, A	527	55.5	11.1	1973	7	US-11-649-663A-5472	Sequence 5472, Ap
455	56	11.2	929	7	US-11-649-663A-3988	Sequence 3988, Ap	528	55.5	11.1	2325	7	US-11-649-663A-2802	Sequence 2802, Ap
456	56	11.2	945	7	US-11-649-663A-782	Sequence 782, App	529	55.5	11.1	3658	7	US-11-649-663A-2802	Sequence 2802, Ap
457	56	11.2	1050	7	US-11-649-663A-720	Sequence 720, App	530	55.5	11.1	3723	7	US-11-360-355-164877	Sequence 164877, A
458	56	11.2	1059	7	US-11-649-663A-1950	Sequence 1950, App	531	55	11.0	136	7	US-10-438-246-6500	Sequence 6500, Ap
459	56	11.2	1135	7	US-11-649-663A-2204	Sequence 2204, App	532	55	11.0	139	6	US-10-438-246-6500	Sequence 134059, A
460	56	11.2	1144	7	US-11-649-663A-506	Sequence 506, App	533	55	11.0	156	6	US-11-360-355-155165	Sequence 155165, A
461	56	11.2	1220	7	US-11-649-663A-1542	Sequence 1542, Ap	534	55	11.0	160	7	US-11-360-355-155165	Sequence 16685, A
462	56	11.2	1285	7	US-11-649-663A-1124	Sequence 1124, Ap	535	55	11.0	176	6	US-10-438-246-16685	Sequence 40420, A
463	56	11.2	1299	7	US-11-649-663A-1524	Sequence 1524, Ap	536	55	11.0	196	6	US-10-438-246-6484	Sequence 6484, Ap
464	56	11.2	1403	7	US-11-649-663A-738	Sequence 738, App	537	55	11.0	200	6	US-10-438-246-6484	Sequence 6488, Ap
465	56	11.2	1437	7	US-11-649-663A-1332	Sequence 1332, App	538	55	11.0	201	6	US-10-438-246-6488	Sequence 48, Appl
466	56	11.2	1459	7	US-11-649-663A-880	Sequence 880, App	539	55	11.0	222	7	US-11-552-437-48	Sequence 24892, A
467	56	11.2	1495	7	US-11-649-663A-1656	Sequence 1656, Ap	541	55	11.0	230	6	US-10-438-246-16684	Sequence 16684, A
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469	56	11.2	1518	7	US-11-649-663A-742	Sequence 742, App	543	55	11.0				

544	55	11.0	387	6	US-10-438-246-24133	Sequence 24133, A	617	54.5	10.9	161	6	US-10-438-246-26350	Sequence 26350, A
545	55	11.0	484	7	US-11-713-768-91092	Sequence 91092, A	618	54.5	10.9	216	6	US-10-438-246-25376	Sequence 25376, A
546	55	11.0	484	7	US-11-713-768-94848	Sequence 94848, A	619	54.5	10.9	221	7	US-11-360-355-135854	Sequence 135854, A
547	55	11.0	485	7	US-11-713-768-91091	Sequence 91091, A	620	54.5	10.9	259	6	US-10-551-004-45	Sequence 45, Appl
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549	55	11.0	486	7	US-11-713-768-91090	Sequence 91090, A	622	54.5	10.9	259	7	US-11-537-235-300	Sequence 300, Appl
550	55	11.0	486	7	US-11-713-768-94846	Sequence 94846, A	623	54.5	10.9	282	6	US-10-553-810-300	Sequence 1230, Appl
551	55	11.0	587	7	US-11-713-768-43888	Sequence 43888, A	624	54.5	10.9	282	6	US-10-529-351A-5217	Sequence 5217, Appl
552	55	11.0	618	6	US-10-529-351A-5433	Sequence 5433, Appl	625	54.5	10.9	282	7	US-11-537-235-312	Sequence 312, Appl
553	55	11.0	619	7	US-11-649-663A-522	Sequence 522, Appl	626	54.5	10.9	282	7	US-11-553-810-312	Sequence 312, Appl
554	55	11.0	642	7	US-11-112-327-11	Sequence 11, Appl	627	54.5	10.9	305	7	US-11-713-768-56489	Sequence 56489, A
555	55	11.0	794	7	US-11-713-768-45043	Sequence 45043, A	628	54.5	10.9	356	7	US-11-713-768-56488	Sequence 56488, A
556	55	11.0	794	7	US-11-713-768-45791	Sequence 45791, A	629	54.5	10.9	371	7	US-11-713-768-56487	Sequence 56487, A
557	55	11.0	794	7	US-11-713-768-46386	Sequence 46386, A	630	54.5	10.9	809	7	US-11-649-663A-5486	Sequence 5486, Appl
558	55	11.0	795	7	US-11-649-663A-1856	Sequence 1856, Appl	631	54.5	10.9	869	7	US-11-673-351-1200	Sequence 1200, Appl
559	55	11.0	853	7	US-11-713-768-45042	Sequence 45042, A	632	54.5	10.9	879	7	US-11-649-663A-1938	Sequence 1938, Appl
560	55	11.0	853	7	US-11-713-768-45790	Sequence 45790, A	633	54.5	10.9	891	7	US-11-649-663A-1484	Sequence 1484, Appl
561	55	11.0	853	7	US-11-713-768-46385	Sequence 46385, A	634	54.5	10.9	1043	6	US-10-438-246-33504	Sequence 33504, A
562	55	11.0	856	7	US-11-713-768-45041	Sequence 45041, A	635	54.5	10.9	1061	7	US-11-649-663A-328	Sequence 328, Appl
563	55	11.0	856	7	US-11-713-768-45789	Sequence 45789, A	636	54.5	10.9	1151	7	US-11-649-663A-556	Sequence 556, Appl
564	55	11.0	856	7	US-11-713-768-46384	Sequence 46384, A	637	54.5	10.9	1170	7	US-11-649-663A-1300	Sequence 1300, Appl
565	55	11.0	987	7	US-11-649-663A-236	Sequence 236, Appl	638	54.5	10.9	1177	7	US-11-649-663A-884	Sequence 884, Appl
566	55	11.0	1017	7	US-11-649-663A-3140	Sequence 3140, Appl	639	54.5	10.9	1195	7	US-11-649-663A-2420	Sequence 2420, Appl
567	55	11.0	1036	7	US-11-234-694-104	Sequence 104, Appl	640	54.5	10.9	1199	7	US-11-649-663A-392	Sequence 392, Appl
568	55	11.0	1037	7	US-11-633-858-230	Sequence 230, Appl	641	54.5	10.9	1201	7	US-11-649-663A-2186	Sequence 2186, Appl
569	55	11.0	1047	7	US-11-649-663A-1534	Sequence 1534, Appl	642	54.5	10.9	1218	6	US-10-594-211-169	Sequence 169, Appl
570	55	11.0	1069	7	US-11-649-663A-1228	Sequence 1228, Appl	643	54.5	10.9	1218	6	US-10-594-211-245	Sequence 245, Appl
571	55	11.0	1073	7	US-11-649-663A-1312	Sequence 1312, Appl	644	54.5	10.9	1218	6	US-10-594-211-252	Sequence 252, Appl
572	55	11.0	1076	7	US-11-537-235-219	Sequence 219, Appl	645	54.5	10.9	1218	7	US-11-625-272-154	Sequence 154, Appl
573	55	11.0	1076	7	US-11-553-810-219	Sequence 219, Appl	646	54.5	10.9	1218	7	US-11-633-858-194	Sequence 194, Appl
574	55	11.0	1117	7	US-11-649-663A-1458	Sequence 1458, Appl	647	54.5	10.9	1224	7	US-11-649-663A-1958	Sequence 1958, Appl
575	55	11.0	1143	7	US-11-649-663A-492	Sequence 492, Appl	648	54.5	10.9	1242	7	US-11-649-663A-1616	Sequence 1616, Appl
576	55	11.0	1263	7	US-11-649-663A-1290	Sequence 1290, Appl	649	54.5	10.9	1244	7	US-11-649-663A-368	Sequence 368, Appl
577	55	11.0	1268	7	US-11-649-663A-744	Sequence 744, Appl	650	54.5	10.9	1270	7	US-11-649-663A-444	Sequence 444, Appl
578	55	11.0	1292	7	US-11-649-663A-750	Sequence 750, Appl	651	54.5	10.9	1287	7	US-11-649-663A-1772	Sequence 1772, Appl
579	55	11.0	1326	7	US-11-649-663A-592	Sequence 592, Appl	652	54.5	10.9	1362	7	US-11-649-663A-448	Sequence 448, Appl
580	55	11.0	1333	7	US-11-649-663A-1258	Sequence 1258, Appl	653	54.5	10.9	1403	7	US-11-649-663A-448	Sequence 448, Appl
581	55	11.0	1349	7	US-11-649-663A-2452	Sequence 2452, Appl	654	54.5	10.9	1407	7	US-11-649-663A-464	Sequence 464, Appl
582	55	11.0	1359	7	US-11-649-663A-3585	Sequence 3585, Appl	655	54.5	10.9	1408	7	US-11-649-663A-2510	Sequence 2510, Appl
583	55	11.0	1424	7	US-11-649-663A-504	Sequence 504, Appl	656	54.5	10.9	1416	7	US-11-649-663A-1480	Sequence 1480, Appl
584	55	11.0	1424	7	US-11-649-663A-2542	Sequence 2542, Appl	657	54.5	10.9	1434	7	US-11-649-663A-1194	Sequence 1194, Appl
585	55	11.0	1431	7	US-11-649-663A-1112	Sequence 1112, Appl	658	54.5	10.9	1459	7	US-11-649-663A-3196	Sequence 3196, Appl
586	55	11.0	1442	7	US-11-649-663A-1084	Sequence 1084, Appl	659	54.5	10.9	1507	7	US-11-649-663A-2476	Sequence 2476, Appl
587	55	11.0	1448	7	US-11-649-663A-2194	Sequence 2194, Appl	660	54.5	10.9	1614	7	US-11-649-663A-484	Sequence 484, Appl
588	55	11.0	1459	7	US-11-649-663A-1350	Sequence 1350, Appl	661	54.5	10.9	1618	7	US-11-649-663A-2748	Sequence 2748, Appl
589	55	11.0	1471	7	US-11-649-663A-2316	Sequence 2316, Appl	662	54.5	10.9	1628	7	US-11-649-663A-2406	Sequence 2406, Appl
590	55	11.0	1473	7	US-11-649-663A-1486	Sequence 1486, Appl	663	54.5	10.9	1633	7	US-11-649-663A-1752	Sequence 1752, Appl
591	55	11.0	1476	7	US-11-649-663A-972	Sequence 972, Appl	664	54.5	10.9	1713	7	US-11-649-663A-5198	Sequence 5198, Appl
592	55	11.0	1482	7	US-11-649-663A-1804	Sequence 1804, Appl	665	54.5	10.9	1730	7	US-11-649-663A-802	Sequence 802, Appl
593	55	11.0	1486	7	US-11-649-663A-684	Sequence 684, Appl	666	54.5	10.9	1753	7	US-11-649-663A-1440	Sequence 1440, Appl
594	55	11.0	1486	7	US-11-649-663A-2236	Sequence 2236, Appl	667	54.5	10.9	1757	6	US-10-438-246-19207	Sequence 19207, A
595	55	11.0	1523	7	US-11-649-663A-786	Sequence 786, Appl	668	54.5	10.9	1783	7	US-11-649-663A-1440	Sequence 1440, Appl
596	55	11.0	1530	7	US-11-649-663A-854	Sequence 854, Appl	669	54.5	10.9	1786	7	US-11-649-663A-602	Sequence 602, Appl
597	55	11.0	1587	7	US-11-649-663A-2652	Sequence 2652, Appl	670	54.5	10.9	1805	6	US-10-438-246-19228	Sequence 19228, A
598	55	11.0	1592	7	US-11-649-663A-5088	Sequence 5088, Appl	671	54.5	10.9	1806	6	US-10-438-246-25826	Sequence 25826, A
599	55	11.0	1601	7	US-11-649-663A-2364	Sequence 2364, Appl	672	54.5	10.9	1917	7	US-11-649-663A-2172	Sequence 2172, Appl
600	55	11.0	1611	7	US-11-649-663A-2234	Sequence 2234, Appl	673	54.5	10.9	2148	7	US-11-649-663A-2000	Sequence 2000, Appl
601	55	11.0	1611	7	US-11-649-663A-2552	Sequence 2552, Appl	674	54.5	10.9	2337	7	US-11-649-663A-1868	Sequence 1868, Appl
602	55	11.0	1629	7	US-11-649-663A-2828	Sequence 2828, Appl	675	54.5	10.9	2433	7	US-11-649-663A-1618	Sequence 1618, Appl
603	55	11.0	1655	7	US-11-649-663A-962	Sequence 962, Appl	676	54.5	10.9	2647	6	US-10-594-211-324	Sequence 324, Appl
604	55	11.0	1665	7	US-11-649-663A-1726	Sequence 1726, Appl	677	54.5	10.9	2647	6	US-10-594-211-325	Sequence 225, Appl
605	55	11.0	1680	7	US-11-649-663A-712	Sequence 712, Appl	678	54.5	10.9	2647	6	US-10-594-211-325	Sequence 235, Appl
606	55	11.0	1696	7	US-11-649-663A-1464	Sequence 1464, Appl	679	54.5	10.9	2647	7	US-11-625-272-182	Sequence 182, Appl
607	55	11.0	1740	7	US-11-649-663A-1390	Sequence 1390, Appl	680	54.5	10.9	2762	7	US-11-649-663A-2672	Sequence 2672, Appl
608	55	11.0	1818	7	US-11-649-663A-2842	Sequence 2842, Appl	681	54.5	10.9	2973	7	US-11-649-663A-1754	Sequence 1754, Appl
609	55	11.0	1964	7	US-11-649-663A-4458	Sequence 4458, Appl	682	54.5	10.9	3018	7	US-11-649-663A-1996	Sequence 1996, Appl
610	55	11.0	2003	7	US-11-649-663A-5496	Sequence 5496, Appl	683	54	10.8	48	7	US-11-528-927-307	Sequence 307, Appl
611	55	11.0	2085	7	US-11-649-663A-954	Sequence 954, Appl	684	54	10.8	48	7	US-11-528-950-307	Sequence 307, Appl
612	55	11.0	2384	7	US-11-649-663A-1740	Sequence 1740, Appl	685	54	10.8	99	6	US-10-767-701-57968	Sequence 57968, A
613	55	11.0	2757	7	US-11-649-663A-1642	Sequence 1642, Appl	686	54	10.8	116	7	US-11-689-173-11222	Sequence 11222, A
614	55	11.0	3291	7	US-11-649-663A-2666	Sequence 2666, Appl	687	54	10.8	116	7	US-11-689-173-11223	Sequence 11223, A
615	55	11.0	3312	6	US-10-529-351A-1133	Sequence 1133, Appl	688	54	10.8	116	7	US-11-689-173-11224	Sequence 11224, A
616	54.5	10.9	123	6	US-10-767-701-48946	Sequence 48946, A	689	54	10.8	132	6	US-10-529-351A-5782	Sequence 5782, Appl

690	10.8	132	7	US-11-699-229-63	Sequence 63, Appl	763	54	10.8	1648	7	US-11-649-663A-670	Sequence 670, App
691	10.8	132	7	US-11-403-116-1251	Sequence 2291, Ap	764	54	10.8	1659	7	US-11-649-663A-984	Sequence 984, App
692	10.8	143	7	US-11-713-768-25639	Sequence 25639, A	765	54	10.8	1659	7	US-11-649-663A-1758	Sequence 1758, Ap
693	10.8	147	6	US-10-438-246-18310	Sequence 18310, A	766	54	10.8	1686	7	US-11-649-663A-866	Sequence 866, App
694	10.8	162	6	US-10-767-701-34897	Sequence 34897, A	767	54	10.8	1753	7	US-11-649-663A-1222	Sequence 1222, Ap
695	10.8	183	7	US-11-713-768-109320	Sequence 109320, A	768	54	10.8	1761	7	US-11-649-663A-1306	Sequence 1306, Ap
696	10.8	186	6	US-10-438-246-33422	Sequence 33422, A	769	54	10.8	1763	7	US-11-649-663A-2674	Sequence 2674, Ap
697	10.8	195	6	US-10-438-246-9719	Sequence 9719, Ap	770	54	10.8	1763	7	US-11-649-663A-2112	Sequence 2112, Ap
698	10.8	209	7	US-11-360-355-133807	Sequence 133807, A	771	54	10.8	1766	7	US-11-649-663A-1944	Sequence 1944, Ap
699	10.8	216	7	US-11-713-768-109319	Sequence 109319, A	772	54	10.8	1767	7	US-11-649-663A-928	Sequence 928, App
700	10.8	224	7	US-11-713-768-109318	Sequence 109318, A	773	54	10.8	1771	7	US-11-649-663A-780	Sequence 780, App
701	10.8	280	7	US-11-713-768-74373	Sequence 74373, A	774	54	10.8	1782	7	US-11-649-663A-1774	Sequence 1774, Ap
702	10.8	280	7	US-11-713-768-107866	Sequence 107866, A	775	54	10.8	1785	7	US-11-649-663A-1192	Sequence 1192, Ap
703	10.8	281	7	US-11-713-768-74372	Sequence 74372, A	776	54	10.8	1792	7	US-11-649-663A-586	Sequence 586, App
704	10.8	281	7	US-11-713-768-107865	Sequence 107865, A	777	54	10.8	1818	7	US-11-649-663A-732	Sequence 732, App
705	10.8	281	7	US-11-360-355-133206	Sequence 133206, A	778	54	10.8	1818	7	US-11-649-663A-1744	Sequence 1744, Ap
706	10.8	322	7	US-11-713-768-107864	Sequence 107864, A	779	54	10.8	1861	7	US-11-649-663A-4320	Sequence 4320, Ap
707	10.8	323	7	US-11-713-768-107864	Sequence 107864, A	780	54	10.8	1868	7	US-11-649-663A-846	Sequence 846, App
708	10.8	516	7	US-11-649-663A-2272	Sequence 2272, Ap	781	54	10.8	1873	7	US-11-649-663A-1358	Sequence 1358, Ap
709	10.8	621	7	US-11-537-235-40	Sequence 40, Appl	782	54	10.8	2010	7	US-11-649-663A-530	Sequence 530, App
710	10.8	621	7	US-11-537-235-40	Sequence 40, Appl	783	54	10.8	2180	7	US-11-649-663A-206	Sequence 206, App
711	10.8	721	7	US-10-581-008-8	Sequence 8, Appl	784	54	10.8	3183	7	US-11-673-351-206	Sequence 1722, Ap
712	10.8	732	6	US-10-529-351A-5932	Sequence 5932, Ap	785	54	10.8	4243	7	US-11-649-663A-1722	Sequence 1722, Ap
713	10.8	732	6	US-10-529-351A-5932	Sequence 5932, Ap	786	53.5	10.7	205	6	US-10-767-701-59788	Sequence 59788, A
714	10.8	732	7	US-11-730-664-4	Sequence 4, Appl	787	53.5	10.7	229	6	US-10-767-701-42171	Sequence 42171, A
715	10.8	770	7	US-11-713-768-75353	Sequence 75253, A	788	53.5	10.7	271	7	US-11-257-477-25	Sequence 25, Appl
716	10.8	931	7	US-11-713-768-103525	Sequence 103525, A	789	53.5	10.7	291	7	US-11-713-768-55600	Sequence 55600, A
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719	10.8	976	7	US-11-649-663A-1470	Sequence 1470, Ap	792	53.5	10.7	353	7	US-11-537-235-296	Sequence 296, App
720	10.8	1039	7	US-11-713-768-75252	Sequence 75252, A	793	53.5	10.7	353	7	US-11-553-810-296	Sequence 296, App
721	10.8	1044	7	US-11-713-768-75251	Sequence 75251, A	795	53.5	10.7	513	7	US-11-649-663A-3284	Sequence 3284, Ap
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724	10.8	1077	7	US-11-649-663A-1630	Sequence 1630, Ap	798	53.5	10.7	831	7	US-11-445-001-85	Sequence 85, Appl
725	10.8	1108	7	US-11-649-663A-1122	Sequence 1122, Ap	799	53.5	10.7	863	7	US-11-649-663A-2446	Sequence 2446, Ap
726	10.8	1136	7	US-11-649-663A-2504	Sequence 2504, Ap	800	53.5	10.7	871	7	US-11-445-001-86	Sequence 86, Appl
727	10.8	1146	7	US-11-649-663A-84	Sequence 84, Appl	801	53.5	10.7	873	7	US-11-649-663A-1072	Sequence 1072, Ap
728	10.8	1146	7	US-11-649-663A-2372	Sequence 2372, Ap	802	53.5	10.7	907	7	US-11-649-663A-1040	Sequence 1040, Ap
729	10.8	1167	7	US-11-649-663A-2734	Sequence 2734, Ap	803	53.5	10.7	979	7	US-11-810-968-55	Sequence 55, Appl
730	10.8	1206	7	US-11-649-663A-916	Sequence 916, App	804	53.5	10.7	979	7	US-11-810-968-58	Sequence 58, Appl
731	10.8	1209	7	US-11-649-663A-360	Sequence 360, App	805	53.5	10.7	987	6	US-10-438-246-25923	Sequence 25923, A
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733	10.8	1217	7	US-11-649-663A-4324	Sequence 4324, Ap	807	53.5	10.7	1111	7	US-11-510-314-4	Sequence 4, Appl
734	10.8	1220	7	US-11-649-663A-1024	Sequence 1024, Ap	808	53.5	10.7	1124	7	US-11-633-858-181	Sequence 181, App
735	10.8	1221	7	US-11-649-663A-1260	Sequence 1260, Ap	809	53.5	10.7	1125	7	US-11-649-663A-650	Sequence 650, App
736	10.8	1250	7	US-11-649-663A-1888	Sequence 1888, Ap	810	53.5	10.7	1143	7	US-11-649-663A-1918	Sequence 1918, Ap
737	10.8	1251	7	US-11-649-663A-426	Sequence 426, App	811	53.5	10.7	1164	7	US-11-649-663A-2218	Sequence 2218, Ap
738	10.8	1288	7	US-11-403-116-1110	Sequence 1110, Ap	812	53.5	10.7	1193	7	US-11-510-314-2	Sequence 2, Appl
739	10.8	1292	7	US-11-649-663A-1736	Sequence 1736, Ap	813	53.5	10.7	1220	7	US-11-649-663A-2404	Sequence 2404, Ap
740	10.8	1293	7	US-11-649-663A-824	Sequence 824, App	814	53.5	10.7	1221	7	US-11-649-663A-362	Sequence 362, App
741	10.8	1296	7	US-11-649-663A-2080	Sequence 2080, Ap	815	53.5	10.7	1289	7	US-11-649-663A-434	Sequence 434, App
742	10.8	1303	7	US-11-649-663A-1570	Sequence 1570, Ap	816	53.5	10.7	1300	6	US-11-649-663A-914	Sequence 13, Appl
743	10.8	1314	7	US-11-649-663A-736	Sequence 736, App	817	53.5	10.7	1329	7	US-10-481-700-13	Sequence 914, App
744	10.8	1324	7	US-11-649-663A-1210	Sequence 1210, Ap	818	53.5	10.7	1342	6	US-10-481-700-15	Sequence 15, App
745	10.8	1326	7	US-11-649-663A-1514	Sequence 1514, Ap	819	53.5	10.7	1346	7	US-11-649-663A-676	Sequence 676, App
746	10.8	1335	7	US-11-649-663A-3964	Sequence 3964, Ap	820	53.5	10.7	1353	6	US-10-481-700-14	Sequence 14, Appl
747	10.8	1346	7	US-11-649-663A-3122	Sequence 3122, Ap	821	53.5	10.7	1413	7	US-11-649-663A-654	Sequence 654, App
748	10.8	1367	7	US-11-649-663A-510	Sequence 510, App	822	53.5	10.7	1413	7	US-11-649-663A-936	Sequence 936, App
749	10.8	1370	7	US-11-649-663A-858	Sequence 858, App	823	53.5	10.7	1456	7	US-11-649-663A-1164	Sequence 1164, Ap
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753	10.8	1393	7	US-11-649-663A-606	Sequence 606, App	827	53.5	10.7	1481	7	US-11-649-663A-878	Sequence 878, App
754	10.8	1439	7	US-11-649-663A-3364	Sequence 3364, Ap	828	53.5	10.7	1493	7	US-11-649-663A-4196	Sequence 4196, Ap
755	10.8	1452	7	US-11-649-663A-38	Sequence 38, Appl	829	53.5	10.7	1518	7	US-11-714-684-212	Sequence 212, App
756	10.8	1480	7	US-11-649-663A-752	Sequence 752, App	830	53.5	10.7	1518	7	US-11-714-684-212	Sequence 212, App
757	10.8	1522	7	US-11-649-663A-3906	Sequence 3906, Ap	831	53.5	10.7	1521	7	US-11-649-663A-1956	Sequence 1956, Ap
758	10.8	1524	7	US-11-649-663A-2656	Sequence 2656, Ap	832	53.5	10.7	1534	7	US-11-649-663A-2156	Sequence 2156, Ap
759	10.8	1532	7	US-11-649-663A-2324	Sequence 2324, Ap	833	53.5	10.7	1542	7	US-11-649-663A-1248	Sequence 1248, Ap
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761	10.8	1605	7	US-11-649-663A-1410	Sequence 1410, Ap	835	53.5	10.7	1557	7	US-11-649-663A-1244	Sequence 1244, Ap
762	10.8	1610	7	US-11-649-663A-1472	Sequence 1472, Ap	836	53.5	10.7	1576	7	US-11-649-663A-594	Sequence 594, App

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838	53.5	10.7	1619	7	US-11-649-663A-2228	Sequence 2228, Ap	911	53	10.6	1159	7	US-11-649-663A-1666	Sequence 1666, Ap
839	53.5	10.7	1626	6	US-10-481-700-12	Sequence 12, Appl	912	53	10.6	1160	7	US-11-649-663A-2370	Sequence 2370, Ap
840	53.5	10.7	1655	7	US-11-649-663A-3630	Sequence 3630, Ap	913	53	10.6	1162	7	US-11-649-663A-2244	Sequence 2244, Ap
841	53.5	10.7	1659	7	US-11-649-663A-1436	Sequence 1436, Ap	914	53	10.6	1164	7	US-11-649-663A-338	Sequence 338, Ap
842	53.5	10.7	1668	6	US-10-481-700-7	Sequence 7, Appl	915	53	10.6	1182	7	US-11-649-663A-1872	Sequence 1872, Ap
843	53.5	10.7	1679	6	US-10-481-700-11	Sequence 11, Appl	916	53	10.6	1192	7	US-11-649-663A-2814	Sequence 2814, Ap
844	53.5	10.7	1691	7	US-11-649-663A-762	Sequence 762, App	917	53	10.6	1194	7	US-11-649-663A-5030	Sequence 5030, Ap
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858	53.5	10.7	1848	7	US-11-649-663A-1372	Sequence 1372, Ap	931	53	10.6	1345	7	US-11-649-663A-1146	Sequence 1146, Ap
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861	53.5	10.7	2175	7	US-11-649-663A-2008	Sequence 2008, Ap	934	53	10.6	1351	7	US-11-649-663A-2808	Sequence 2808, Ap
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863	53.5	10.7	2196	7	US-11-691-000-122	Sequence 122, App	936	53	10.6	1375	7	US-11-649-663A-2276	Sequence 2276, Ap
864	53.5	10.7	2411	7	US-11-649-663A-4618	Sequence 4618, Ap	937	53	10.6	1394	7	US-11-649-663A-640	Sequence 640, App
865	53.5	10.7	2598	7	US-11-649-663A-1488	Sequence 1488, Ap	938	53	10.6	1400	7	US-11-649-663A-446	Sequence 446, App
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868	53	10.6	187	7	US-11-713-768-38622	Sequence 38622, A	941	53	10.6	1409	7	US-11-649-663A-1732	Sequence 1732, Ap
869	53	10.6	187	7	US-11-713-768-77611	Sequence 77611, A	942	53	10.6	1422	7	US-11-649-663A-690	Sequence 690, App
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871	53	10.6	199	7	US-11-360-355-141763	Sequence 141763, A	944	53	10.6	1449	7	US-11-649-663A-1012	Sequence 1012, Ap
872	53	10.6	220	7	US-11-713-768-38621	Sequence 38621, A	945	53	10.6	1450	7	US-11-649-663A-2578	Sequence 2578, Ap
873	53	10.6	220	7	US-11-713-768-77611	Sequence 77611, A	946	53	10.6	1452	7	US-11-649-663A-4154	Sequence 4154, Ap
874	53	10.6	241	6	US-10-533-069-1535	Sequence 1535, Ap	947	53	10.6	1462	7	US-11-649-663A-1174	Sequence 1174, Ap
875	53	10.6	250	7	US-11-713-768-77610	Sequence 77610, A	948	53	10.6	1467	7	US-11-649-663A-1854	Sequence 1854, Ap
876	53	10.6	251	7	US-11-713-768-38620	Sequence 38620, A	949	53	10.6	1478	7	US-11-649-663A-1476	Sequence 1476, Ap
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878	53	10.6	314	7	US-11-713-768-13288	Sequence 13288, A	951	53	10.6	1484	7	US-11-649-663A-2594	Sequence 2594, Ap
879	53	10.6	322	7	US-11-713-768-54922	Sequence 54922, A	952	53	10.6	1494	7	US-11-649-663A-876	Sequence 876, App
880	53	10.6	332	7	US-11-713-768-10931	Sequence 10931, A	953	53	10.6	1495	7	US-11-649-663A-776	Sequence 776, App
881	53	10.6	349	7	US-11-713-768-16833	Sequence 16833, A	954	53	10.6	1521	7	US-11-649-663A-36	Sequence 36, Appl
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885	53	10.6	378	7	US-11-713-768-13296	Sequence 13296, A	958	53	10.6	1674	7	US-11-649-663A-1328	Sequence 1328, Ap
886	53	10.6	499	7	US-11-360-355-133188	Sequence 133188, A	959	53	10.6	1676	7	US-11-649-663A-546	Sequence 546, App
887	53	10.6	514	6	US-10-438-246-18087	Sequence 18087, A	960	53	10.6	1722	7	US-11-649-663A-350	Sequence 350, App
888	53	10.6	514	6	US-10-438-246-25226	Sequence 25226, A	961	53	10.6	1723	7	US-11-649-663A-908	Sequence 908, App
889	53	10.6	562	7	US-11-649-663A-3662	Sequence 3662, Ap	962	53	10.6	1775	7	US-11-649-663A-1538	Sequence 1538, Ap
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892	53	10.6	725	6	US-10-481-700-1	Sequence 1, Appl	965	53	10.6	1944	7	US-11-649-663A-2442	Sequence 2442, Ap
893	53	10.6	738	7	US-11-649-663A-816	Sequence 816, App	966	53	10.6	1957	7	US-11-649-663A-2230	Sequence 2230, Ap
894	53	10.6	785	6	US-10-438-246-32424	Sequence 32424, A	967	53	10.6	1968	7	US-11-649-663A-730	Sequence 730, App
895	53	10.6	906	7	US-11-649-663A-2610	Sequence 2610, Ap	968	53	10.6	2062	7	US-11-649-663A-876	Sequence 876, App
896	53	10.6	914	7	US-11-649-663A-2084	Sequence 2084, Ap	969	53	10.6	2073	7	US-11-649-663A-2678	Sequence 2678, Ap
897	53	10.6	929	7	US-11-360-355-120849	Sequence 120849, A	970	53	10.6	2195	7	US-11-649-663A-5412	Sequence 5412, Ap
898	53	10.6	945	7	US-11-649-663A-1700	Sequence 1700, Ap	971	53	10.6	2228	7	US-11-649-663A-920	Sequence 920, App
899	53	10.6	994	7	US-11-649-663A-918	Sequence 918, App	972	53	10.6	2973	7	US-11-649-663A-1566	Sequence 1566, Ap
900	53	10.6	1035	7	US-11-649-663A-1704	Sequence 1704, Ap	973	53	10.6	3060	7	US-11-649-663A-1532	Sequence 1532, Ap
901	53	10.6	1045	7	US-11-649-663A-1030	Sequence 1030, Ap	974	53	10.6	4590	6	US-10-586-772A-3	Sequence 3, Appl
902	53	10.6	1053	7	US-11-649-663A-596	Sequence 596, App	975	53	10.6	4602	6	US-10-586-772A-5	Sequence 5, Appl
903	53	10.6	1055	7	US-11-649-663A-3194	Sequence 3194, Ap	976	52.5	10.5	70	7	US-11-214-372B-483	Sequence 483, App
904	53	10.6	1078	7	US-11-649-663A-848	Sequence 848, App	977	52.5	10.5	83	6	US-10-767-701-33968	Sequence 33968, A
905	53	10.6	1086	7	US-11-649-663A-600	Sequence 600, App	978	52.5	10.5	149	7	US-11-360-355-166420	Sequence 166420, A
906	53	10.6	1104	7	US-11-649-663A-1330	Sequence 1330, Ap	979	52.5	10.5	151	7	US-11-360-355-153624	Sequence 153624, A
907	53	10.6	1132	7	US-11-649-663A-1014	Sequence 1014, Ap	980	52.5	10.5	154	6	US-10-767-701-36170	Sequence 36170, A
908	53	10.6	1145	7	US-11-649-663A-2560	Sequence 2560, Ap	981	52.5	10.5	192	7	US-11-360-355-165844	Sequence 165844, A
909	53	10.6	1148	7	US-11-649-663A-2150	Sequence 2150, Ap	982	52.5	10.5	222	7	US-11-360-355-157293	Sequence 157293, A
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983	52.5	10.5	261	6	US-10-438-246-10723	Sequence 10723, A	1056	52.5	10.5	1011	7	US-11-649-663A-1528	Sequence 1528, Ap
984	52.5	10.5	261	6	US-10-438-246-10725	Sequence 10725, A	1057	52.5	10.5	1048	6	US-10-438-246-19235	Sequence 19235, A
985	52.5	10.5	300	6	US-10-438-246-10724	Sequence 10724, A	1058	52.5	10.5	1050	7	US-11-649-663A-2216	Sequence 2216, Ap
986	52.5	10.5	311	7	US-11-360-355-150831	Sequence 150831,	1059	52.5	10.5	1079	7	US-11-649-663A-4958	Sequence 4958, Ap
987	52.5	10.5	328	7	US-11-741-492-22	Sequence 22, App1	1060	52.5	10.5	1079	7	US-11-649-663A-1016	Sequence 1016, Ap
988	52.5	10.5	348	7	US-11-713-768-75425	Sequence 75425, A	1061	52.5	10.5	1168	7	US-11-649-663A-2532	Sequence 2532, Ap
989	52.5	10.5	350	6	US-10-438-246-26130	Sequence 26130, A	1062	52.5	10.5	1169	7	US-11-649-663A-284	Sequence 284, App
990	52.5	10.5	352	7	US-11-713-768-71670	Sequence 71670, A	1063	52.5	10.5	1220	7	US-11-649-663A-1052	Sequence 1052, Ap
991	52.5	10.5	352	7	US-11-713-768-75424	Sequence 75424, A	1064	52.5	10.5	1234	7	US-11-649-663A-656	Sequence 656, App
992	52.5	10.5	356	7	US-11-713-768-71669	Sequence 71669, A	1065	52.5	10.5	1234	7	US-11-649-663A-2566	Sequence 2566, App
993	52.5	10.5	358	7	US-11-713-768-75423	Sequence 75423, A	1066	52.5	10.5	1249	7	US-11-649-663A-346	Sequence 346, App
994	52.5	10.5	362	7	US-11-713-768-71668	Sequence 71668, A	1067	52.5	10.5	1278	7	US-11-649-663A-1626	Sequence 1626, Ap
995	52.5	10.5	380	7	US-11-714-841-543	Sequence 543, App	1068	52.5	10.5	1286	7	US-10-438-246-19548	Sequence 19548, A
996	52.5	10.5	380	7	US-11-783-419-543	Sequence 543, App	1069	52.5	10.5	1286	6	US-10-438-246-19071	Sequence 19071, A
997	52.5	10.5	391	7	US-11-360-355-152928	Sequence 152928,	1070	52.5	10.5	1287	6	US-11-649-663A-1250	Sequence 1250, Ap
998	52.5	10.5	401	7	US-11-714-841-528	Sequence 528, App	1071	52.5	10.5	1300	7	US-11-649-663A-2820	Sequence 2820, Ap
999	52.5	10.5	401	7	US-11-714-841-529	Sequence 529, App	1072	52.5	10.5	1342	7	US-11-649-663A-2516	Sequence 2516, Ap
1000	52.5	10.5	401	7	US-11-714-841-542	Sequence 542, App	1073	52.5	10.5	1342	6	US-10-438-246-19034	Sequence 19034, A
1001	52.5	10.5	401	7	US-11-714-841-1238	Sequence 1238, Ap	1074	52.5	10.5	1357	7	US-11-649-663A-1946	Sequence 1946, Ap
1002	52.5	10.5	401	7	US-11-714-841-1239	Sequence 1239, Ap	1075	52.5	10.5	1358	7	US-11-649-663A-2238	Sequence 2238, Ap
1003	52.5	10.5	401	7	US-11-714-841-1240	Sequence 1240, Ap	1076	52.5	10.5	1382	6	US-10-438-246-19100	Sequence 19100, A
1004	52.5	10.5	401	7	US-11-714-841-1241	Sequence 1241, Ap	1077	52.5	10.5	1417	6	US-10-438-246-19036	Sequence 19036, A
1005	52.5	10.5	401	7	US-11-714-841-1242	Sequence 1242, Ap	1078	52.5	10.5	1420	6	US-11-649-663A-2516	Sequence 2516, Ap
1006	52.5	10.5	401	7	US-11-714-841-1243	Sequence 1243, Ap	1079	52.5	10.5	1434	6	US-10-438-246-19034	Sequence 19034, A
1007	52.5	10.5	401	7	US-11-714-841-1244	Sequence 1244, Ap	1080	52.5	10.5	1464	7	US-11-649-663A-2038	Sequence 2038, Ap
1008	52.5	10.5	401	7	US-11-714-841-1245	Sequence 1245, Ap	1081	52.5	10.5	1465	7	US-11-649-663A-1890	Sequence 1890, Ap
1009	52.5	10.5	401	7	US-11-783-419-528	Sequence 528, App	1082	52.5	10.5	1469	7	US-11-649-663A-1180	Sequence 1180, Ap
1010	52.5	10.5	401	7	US-11-783-419-529	Sequence 529, App	1083	52.5	10.5	1470	7	US-11-649-663A-1290	Sequence 1290, Ap
1011	52.5	10.5	401	7	US-11-783-419-542	Sequence 542, App	1084	52.5	10.5	1481	7	US-11-649-663A-5082	Sequence 5082, Ap
1012	52.5	10.5	401	7	US-11-783-419-1238	Sequence 1238, Ap	1085	52.5	10.5	1483	7	US-11-649-663A-696	Sequence 696, App
1013	52.5	10.5	401	7	US-11-783-419-1239	Sequence 1239, Ap	1086	52.5	10.5	1487	7	US-10-438-246-19262	Sequence 19262, A
1014	52.5	10.5	401	7	US-11-783-419-1240	Sequence 1240, Ap	1087	52.5	10.5	1494	6	US-10-438-246-19262	Sequence 19262, A
1015	52.5	10.5	401	7	US-11-783-419-1241	Sequence 1241, Ap	1088	52.5	10.5	1494	6	US-10-438-246-19262	Sequence 19262, A
1016	52.5	10.5	401	7	US-11-783-419-1242	Sequence 1242, Ap	1089	52.5	10.5	1502	7	US-11-649-663A-632	Sequence 632, App
1017	52.5	10.5	401	7	US-11-783-419-1243	Sequence 1243, Ap	1090	52.5	10.5	1502	7	US-11-649-663A-2358	Sequence 2358, Ap
1018	52.5	10.5	401	7	US-11-783-419-1244	Sequence 1244, Ap	1091	52.5	10.5	1523	7	US-10-438-246-19214	Sequence 19214, A
1019	52.5	10.5	401	7	US-11-783-419-1245	Sequence 1245, Ap	1092	52.5	10.5	1559	6	US-11-649-663A-1846	Sequence 1846, Ap
1020	52.5	10.5	405	6	US-10-438-246-19506	Sequence 19506, A	1093	52.5	10.5	1560	7	US-11-649-663A-2208	Sequence 2208, Ap
1021	52.5	10.5	466	7	US-11-649-663A-1342	Sequence 1342, Ap	1094	52.5	10.5	1566	7	US-10-438-246-19080	Sequence 19080, A
1022	52.5	10.5	493	6	US-10-594-211-265	Sequence 265, App	1095	52.5	10.5	1595	6	US-11-649-663A-3990	Sequence 3990, Ap
1023	52.5	10.5	493	6	US-10-594-211-281	Sequence 281, App	1096	52.5	10.5	1632	7	US-11-649-663A-860	Sequence 860, App
1024	52.5	10.5	518	7	US-11-649-663A-3402	Sequence 3402, App	1097	52.5	10.5	1649	7	US-11-649-663A-682	Sequence 682, App
1025	52.5	10.5	586	7	US-11-584-820-90	Sequence 90, App1	1098	52.5	10.5	1657	7	US-11-649-663A-19070	Sequence 19070, A
1026	52.5	10.5	592	7	US-11-542-670-52	Sequence 52, App1	1099	52.5	10.5	1663	6	US-10-438-246-19061	Sequence 19061, A
1027	52.5	10.5	711	7	US-11-649-663A-4400	Sequence 4400, App	1100	52.5	10.5	1670	6	US-10-438-246-25934	Sequence 25934, A
1028	52.5	10.5	778	7	US-11-714-841-1224	Sequence 1224, Ap	1101	52.5	10.5	1697	6	US-10-438-246-19086	Sequence 19086, A
1029	52.5	10.5	778	7	US-11-714-841-1227	Sequence 1227, Ap	1102	52.5	10.5	1701	6	US-10-438-246-19086	Sequence 19086, A
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1031	52.5	10.5	778	7	US-11-783-419-1227	Sequence 1227, Ap	1104	52.5	10.5	1706	7	US-11-649-663A-2342	Sequence 2342, Ap
1032	52.5	10.5	779	7	US-11-714-841-1223	Sequence 1223, Ap	1105	52.5	10.5	1706	6	US-10-438-246-19118	Sequence 19118, A
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1034	52.5	10.5	779	7	US-11-783-419-1223	Sequence 1223, Ap	1107	52.5	10.5	1708	6	US-11-649-663A-3676	Sequence 3676, Ap
1035	52.5	10.5	779	7	US-11-783-419-1228	Sequence 1228, Ap	1108	52.5	10.5	1720	6	US-10-438-246-19044	Sequence 19044, A
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1053	52.5	10.5	989	7	US-11-714-841-327	Sequence 327, App	1126	52.5	10.5	1803	6	US-10-438-246-19216	Sequence 19216, A
1054	52.5	10.5	989	7	US-11-783-419-313	Sequence 313, App	1127	52.5	10.5	1803	6	US-10-438-246-19216	Sequence 25914, A
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1130	52.5	10.5	1804	6	US-10-438-246-19116	Sequence 19146, A	1203	52	10.4	300	7	US-11-714-841-494	Sequence 494, App
1131	52.5	10.5	1804	6	US-10-438-246-19161	Sequence 19161, A	1204	52	10.4	300	7	US-11-783-419-439	Sequence 439, App
1132	52.5	10.5	1804	6	US-10-438-246-19162	Sequence 19162, A	1205	52	10.4	300	7	US-11-783-419-452	Sequence 452, App
1133	52.5	10.5	1804	6	US-10-438-246-19641	Sequence 19641, A	1206	52	10.4	300	7	US-11-783-419-491	Sequence 491, App
1134	52.5	10.5	1804	6	US-10-438-246-25900	Sequence 25900, A	1207	52	10.4	300	7	US-11-783-419-494	Sequence 494, App
1135	52.5	10.5	1805	6	US-10-438-246-19132	Sequence 19132, A	1208	52	10.4	341	6	US-10-438-246-8788	Sequence 8788, App
1136	52.5	10.5	1805	6	US-10-438-246-25905	Sequence 25905, A	1209	52	10.4	359	7	US-11-360-355-120013	Sequence 120013, App
1137	52.5	10.5	1805	6	US-10-438-246-25929	Sequence 25929, A	1210	52	10.4	361	7	US-11-726-028-9	Sequence 9, Appl
1138	52.5	10.5	1808	7	US-11-649-663A-1788	Sequence 1788, App	1211	52	10.4	395	7	US-11-360-355-120911	Sequence 120911, App
1139	52.5	10.5	1809	6	US-10-438-246-19176	Sequence 19176, A	1212	52	10.4	430	6	US-11-649-663A-198	Sequence 198, App
1140	52.5	10.5	1809	6	US-10-438-246-19183	Sequence 19183, A	1213	52	10.4	435	6	US-10-529-351A-3477	Sequence 3477, App
1141	52.5	10.5	1816	7	US-11-649-663A-590	Sequence 590, App	1214	52	10.4	441	6	US-10-438-246-30110	Sequence 30110, A
1142	52.5	10.5	1828	6	US-10-438-246-25902	Sequence 25902, A	1215	52	10.4	455	6	US-10-438-246-18589	Sequence 18589, A
1143	52.5	10.5	1832	6	US-10-438-246-25962	Sequence 25962, A	1216	52	10.4	643	6	US-10-438-246-30106	Sequence 30106, A
1144	52.5	10.5	1844	6	US-11-649-663A-930	Sequence 930, App	1217	52	10.4	746	6	US-10-594-211-218	Sequence 218, App
1145	52.5	10.5	1846	6	US-10-438-246-25954	Sequence 25954, A	1218	52	10.4	751	7	US-11-649-663A-2896	Sequence 2896, App
1146	52.5	10.5	1849	6	US-10-438-246-19171	Sequence 19171, A	1219	52	10.4	787	7	US-11-633-858-172	Sequence 172, App
1147	52.5	10.5	1857	6	US-10-438-246-25967	Sequence 25967, A	1220	52	10.4	787	7	US-11-741-432-98	Sequence 98, Appl
1148	52.5	10.5	1864	6	US-10-438-246-19035	Sequence 19035, A	1221	52	10.4	864	7	US-11-714-841-220	Sequence 220, App
1149	52.5	10.5	1867	6	US-10-438-246-19226	Sequence 19226, A	1222	52	10.4	864	7	US-11-783-419-220	Sequence 220, App
1150	52.5	10.5	1868	6	US-10-438-246-25916	Sequence 25916, A	1223	52	10.4	868	7	US-11-714-841-219	Sequence 219, App
1151	52.5	10.5	1897	7	US-11-649-663A-2894	Sequence 2894, App	1224	52	10.4	868	7	US-11-783-419-219	Sequence 219, App
1152	52.5	10.5	1917	6	US-10-438-246-25937	Sequence 25937, A	1225	52	10.4	870	7	US-11-783-419-235	Sequence 235, App
1153	52.5	10.5	1941	7	US-11-649-663A-1768	Sequence 1768, App	1226	52	10.4	870	7	US-11-783-419-235	Sequence 235, App
1154	52.5	10.5	1943	6	US-10-438-246-19224	Sequence 19224, A	1227	52	10.4	874	7	US-11-714-841-218	Sequence 218, App
1155	52.5	10.5	1990	7	US-11-649-663A-862	Sequence 862, App	1228	52	10.4	874	7	US-11-714-841-234	Sequence 234, App
1156	52.5	10.5	2133	7	US-11-649-663A-894	Sequence 894, App	1229	52	10.4	874	7	US-11-783-419-218	Sequence 218, App
1157	52.5	10.5	2187	6	US-10-438-246-19643	Sequence 19643, A	1230	52	10.4	874	7	US-11-783-419-234	Sequence 234, App
1158	52.5	10.5	2205	7	US-11-649-663A-1876	Sequence 1876, App	1231	52	10.4	876	7	US-11-714-841-236	Sequence 236, App
1159	52.5	10.5	2273	6	US-10-438-246-25956	Sequence 25956, A	1232	52	10.4	876	7	US-11-783-419-236	Sequence 236, App
1160	52.5	10.5	2333	6	US-10-438-246-19029	Sequence 19029, A	1233	52	10.4	879	7	US-11-714-841-224	Sequence 224, App
1161	52.5	10.5	2355	6	US-10-438-246-25897	Sequence 25897, A	1234	52	10.4	879	7	US-11-783-419-224	Sequence 224, App
1162	52.5	10.5	4655	7	US-11-542-670-17	Sequence 17, Appl	1235	52	10.4	880	7	US-11-714-841-217	Sequence 217, App
1163	52	10.4	122	6	US-10-438-246-9364	Sequence 9364, App	1236	52	10.4	880	7	US-11-714-841-221	Sequence 221, App
1164	52	10.4	130	6	US-10-438-246-32936	Sequence 32936, A	1237	52	10.4	880	7	US-11-714-841-222	Sequence 222, App
1165	52	10.4	138	7	US-11-713-768-6842	Sequence 6842, App	1238	52	10.4	880	7	US-11-714-841-227	Sequence 227, App
1166	52	10.4	143	7	US-11-713-768-6841	Sequence 6841, App	1239	52	10.4	880	7	US-11-714-841-233	Sequence 233, App
1167	52	10.4	146	7	US-11-403-116-1218	Sequence 1218, App	1240	52	10.4	880	7	US-11-714-841-274	Sequence 274, App
1168	52	10.4	180	6	US-10-767-701-42840	Sequence 42840, A	1241	52	10.4	880	7	US-11-714-841-279	Sequence 279, App
1169	52	10.4	183	6	US-10-767-701-42840	Sequence 42840, A	1242	52	10.4	880	7	US-11-783-419-217	Sequence 217, App
1170	52	10.4	188	7	US-11-360-355-140730	Sequence 140730, App	1243	52	10.4	880	7	US-11-783-419-221	Sequence 221, App
1171	52	10.4	193	7	US-11-713-768-110200	Sequence 110200, App	1244	52	10.4	880	7	US-11-783-419-222	Sequence 222, App
1172	52	10.4	207	7	US-11-360-355-164986	Sequence 164986, App	1245	52	10.4	880	7	US-11-783-419-227	Sequence 227, App
1173	52	10.4	224	6	US-10-767-701-31808	Sequence 31808, A	1246	52	10.4	880	7	US-11-783-419-233	Sequence 233, App
1174	52	10.4	271	7	US-11-714-841-433	Sequence 433, App	1247	52	10.4	880	7	US-11-783-419-274	Sequence 274, App
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1176	52	10.4	271	7	US-11-714-841-435	Sequence 435, App	1249	52	10.4	885	7	US-11-714-841-275	Sequence 275, App
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